Title: Perfect s Sequence:

score:

US-08-956-518A-103

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nucleic 9

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Scoring table:

IDENTITY\_NUC

Issued\_Patents\_NA: \*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 1998 Compugen Ltd.
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/cgn2_6/ptodata/1/lna/5C_COMB.seq:*
/cgn2_6/ptodata/1/lna/5D_COMB.seq:*
/cgn2_6/ptodata/1/lna/5D_COMB.seq:*
/cgn2_6/ptodata/1/lna/backfiles1.seq:*
                                                                                                                                                                 US-08-306-691B-46
US-07-642-734C-1
PCT-US93-06251-23
US-08-496-855A-1
US-08-086-439C-2
US-08-458-568A-11
US-08-690-473-1
US-08-690-473-1
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US-08-377-292-6
US-07-989-847-7
US-08-38-373-948-1
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PCT-USS-04467-6
US-07-945-283-1
US-08-166-316-1
US-08-343-428-1
US-07-626-6188-1
US-08-333-977-1
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US-08-444-083-6
US-08-444-745-6
US-08-443-745-6
US-08-443-129-6
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FILING DATE: March 8, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: cDNA FEATURE:
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PRIOR APPLICATION DATA:
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ADDRESSEE: Brown, Martin,
STREET: 1660 Union Street
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APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael
TITLE OF INVENTION: HUMAN NE
TITLE OF INVENTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                                                           526 CTGCGATATTGCTGATGAGCGCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTC 585
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STRANDEDNESS: both
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US-08-073-384C-3
US-08-254-359A-3
US-08-284-490-30
US-08-483-043-3
US-08-483-043-3
US-08-459-383-30
US-08-458-819-9
US-08-481-238-3
                                                                                                                                                                                                                                                                                                                 Score 108; DB 4;
Pred. No. 7.6e-22;
0; Mismatches 5;
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No. 5824790
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MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER:
                                                                                                118 CCGCCTGGTGGCCGCGCCATGACAGCGGCTCGGACTGGCTCCTTTTCCGCCGCCCCTCC 177
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                 Patent No. 5837489
GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,7
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VENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
VENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
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Ellis, Steven B.
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                                               103 CGGAGCGTACCCAGCGCGGGAGTACCTCCCGCTCACACCTCGGGCTGCAGTTCCCTGGG 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Infections NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Schafter APPLICANT: Yeh, Lil FITLE OF INVENTION:
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CTGCACG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               441 CTGCACG 447
                                                                                                  43 GECCTGGCCAGAGGCGCAGAGGCCCGAGAGCCTCGGTGGAGACTGGGGGGTGGAGGTGCC 102
                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/065,146 FILING DATE: 05-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                   ENGTH:
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                                                                         19103
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                                                                                                                                                                                                                                                                                                                    nucleic acid
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                                                                                                                                                                                                              Herpes simplex virus
Herpes Simplex Virus Type 1
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                                                                                                                                 Conservative
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02-JUNE-1995
                                                                                                                                                                                                                                                                              DNA (genomic)
                                                                                                                                                                                                                                                                                                          double
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                                                                                                                                          Score 56.4; DB 3
Pred. No. 0.0027;
                                                                                                                               Mismatches
                                                                                                                                                        DB 3; Length 12001;
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US-08-458-568A-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11,
                                                                                                                                                                        TELEFAX: (215) 568-34 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                     MOLECULE TYPE: D
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Herp
                                                                                                                                                                                                                                                   CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2020 GAGGGGCGGAGGGGCGAGGGGCGG 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283 CTTAAAGGCGCGAGCCGAGCGGCGAGGTGCCTCTGTGGCCGCAGGCGCAGGCCCGGGC 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343 GACAGCCGAGACGTGGAGCGCGCCGG 368
                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 02-JU
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: One Liberty
CITY: Philadelphia
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                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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         Herpes simplex virus
Herpes Simplex Virus Type 1
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(215) 568-3439
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                                                                                    DNA (genomic)
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                                                                                                                 double
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Place, 46th floor
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Query Match 11.6%; Best Local Similarity 48.7%; Matches 172; Conservative

88 GGGGTGGAGGTGCCCGGAGCGTACCCAGCGCCGGGAGTACCTCCCGCTCACACCTCGGG 147

Score 53; DB 3; Length 12001; Pred. No: 0.011; 0; Mismatches 180; Indels

1;

Gaps

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Title: Perfect score: Sequence:

US-08-956-518A-99 100 1 CTGTTTCTAGTGCTG

CTGTTTCTAGTGCTGATGAG.....

.CTGCCTCCAGGTAAGCTGCA 100

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nucleic search, using sw model

GenCore version 4.5 Compugen Ltd.

September 17, 1999, 22:05:13;

13 ; Search time 234.98 Seconds
(without alignments)
39.015 Million cell updates/sec

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Scoring table:

IDENTITY\_NUC

176461 seqs, 45838279

residues

abase :

Issued\_Patents\_NA:\*

1: /cgn2\_6/ptcdata/
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/cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

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1 Appli
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LOCATION:
US-08-466-589-7
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US-08-466-589-7
                                                    Query Match
Best Local S
Matches 84
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                                                                                                                                                                                                                                                                                                      COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,589
FILING DATE: June 5, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: MARCH 8, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 362-9950
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
SEQUENCE 1876 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Elliot, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURO)
TITLE OF INVENTION: RECEPTOR CONUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      444444
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ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                   MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
421 AGTGCTGATGAGCGCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTCTTCTGGG 480
                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Brown, Martin, STREET: 1660 Union Street
                          9
                AGTGCTGATGAGCGCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTCTTCTGGG
                                                   ch 83.4%;
l Similarity 98.8%;
84; Conservative
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US-08-899-575-170
US-08-899-575-170
US-08-899-575-170
US-08-580-038-26
US-08-710-249-3
US-08-750-524-2
PCT-US95-08743-170
                                                   Score 83.4; DB 4;
Pred. No. 2.6e-22;
0; Mismatches 1;
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                                                                               Length 1876;
                                                      Indels
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170, App
156, App
170, App
26, Appl
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170, App
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Result No.

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US-08-299-849B-20 US-08-770-379-17 US-08-484-101B-37

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CATTGCCAGTACCTGCCTCCAGGTA

19, Appl 23, Appl 11, Appl 2, Appl 2, Appl 5, Appl

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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US-08-222-617A-3/c; Sequence 3, Application US/08222617A; Patent No. 5882879; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                     us-07-607-538C-1
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                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patentin Release #1.0, Ver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: CRITELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 943-1931
TELEPAX: (510) 943-1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/607,538C
                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
APPLICANT:
                                                                                                                                                                                                         631 CTGCGCCTGGAGCTGCTGGGCCTGTTAGTGGCCACCTGCCACCCCAGGTCTTCCTGCTTT 690
                                                                                                                                      691 C 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481 CATTGCCAGTACCTGCCTCCAGGCA 505
                                                                                                                                                                                                                                                                     Local Similarity 62.3%; tes 38; Conservations
                                                                                                                                                                      61 C 61
                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                         1 CTGTTTCTAGTGCTGATGAGCGCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     r: 2055 No. 5455031th Broadway Walnut Creek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94596
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                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   1384 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIFFERENTIATION ANTIGEN BINDING SPECIFITY AND CLOTTING FACTORS V AND VIII LIGHT-CHAIN HOMOLOGIES, FUSION PROTEIN, POLYNOCLEOTIDE AND POLYRIBO-
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                                                                                                                                                                                                                                                                          Score 24.2; DB Pred. No. 2.8; 0; Mismatches
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Best Local Similarity
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SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/222,617A
FILING DATE: 04-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 97,157
INFORMATION FOR SEQ. ID NO: 3:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                tent No.
                                             APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                         8012 TTTCTAGTGGTGATGAGCGTCCTGGCACTAGATTCCTC 7975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: lin
MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 11601 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 8050..8052

OTHER INFORMATION: /note= "NNN=GCC, AGU, AGC, UCU, UCC, UCA, or UCG;
OTHER INFORMATION: Xaa=Ala or Ser "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 388..11526
OTHER INFORMATION: /function= "Enzyme"
OTHER INFORMATION: /product= "ACV Synthetase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: UZIF: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
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                                                                                                   INFORMATION:
                                                                                                                  Application US/08222617A 5882879
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300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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Montenegro, Eduardo P.
Montenegro, Eduardo P.
VENTION: A Method for Influencing Beta-Lactam
VENTION: Antibiotic Production and for Isolation of Large
VENTION: Quantities of ACV Synthetase
         Gutierrez, Santiago
Barredo, Jose L.
                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Martin, Juan F. Garcia, Bruno D.
                                             Martin, Juan F. Garcia, Bruno D.
                                                                               Veenstra,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gutierrez,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barredo, Jose L.
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                                                                               Annemarie E.
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Pred. No. 9.
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Scoring table:
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      ACCCACAGGCATATTCAAGAGTTCCTGCTACA1 G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn2_6/ptodata/1/ina/FD_COMB.seq:*
/cgn2_6/ptodata/1/ina/Bockfiles1.seq:*
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US-07-721-761A-28
US-07-978-687-28
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PCT-US91-05801-27
PCT-US91-05801-28
US-07-959-943-8
US-07-959-943-8
US-07-959-943-1
US-08-562-985A-1
US-08-562-985A-7
PCT-US91-02311-8
PCT-US91-02311-8
PCT-US91-02311-8
PCT-US91-02311-1
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US-07-648-796A-11
US-07-648-796A-11
US-07-648-796A-11
US-07-648-796A-12
US-07-648-796A-14
US-07-648-796A-17
US-07-648-796A-17
US-07-648-796A-17
US-07-648-796A-17
US-07-648-796A-17
US-07-946-232-4
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(without alignments)
14.435 Million cell updates/sec
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US-08-466-589-7
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US-08-466-589-7
                                                                                                   Matches
                                                                                                               Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM COMPATIBLE

COMPUTER: IBM COMPATIBLE

OPERATING SYSTEM: DOS

SOFTWARRE: FESTSEO VERSION 1.5

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,589

FILING DATE: June 5, 1995

CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031

FILING DATE: MAICH 8, 1993

ATTORNEY/ACENT INFORMATION:

MANCE: GALFER ST. DESCRIPTION:
                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1876 base pairs
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ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                  TOPOLOGY: bot MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 63
TELECOMMUNICATION INFORMATION: 619-238-0999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin,
STREET: 1660 Union Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ellis, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
                                 500
                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,77
                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 619-238-0062
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                                                  CAGGCATATTCAAGAGTTCCTGCTACATCG 37
                               CAGGCATATTCAAGAGTTCCTGCTACATCG 529
                                                                                                Similarity
30; Conserv
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llarity 100.0%;
Conservative
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US-08-637-640-1
US-08-630-963-4
PCT-US91-02311-7
US-08-657-192-13
US-08-657-192-13
US-08-461-5928-5
PCT-US95-07349-1
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Pred. No. 0.0
0; Mismatches
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                                                                                                                                         ent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: 519-238-0999
                                                                                                                                                                                                                                  637 ACTCCCCCGGCCATTTACAAGAGCTCCTGCAGCATCG 673
                                                                                                                                                                                                                                                                                                                                                                                                                                      OLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 0 FILING DATE: March 8, 19 NTTORNEY/AGENT INFORMATION:
                                                                                                          PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/466,589 FILING DATE: June 5, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                      1 ACCCACACAGGCATATTCAAGAGTTCCTGCTACATCG 37
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92101-2926
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                                                                                                                                                    Application US/08496855A
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                                                                                                                                                                                                                                                                                              Conservative
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184. 2067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Elliot, Kathryn J.
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rown, Martin, Haller & McClain
                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Stephanie L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Steven
                                                                                                         Kathryn J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMAN NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
                                                                                                                                                                                                                                                                                                           56.8%;
73.0%;
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                                             METHODS EMPLOYING SAME
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Best Local :
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INFORMATION FOR SEQ ID NO:
                                                                  ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                          tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/149,503 FILING DATE: 08-NOV-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                CORRESPONDENCE ADDRESS
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LOCATION:
                                     COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                 CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 08-MAR-1993
TORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 0 FILING DATE: 08-MAR-1993
APPLICATION NUMBER:
                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
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25; Conserv
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              RE: FastSEQ Version 1.5
APPLICATION DATA:
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                                                                                                                                                                                                                              HUMAN NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR COMPOSITIONS AND METHODS EMPL
US/08/466,589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US 08/028,031
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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen

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Sequence Sequence Sequence Sequence Sequence Sequence Sequence

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September 17, 1999, 22:05:18;

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Scoring table:

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Score

Match

Length

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US-08-466-589-7
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                                                                                                  Matches
                                                                                                                    Best
                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 636:
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEFAX: 619-238-0062
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/466,589
FILING DATE: June 5, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: March 8, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Seldman, Stephanie L
REGISTRATION NUMBER: 33,779
                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ellis, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
APPLICANTINIC HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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OPERATING SYSTEM: DOS
SOFTWARE: FASTEG Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClaim
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                                               321 GGCCGCAGGCCCAGGCCCGGGCGACAGCCGAGACGTGGAGCGCGCCGGCCTCGCTGCAGCT 380
381
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TOPOLOGY: both
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                                                                                                72;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/5D_COMB.seq:*
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US-07-885-972A-3
US-08-833-761-1
US-08-383-761-1
US-08-306-691B-42
US-08-306-691B-42
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US-08-400-422-2
US-08-409-8611-12
US-08-49-169A-1
US-08-487-811A-12
US-08-487-811A-12
US-08-487-811A-12
US-08-487-811A-12
US-08-487-811A-21
US-08-487-811A-12
US-08-487-811A-12
US-08-488-4
US-08-488-4
US-08-488-68-4
US-08-488-68-4
US-08-488-68-1
US-08-388-68-1
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US-08-458-568A-11/c
                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 164; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                            2259
                               ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA
APPLICATION UMBER: US 0)
FILING DATE: 05-MAY-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
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                                                                                                                     103
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                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn R.
REGISTRATION NUMBER: 36,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Composition Infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Schaffer, Priscilla A. APPLICANT: Yeh, Lily
163
                                                                                                                                                                          43 GGCCTGGCCAGAGGCGCGAGGCCCGAGAGCCCGCTCGGTGGAGACTGGGGGGGTGGAGGTGCC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Herpes simplex virus Type
                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/458,568A FILING DATE: 02-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
                                                                                    CGGAGCGTACCCAGCGCCGGGAGTACCTCCCGCTCACACCTCGGGCTGCAGTTCCCTGGG 162
                                                          INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1, Application US/08458568A 5821339
                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
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                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                      14.48;
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                                                                                                                                                                                                      Score 56.4; DB 3; Length 1
Pred. No. 0.002:
0; Mismatches 151; Indels
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Similarity

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Conservative 217; Mismatches 153;

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US-08-232-463-14
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Query Match
Best Local S
Matches 14
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                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0 CURRENT APPLICATION DATA:
                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pair
                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                      IMMEDIATE SOURCE:
CLONE: pTZgpt-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 22313-0299
                                                                                                               TOPOLOGY:
                                                                                                                            STRANDEDNESS:
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                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Alexandria
                                                                                                                                                                                                                           TELEPHONE:
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5670367
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                                                                                 pTZgpt-F1s
                                                                                                                                                    7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Foley & Lardner
1800 Diagonal Road, Suite 500
                                                                                                                                                                                                              (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCHEIFLINGER, FALKNER, F. G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DORNER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FALKNER,
                                                                                                                                          leic acid
                                                                                                                Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
                                                                                                                                                                                                                                                                                                                 26-AUG-1991
                                                                                                                            single
             13.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                             EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                                         US/07/935,313
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                                                                                                                                                                                                                                                                     29,768
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             Score 52.4; DB
Pred. No. 0.014;
                         DB 2;
                          Length 7218;
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Perfect s Sequence:

score:

US-08-956-518A-102 689 1 AGCCCTTTCCCAGGCGG

AGCCCTTTCCCAGGCGGTAG.....

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nucleic search, using sw model

GenCore version 4.5 Compugen Ltd

September 17, 1999, 22:05:28;

Scoring table:

IDENTITY\_NUC

base:

Issued\_Patents\_NA: \* 176461 seqs, 45838279

residues

/cgn2\_6/ptodata/1/ina/5a\_COMB.seq:\*
/cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*
/cgn2\_6/ptodata/1/ina/5E\_COMB.seq:\*
/cgn2\_6/ptodata/1/ina/5D\_COMB.seq:\*
/cgn2\_6/ptodata/1/ina/5D\_COMB.seq:\*
/cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

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; LOCATION:
US-08-466-589-7
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                                                                             Query Match
Best Local S
Matches 111
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                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRASISEQ VERSION 1.5
SOFTWARE: FRASISEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,589
FILING DATE: June 5, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/028,031
APPLICATION NUMBER: US 08/028,031
FILING DATE: MARCH 8, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Scidman, Stephanie L
REGISTRATION NUMBER: 33,779
REGISTRATION NUMBER: 33,779
REGISTRATION NUMBER: 6362-9950
TELEPHONE: 619-238-0099
TELEPHONE: 619-238-0099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Ellist, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: RECEPTOR COMPOS
                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1876 base pair:
                                                                                                                                                                                      MOLECULE TYPE: FEATURE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
                     414 CTATAACAGTGCTGATGAGCGCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTC
                                                                             Local Similarity
nes 111; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1660 Uni
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                                    CTGCGATATTGCTGATGAGCGCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTC 633
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1660 Union Street
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                                                                             Conservative
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                                                                                                                                                                                                                                                       pairs
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US-08-353-948-1
US-08-277-034-2
US-08-216-260-1
US-07-977-434-9
US-08-073-384C-3
US-08-428-732-3
US-08-254-359A-3
                                                                           Score 108; DB 4; I
Pred. No. 2.5e-21;
D; Mismatches 5;
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SUMMARIES

US-08-466-589-11 US-08-604-989A-11 US-08-323-443B-1 US-08-458-568A-11 US-08-466-589-5

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US-08-444-083-6
US-08-442-745-6
US-08-443-129-6
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US-08-443-130-6
US-08-443-130-6
US-08-443-130-6
US-08-443-130-1
US-07-945-2316-1
US-07-945-233-3
US-08-343-428-1
US-08-333-971-51
US-08-333-971-6
US-08-333-971-1
US-08-383-971-2
US-08-434-877-2
US-08-434-877-2
US-08-377-298-847-7

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Best Local :
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**FORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 2990 har-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                            TOPOLOGY: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2
FILING DATE: 21-JUN-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 22:
RELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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IITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                         230 CCGCCTGGTGGCCGCGCCATGACAGCGGCTCGGGACTGGCTCCTTTTCCGCGCCCCCCC 289
                                                                                                                         170 GCTCCCACGAGGGTCACGGCGGGGGAGAG:TGGAGCCGCGAGAGCTCGGCCGGGGGCC 229
                                290 CGCCG 294
                                                                  753
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Local Similarity 57.6%;
nes 72; Conservativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 29 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/346,602 FILING DATE: 29-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/572,951 FILING DATE: 15-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ.
GGCCG 817
                                                             Washington
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                                                                                                                                                                                                                                                                                                                                              nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KNIGHT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GUAN, HANPING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEELING, PETER L.
KNIGHT, MARY E.
                                                                                                                                                                                                                                                                                                linear
E: cDNA
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                                                                                                                                                                                                                                                                                                                               both
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SYNTHESIS IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08/263,921
                                                                                                                                                                                           Score 40.2; DB 3;
Pred. No. 0.025;
0; Mismatches 53;
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US-08-681-129-1
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Best Local Similarity 50.9
Matches 92; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/24/
FILING DATE: 02-7UN-1994
CLASSIFICATION: 424
APPLICATION NUMBER: EP 92.
FILING DATE: 06-0CT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: D
ORIGINAL SOURCE:
ORGANISM: Pseu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (301) 258-5
                                                                                                                                   1079 GCGGCCACGGCGCCTCTCGGGCCGCGAGCGCCGTGGCCCACGCCGTCAACCGCGTGCTGC 1138
                                                                                                                                                                                                        1199 CC 1200
                                                                  1139 GCGAGGCGACCGTCTTCGGCGAGGTGATGCGGATGCTCGTGAACGCCGCGTGGTGCACG 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/681,129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                    233 CC 234
                                                                                                 173 CCCACGAGGGTCACGGCGGCGGGAGAGGTGGAGCCGCGAGAGCTCGGCCGGGGGCCCCG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                      113 CAGGCCGCCACATAGCTCCCGCCAAGTCCTCGGTGCCCCTTGCCATTTTCCAGCCGCGCT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Pseudorabies virus vaccine NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                       53 GCGGCTTGACGGGAGCCGCGCCTCCTGTCGGTGGAGTCGGTTATAAAGGGAGCAGCCCCG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPLICANT: Metten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Gormley, Mary E. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: UZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                  Kaplan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1578 base pairs
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1330 Piccard Drive
                                                                                                                                                                                                                                                                                                                                                                                                  Pseudorabies virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA (genomic)
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06-OCT-1992
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Pred. No. 0.08;
0; Mismatches
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RESULT 4 US-07-980-528-1/c

Title: Perfect score: Sequence:

US-08-956-518A-84 55

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2 HUMMOMOSEOS
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em\_est9:\* em\_est7: em\_est5:

em\_est12:\* em\_est10:\*

em\_est18: em\_est17: em\_est15:\* em\_est13:\*

em\_est16:

gb\_est5:\* gb\_est3:\* gb\_est2:\* gb\_est1:\* em\_est19:

gb\_est4:\*

gb\_est28: gb\_est29: gb\_est30: gb\_est31: gb\_est32:

gb\_est26:

gb\_est2 jp\_est23:

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gb\_est16: gb\_est15: gb\_est14: Run

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No.
RESULT
HS469201
ID HS46
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AC H504
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SV H504
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
     H50469.1
                H50469;
                           HS469201
                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                                                                                 Query
Match
                           standard; RNA; EST; 437 BP
                                                                                                                                                                                                                                                                                                                                                                                 em_est22:*
em_est23:*
em_est24:*
em_est25:*
                                                                                                                                                                                                                                                                                                                                 Length DB
                                                                       IJ
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                                                                       D15892
D15918
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                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu High quality sequence stops: 313 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. NCBI gi: 990310
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 437 BP;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Primates; Catarrhini; Hominidae; Homo.
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                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 480) Okubo,K., Hori,N., Matoba,R., Nilyama,T., Fukushima,
                                                                                      and Matsubara, K.
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/organism="Homo sapie
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Fukushima, Yuko Kojima &
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1-3 Yamada-oka, Suita, Osa
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Okubo,K., Hori,N., Matoba,R., Niiyama,T., Fukushima, and Matsubara,K.
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1-3 Yamada-oka, Suita, Osaka 565, Japan
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/lab_host="E.coli"
/note="3 -directed regional cDNA library. Cleaved by and transformed into E.coli."
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/db_xref="taxon:9606"
/clone="a20"
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/db_xref="GDB:D0S7502E"
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                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 376)
Okubo,K., Hori,N., Matoba,R., Niiyama,T., Fukushima
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Niiyama, Atsushi Fukushima, Yuko Kojima & Kenichi Matsubara
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Contact: Kousaku Okubo, Naohiro Hori, Ryo Matoba, Toshiyuki
Niiyama, Atsushi Fukushima, Yuko Kojima & Kenichi Matsubara
                                                                                                                           and Matsubara, K.
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1-3 Yamada-oka,S
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/clone="c12d08"
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/lab_host="E.coli"
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/db_xref="GDB:D058062E"
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Nature Genet. 2, 173-179 (1992)
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1 (bases 1 to 411)

1 (bases 1, Hori,N., Matoba,R., Nilyama,T., Fukushima,A., Kojimo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Matsubara, K.
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Location/Qualifiers
                                                                                                                                                     116
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ilarity 100.0%;
Conservative (
                                                         12.7%;
llarity 100.0%;
Conservative
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                                                                                                                                                /clone_llb="Liver HepG2 cell line."
/lab_host="E.coli"
/note="3'-directed regional cDNA library. Cleaved by MboI and transformed into E.coli."
119 c 109 g 65 t 2 others
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107 c 105 g 57 t
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/db_xref="GDB:DOS7516E"
/db_xref="taxon:9606"
/clone="c202"
                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="GDB:D0S8337E"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                /clone="hm01g02"
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/lab_host="E.coli"
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                                                         Score 7; DB 2; Pred. No. 5.4
0; Mismatches
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Pred. No.
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                                                                        DB 20; Le
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o. 5.3e+04
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                                                                                      Length 411;
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Best Local
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D11889.1
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D11893.1
                                          Large scale cDNA sequencing for analysis of quantitative qualitative aspects of gene expression Nature Genet. 2, 173-179 (1992)
                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 244)
Okubo, K., Hori, N., Matoba, R., Nijama, T., Fukushima, A., Kojim
                                                                                                                                                                                                                                                                      D11893 244 bp
HUMHM05F08 Liver HepG2
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1-3 Yamada-oka,Suita,Osaka 565,Japan.
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Niiyama, Atsushi Fukushima, Yuko Kojima & Kenichi
Institute for Molecular and Cellular Biology
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 Contact: Kousaku Okubo,
                                                                                      and Matsubara, K.
                                                                                                                                                                Homo sapiens
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/db_xref="GDB:DOS8435E"
/db_xref="taxon:9606"
/clone="hm05e09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="3'-directed regional cDNA library.
and transformed into E.coli."
125 c 96 g 84 t 5 others
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/lab_host="E.coli"
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Naohiro Hori, Ryo Matoba, Toshiyuki
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MEDLINE
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49 CTGCACG
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1-3 Yamada-oka, Suita, Osaka 565, Japan
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                         Contact: Kousaku Okubo, Naohiro Hori, Ryo Matoba,
Niiyama, Atsushi Fukushima, Yuko Kojima & Kenichi
Institute for Molecular and Cellular Biology
                                                                                                                                                                                                                                                                                                                                                                                                Large scale cDNA sequencing for analysis qualitative aspects of gene expression Nature Genet. 2, 173-179 (1992)
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                                           Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                            and Matsubara, K.
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Institute for Molecular and
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                                            Conservative
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1 72 c 49 g 51 t
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/lab_host="E.coli"
/lab_host="6".coli"
/note="3'-directed regional cDNA library. Cleaved and transformed into E.coli."
105 c 109 g 101 t 9 others
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/clone="hm05f08"
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/db_xref="GDB:D0S8439E"
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/lab_host="E.coli"
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/clone="s155"
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ob_xref="GDB:D057600E"
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Cellular Biology
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b. 5e+04;
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Matsubara
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                                                                                                      g2148499
D12355.1
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Murakawa,K., Matsubara,K., Fukushima,A., Yoshii,J. and Okubo,K.

Chromosomal assignments of 3'-directed partial cDNA sequences representing novel genes expressed in granulocytoid cells Genomics 23, 379-389 (1994)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 356)
                                                                                                                                                                    HUM000TB04 Liver HepG2
                                                                                                                                                   mRNA sequence.
                                                                                                                                                                                      D12355
                                                                                                                                                                                                                                                                                                                                 h 12.7%;
Similarity 100.0%;
7; Conservative
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1-3 Yamada-oka,s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Kousaku Okubo, Naohiro Hori, Ryo Matoba, Niiyama, Atsushi Fukushima, Yuko Kojima & Kenichi Institute for Molecular and Cellular Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Large scale cDNA sequencing for analysis of quantitative qualitative aspects of gene expression Nature Genet. 2, 173-179 (1992)
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1 (bases 1 to 397)
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HUM000S173 Liver HepG2 cell line.
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                                                                                                       GI:2148499
                                                                                                                                                                                                                                                                                                                                                                                                                          /note="3'-directed regional cDNA library.
and transformed into E.coli."
80 c 109 g 93 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="GDB:D0S7613E"
/db_xref="taxon:9606"
/map="17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Liver HepG2 cell line."
/lab_host="E.coli"
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Pred. No. 5.4
0; Mismatches
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                                                                                                                                                                  cell line. Homo
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                                                                                                                                                               sapiens cDNA clone tb04,
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Matsubara
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D15140/c
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Best Local S
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
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D15140.1
                                                                                                                                                                                            Tel: 0298-38-7441
Fax: 0298-38-7468
                                                                                                                                                                                                                                                                     Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                   Sasaki, T. and Minobe, Y Rice cDNA from callus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RICC0143A Rice callus
                                                                                                                                             Seq
                                                                                                                                                                          Email: tsasaki@abr.affrc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa
                                                                                                                                                             PROJECT ='RGP'
                                                                                                                                                                                                                           Japan 305
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Nilyama, Atsushi Fukushima, Yuko Kojima & Kenichi Matsubara
Institute for Molecular and Cellular Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Large scale cDNA sequencing for analysis qualitative aspects of gene expression Nature Genet. 2, 173-179 (1992)
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Similarity 100.0%;
7; Conservative
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Location/Qualifiers
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                                                                                                                                             primer: oligo(dT)
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/note="3'-directed regional cDNA library.
and transformed into E.coli."
9 c 100 g 56 t 3 others
/clone_lib="Rice callus"
/note="Vector: pBluescript II
NotI; cDNA prepared from rice
                                                            /organism="oryza sativa"
/strain="cultivar Nipponbare,
/db_xref="taxon:4530"
                                                                                                                            Location/Qualifiers
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/db_xref="GDB;D0S7837E"
/db_xref="taxon;9606"
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s; Pred. No. 5.3
0; Mismatches
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Oryza sativa cDNA clone R,
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No. 5.3e+04;
0;
 SK+; Site_1:
callus mRNAs
                                                                           sub_species Japonica"
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by us'
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D15143/c
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D15154
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                                                                                                        CIGCACG
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D15143
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Sasaki,T. and Minobe,Y.
Rice cDNA from callus
Unpublished (1994)
                                                                                                                                                                    l Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
2-1-2 Kannondai, Tsukuba
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Oryza sativa
D15154 273 bp mRNA EST RICCO177A Rice callus Oryza sativa cDNA clone D15154
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euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: tsasaki@abr.affrc.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 0298-38-7441
Fax: 0298-38-7468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Poaceae; Oryza.
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Similarity 100.0%;
7; Conservative
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                                                                                                                                                                      Conservative
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83 c 85 g 91 t 10 others
                                                                                                                                                                                                                                                          /Glone_lib="Rice callus"
/rote="Vector: pBluescript II SK+; Site_1: SalI; Site_2:
NotI; cDNA prepared from rice callus mRNAs by using
oligo(dT) as a primer and ligating to the SalI-NotI site
of pBluescript II SK+ phagemid.
a 85 c 96 g 80 t 2 others
                                                                                                                                                                                                                                                                                                                                                                       /organism="Oryza sativa"
/strain="cultivar Nipponbare,
/db_xref="taxon:4530"
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                              273 bp
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                                                                                                                                                                                                   Length 332;
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D15173.1
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Oryza sativa
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euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Poaceae; Oryza.
1 (bases 1 to 356)
5 Sasakl.T. and Minobe, Y.
Rice cDNA from callus
Unpublished (1994)
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Sasaki, T. and Minobe, Y.
Rice cDNA from callus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                           Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
2-1-2 Kannondai, Tsukuba
                                                                                                                                                                                                                                 Oryza sativa.
Oryza sativa
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Fax: 0298-38-7468
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National Institute of Agrobiological Resources
Rice Genome Research Program
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   Japan 305
Tel: 0298-38-7441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROJECT - 'RGP'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /Glone_lib="Rice callus"
/Glone_lib="Rice callus"
/note="Vector: pBluescript II SK+; Site_1: SalI; Site_2:
NotI; cDNA prepared from rice callus mRNAs by using
NotI; cDNA prepared from rice callus mRNAs by using
Oligo(dT) as a primer and ligating to the SalI-NotI site
of pBluescript II SK+ phagemid. "
of pBluescript II SK+ phagemid. "
11 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Oryza sativa"
/strain="cultivar Nipponbare,
/db_xref="taxon:4530"
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100.0%; Pred. No. 5.1e+04;
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Gaps

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Page 7
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Searched:

Af120344 Homo sapi D12193 HUM000S317 D20010 HUMGS00981

Description

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1 TGTGTGTCAG 10
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em_est3:*
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F02697 HSC178112 n
F03251 HSC117812 n
N78805 EST00987 H1
M78805 EST000987 H1
M79816 WEST00034 H
M79816 WEST00254 F
M86024 EST00254 F
M86024 EST00254 F
M86024 EST00254 F
M86024 EST00256 E
T02241 WEST00296 E
T00237 EST06218 In
T08749 EST06241 In
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T09101 EST06294 In
T115405 IB1093 Infa
T15405 IB1093 Infa
T15405 IB1514 Nor
T12041 S1832 Norm
T20612 EST82488 Hu
T2061 EST8524 H0
T32366 EST47555 Hu
T32366 EST47556 Hu
T33364 EST85866 Hu
T33412 EST818801 Hu
T33412 EST818801 Hu
T33532 EST818801 Hu
T35332 EST818801 Hu

A1044699 Homo sapi

Toshiyuki Matsubara

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Eukaryota; Metazoa; Chordata; Craniata;
Primates; Catarrhini; Hominidae; Homo.
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l similarity 100.0%;
l0; Conservative (
Nature Genet.
94258199
           Large scale cDNA sequencing for analysis qualitative aspects of gene expression Nature Genet. 2, 173-179 (1992)
                                                                  1 (bases 1 to 389)
Okubo, K., Hori, N., Matoba, R., Niiyama, T.,
                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                      and Matsubara, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                  Fukushima, A.,
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6 TGTGTGTCAG 295
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Gene expression of human promyelocytic cell line HL60 before and after induction of differentiation. A new application of 3'directed cDNA sequencing Unpublished (1993)
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Niiyama, Atsushi Fukushima, Yuko Kojima & Kenichi
Institute for Molecular and Cellular Biology
                                                                                                                                                                            Contact: Okubo,K., Fukushima,A., Yoshii,J., Yoshinari,H., Arimoto,J. and Matsubara,K. Institute for Molecular and Cellular Biology
                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1-3 Yamada-oka,Suita,Osaka 565,Japan.
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Location/Qualifiers
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                       promyelocyte.
                                         /note="Female, adult,
                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="pm2779"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Liver HepG2 cell line."
/lab_host="E.coli"
/note="3' directed regional cDNA library.
and transformed into E.coli."
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/db_xref="GDB:D0S7694E"
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Niiyama, T.,

Kojima,Y.,

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Best Local
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                                                                                                              g643978
D31098.1
EST.
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                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 199)
Sudo,K., Chinen,K. and Nakamura,Y.
                                                                                                human.
                                                                                                                                                               D31098 199 bp mRt
HUML12503 Human fetal lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Okubo, K., Fukushima, A., Yoshii, J., Niiyama, T., Yoshinari, H., Arimoto, J. and Matsubara, K.
Institute for Molecular and Cellular Biology
Osaka University
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10; Conserv
                                                                                    Homo sapiens
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 88)
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D20990.1 GI:504810
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                expressed sequence tags (ESTs) from a human fetal lung cDNA
                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="mpy519"
/clone=lib="Human promyelocyte"
/note="Female, adult, cell_line =
promyelocyte."
                                                                                                                                                                                                                                                                                                                                                                                                 promyelocyte.
                                                                                                                           GI:643978
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Pred. No. 5.
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Homo sapiens cDNA 5',
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cDNA clone mp2519
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                                                      BASE COUNT
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AUTHORS
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SOURCE
ORGANISM
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MEDLINE
COMMENT
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Matches 10
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100.0%;

Score 10; Pred. No.

; DB 20; . 5.5e+03;

Length 374;

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TGTGTGTCAG 171
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CELKO13G6R Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA
clone ykl3g6 3′, mRNA sequence.
D32407
                                                                                                                                                                                                                                            National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411,
Tel: 0559-75-0771
Fax: 0559-75-6240
                                                                                                                                                                                                                                                                                                                                                                             Toward an expression map 
Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                        Contact: Yuji Kohara
Gene Library Lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi (bases 1 to 374)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Kohara, Y., Mitsuki, H., Nishigaki, A., Motohashi, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: yusuke@ims.u-tokyo.ac.jp
Insert Length: 552 Std Error:
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 81-3-5449-5372 Fax: 81-3-5449-5433
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Institute of Medical Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                 ykohara@ddbj.nig.ac.j.
Location/Qualifiers
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/clone_lib="Yuj1 Kohara unpublished cDNA"
/note="dev_stage="varied", sex=Hermaphrodite
tissue_type=whole animal;
70 c 67 g 118 t
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/db_xref="taxon:9606"
/map-"17g21"
/clone_11b-"Human fetal lung"
/clone_10 36 g 59 t
                                                                                    /clone="yk13g6"
                                                                                                  /map="978E04;
                                                                                                      /organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="faxon:6239"
/map="978E04; 1"
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Pred. No. 5.4e+03;
; Mismatches 0;
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                                         male,
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KEYWORDS
SOURCE
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1 (bases 1 to 344)
Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
Pevignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot
                                                                                                                                                                                                                                                                                                                        F02697 344 bp mRNI
HSC17B112 normalized infant
c-17b11 3', mRNA sequence.
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Caenorhabditia; Rhabditida; Rhabditida; Rhabditida; Rhabditida; Rhabditida; Rhabditida; Rhabditida; Rhabditida; Rhabditidae; 
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                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Frimates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                             g646254
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Yata 1111, Mishima, Shizuoka 411,
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D33452
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                                                                                                                                      Eukaryota;
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ilarity 100.0%;
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Location/Qualifiers
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/note="dev_stage=varied, sex=Hermaphrodite male,
tissue_type=whole animal;
40 c 100 g 104 t
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/strain-"CB1489 him-8(e1489)"
/db_xref="taxon:6239"
/clone-"yk31b8"
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                                                                                                             Homo.
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1 (bases 1 to 265)

Auffray,C., Behar,G., Bols,F., Bouchier,C., da Silva,C.,
Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pletu,G., Pouliot
Sebastiani-Kabaktchis,C. and Tessier,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
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     Genexpress-Genethor
                                Contact: Genethon
                                                                                                                                                         and its expression
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                                                                                  On Apr 14,
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1,rue de 1'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
                                                                                                                                                                                  IMAGE: molecular integration of the analysis of the human
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Senexpress_library_idt: C; Genexpress_sequence_idt: alc-17b11
Seq primer: (-21)M13_universal.
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/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total
brain; total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"

Bento Soares, P.N.A.S in press"
2 others
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/sex="Female"
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                                                                                                                                                                                                                                                                                                                    Polymeropoulos,M.H., Xiao,H., Sikela,J.M., Adams,M., Venter,J.C. and Merrill,C.R. Chromosomal distribution of 320 genes from a brain cDNA library Nature Genet. 4, 381-386 (1993) 94004966
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EST00953 Hippocampus, Strataç
clone HHCMG02, mRNA sequence
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Genexpress_library_idt: C; Genexpress_sequence_idt: alc-lra10
Seq primer: (-21)M13_universal
                                                                                                                                       The Institute for Genomic Research 9712 Medical Center Drive, Rockville,
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1,rue de 1'Internationale, BP60 91002 EVRY Cedex, FRANCE
Tel: 33169472800
Fax: 33160778698
                                                                                                                                                                                                             Bioinformatics
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/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
/note="Organ: bex="female; dev_stage="3 months old;
/isolate=muscular atrophy patient; tissue_type=total
/isolate="Organ: brain; vector: lafmid BA; Site_1: HindIII;
/isolate="Organ: lafmid BA; Site_1: L
                                 arkerlav@tigr.org
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                                                                                                                                                                                                                                                                                           Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 290)

1 Adams, M.D., Dubnick, M., Kerlavage, A.R., Moreno, R., Kelley, J.M., Utterback, T.R., Nagle, J.W., Fields, C. and Venter, J.C.

Sequence identification of 2,375 human brain genes

Nature 355, 632-634 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M78839 290 bp mRNA EST00987 Hippocampus, Strata clone HHCMG95, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                              Polymeropoulos, M.H., Xiao, H., Sikela, J.M., Adams, M., Venter, J.C. and Merrill, C.R. Chromosomal distribution of 320 genes from a brain cDNA library Nature Genet. 4, 381-386 (1993)
                                                                                                                                                                                                                                                                  Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                       Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                            Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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       /clone_lib="Hippocampus, Stratagene (cat. #936205)"
/note="Vector: lambdazAP-II; Female, 2 years; oligo-
random primed cDNA synthesis; lambdazAP-II vector, 1
average insert size."
a 99 c 52 g 61 t 2 others
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a 67 c 80 g 94 t 3 others
                                                                                                                      /db_xref="taxon:9606"
/map="10"
                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="ATCC (inhost):
                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                       /db_xref="ATCC (inhost):78292"
/db_xref="GDB:D10S238E"
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/db_xref="ATCC (inhost):78249"
/db_xref="GDB:D12S110E"
                                                                                                     'clone="HHCMG95"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /map="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'clone="HHCMG02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
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Stratagene (cat. #936205) Homo sapiens cDNA
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Pred.
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5.5e+03;
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-II; Female, 2 years; oligo
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Best Local
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M79816.1
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M78856.1
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10; Conserv
                                                        M79816 390 bp mRNA ES WESTOO353 Mixed stage, Stratagene (cat. #9 elegans cDNA clone CEMSE23, mRNA sequence. M79816
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1 (bases 1 to 332)

Adams,M.D., Dubnick,M., Kerlavage,A.R., Moreno,R., Kelley,J.M. Utterback,T.R., Nagle,J.W., Fields,C. and Venter,J.C. Sequence identification of Sequence 1dentification of 2,375 human brain genes

Nature 355, 632-634 (1992)
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Institute for Genomic Research
9712 Medical Center Drive, Rockvil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST01004 Hippocampus, Stratagene clone HHCMH72, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            il: arkerlav@tigr.org
primer: M13 Forward.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                    /clone_lib-"Hippocampus, Stratagene (cat. #936205)"
/note-"Vector: lambdaZAP-II; Remale, 2 years; oligo-dT +
random primed cDNA synthesis; lambdaZAP-II vector, 1.0kb
average insert size."

1 11 c 59 g 71 t
                              GI:271835
                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="ATCC (inhost):78321"
/db_xref="GDB:D0S1837E"
                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="HHCMH72"
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Pred. No. 5.5e+03;
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                                                                                                                                                                                                                               . 5.5e+03;
ches 0;
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                                                                                                                                                                                                                                                            Length 332;
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M85650/c
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Best Local S
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EST02167 Fetal 1
clone HFBCL38, 1
M85650
                                                                                                                                                            1 (bases 1 to 25)
Adams, M.D., Dubnick, M., Kerlavage, A.R., Moreno, R.,
Utterback, T.R., Nagle, J.W., Fields, C. and Venter, J.
Sequence identification of 2,375 human brain genes
Nature 355, 632-634 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                                 Contact: Kerlavage, Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
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McCombie,W.R., Adams,M.D., Kelley,J.M.,
Utterback,T.R., Khan,M., Dubnick,M., Kel
               Fax: 3018699423
Email: arkerlav@tigr.org
Seq primer: M13 Forward.
                                                                 9712 Medical Center Drive, Tel: 3018699056
                                                                             The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                            M85650.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 3018699423
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primer: Ml3 Foward.
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Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Mixed stage, Stratagene (cat. #937006)"
/note="Yector: Uni-ZAP XR; C. elegans mixed stage cDNA
library. Strategene catalog #937006. The library is oligo
                                                                                                                                                                                                                                                                                                                                            GI:274297
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/db_xref="taxon:6239"
/clone="CEMSE23"
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sequence.
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5.5e+03;
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M86021
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MEDLINE
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1 TGTGTGTCAG 10
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8 TGTGTGTCAG 27
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EST02546 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA
Clone HFBCY34, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 345)
Adams,M.D., Dubnick,M., Kerlavage,A.R., Moreno,R., Kelley,J.M., Utterback,T.R., Nagle,J.W., Fields,C. and Venter,J.C.
Sequence identification of 2,375 human brain genes
Nature 355, 632-634 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M8602
                                                                                                                                                                                                                                                                                                                                                                                                             Email: arkerlav@tigr.org
Seg primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M86021.1 GI:274672
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nilarity 100.0%;
Conservative 0
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/note="Vector: LambdaZAP-II; 17-18 wk gestation, female;
oligo-dr + random primed cDNA synthesis; lambdaZAP-II
vector, 1.0kb average inser size."

1 others
                                                                                                                                                                                    /Clone_lib="Fetal brain, Stratagene (cat#936206)"
/note="Vector: LambdaZAP-II; 17-18 wk gestation, female;
oligo-dT++random primed cDNA synthesis; lambdaZAP-II
vector, 1.0kb average inser size."
a 68 c 63 g 104 t
                                                                                                                                                                                                                                                                             /db_xref="ATCC (inhost):81598"
/db_xref="GDB:D0S709E"
/db_xref="taxon:9606"
/clone="HFBCY34"
                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
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Gb_xref="ATCC (inhost):81227"
Gb_xref="GDB:DOS343E"
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one="HFBCL38"
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                                                                         Score 10; DB 20;
Pred. No. 5.5e+03;
Mismatches 0;
                                                                                                            Length 345;
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18

Search completed: September 17, 1999, 21:27:57 Job time: 14261 sec

Title: Perfect score: Sequence:

US-08-956-518A-86

Run on: OM nucleic

nucleic search, using sw model

Scoring table: Searched:

2546578 seqs, IDENTITY\_NUC TTTTTTGAAG 10

986266752 residues

em\_est2

em\_est8:\* em\_est6: em\_est5 em\_est4: em\_est3 em\_est1

em\_est10:\*

em\_esti

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gb\_est10:

AF123245.1

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September 17, 1999, 21:27:55; Search time 2825.05 Seconds (without alignments) 6.982 Million cell updates/sec
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RESULT 1
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em_est25: *
em_est26: *
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                                                       ALIGNMENTS
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D20170 HDWGS01144
D22028 RICC10206A
D22533 RICC0190B R
D23618 RICC3103A R
                                                                            D33071 CELK025G7R
D33081 CELK026A9R
D33087 CELK027DYR
D33182 CELK031AXR
D33477 CELK031FXR
D33502 CELK031F7R
D33502 CELK036F3R
D33948 CELK038E9R
D33948 CELK038F4R
D34048 CELK034F4R
D34048 CELK040A9R
D34048 CELK040A9R
D34048 CELK040A9R
D340492 CELK0445A2R
D34370 CELK045A2R
D34370 CELK045A2R
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MEDLINE
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AUTHORS
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypiu
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11-MAR-1999
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                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 314)

Murakawa, K., Matsubara, K., Fukushima, A., Yoshii, J. and Okubo, K.

Chromosomal assignments of 3'-directed partial cDNA sequences representing novel genes expressed in granulocytoid cells
 Okubo,K., Fukushima,A., 1
Yoshinari,H., Arimoto,J.
Gene expression of human
                                                representing novel genes expressed Genomics 23, 379-389 (1994) 95137584
                                                                                                                                                                                                                        HUMGS01144 Human promyelocyte Homo sapiens cDNA clone pm1519
                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ed (23-JAN-1999) to the EMBL/GenBank/DDBJ databases. University of Texas at Austin, Austin, TX 78713, USA
                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                              540
                                     (bases 1 to 314)
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milarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="24 days postanthesis
/clone="CF16S"
/cell_type="seed epidermal cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Gossypium hirsutum"
/strain="Texas Marker-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                 GI:501267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'db_xref="taxon:3635"
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26
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Yoshii,J., Niiyama,T.,
. and Matsubara,K.
n promyelocytic cell lir
                                                                                                                                                                                                                                          mRNA
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                                                                                                                                                                                                                                                                                Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                              Tel: 0298-38-7441
Fax: 0298-38-7468
                                                                                                                                                                                                                                            Japan
                                                                                                                                                                                                                                                                                                                                             Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D22028 288 bp
RICC10206A Rice callus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             after induction of differentiation. A new application cDNA sequencing Unpublished (1993)
                                                                                                                                                                                                                                                                                                                                                        Sasaki, T. and Minobe, Y. Rice cDNA from callus
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trac)
euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Okubo,K., Fukushima,A., Yoshii,J., Yoshiari,H., Arimoto,J. and Matsubara,K. Institute for Molecular and Cellular Biology Osaka University
                                                                                                                                                                                                                                                                                                                                                                                                     Poaceae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa.
                                                                                                                                                                                                                                                           baraki
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Location/Qualifiers
              78
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                                                                                                                                                                                                                                                                     Kannondai, Tsukuba
                                                                                                                                                                                               tsasaki@abr.affrc.go.jp
          /clone_lib="Rice callus"
/note="Vector: pBluescript II SK+; Site_1:
NotI; Chap prepared from rice callus mRNAs;
Oligo(dT) as a primer and ligating to the s
of pBluescript II SK+ phagemid."
a 57 c 59 g 92 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131
                                                                                                           /organism="Oryza sativa"
/strain="cultivar Nipponbare,
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 promyelocyte.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /Cloue- p..../Clone_lib="Human prom/clone_"Female, adult,
                                                                                               clone-"R"
                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:426169
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/db_xref="taxon:9606"
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.lt, cell_line =
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Cellular Biology
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                                   l: SalI; Site_2:
As by using
SalI-NotI site
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                                                                                                                        Japonica"
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sida; Poales;
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19 TTTTTTGAAG 310
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RICC3103A Rice of
D23618
                                           9427550
D23618.1
EST.
Oryza sativa.
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: tsasaki@abr.affrc.go.jp
PROJECT ='RGP'.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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Fax: 0298-38-7468
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National Institute of Agrobiological Resources
Rice Genome Research Program
2-1-2 Kannondai, Tsukuba
                                                                                                                                                                                                                            Similarity 100
10; Conservative
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Rice cDNA from callus
Unpublished (1994)
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euphyllophytes; Spermatophyta;
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                                                                                                                                                                                                                                                                                                           96
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llarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                          /Clone_lib="Rice callus"
/Clone_lib="Rice callus"
/note="Vector: pBluescript II SK+; Site_1: Sall; Site_2:
/note="Vector: pBluescript II SK+ callus mRNAs by using
oligo(dT) as a primer and ligating to the Sall-NotI site
of pBluescript II SK+ phagemid.
a 69 c 81 g 78 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                      /clone="R"
                                                                                                                                                                                                                                                                                                                                                                                               /organism="Oryza sativa"
/strain="cultivar Nipponbare, sub_species Japonica"
/db_xref="taxon:4530"
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callus Oryza sativa
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Pred. No. 3.4e+04;
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lyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                    BB
                                                                                             CDNA
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                                                                                                                                                                                                                                                   Length 328;
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                                                          Tel: 0298-38-7441

Fax: 0298-38-7468

Email: minobe@rtcs0.riken.go.
                                                                                                                                                Contact: Yuzo Minobe National Institute of Agrobiological Resources
                                                                                                                                                                                              Unpublished (1995)
                                                                                                     Japan
                                                                                                                                        Rice Genome Research Program
                                                    PROJECT -'RGP'
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TTTTTTGAAG 242
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1 (bases 1 to 261)
Sasaki, T. and Minobe, Y.
Rice CDNA from callus
Unpublished (1994)
1 (bases 1 to 331)
Minobe, Y. and Sasaki, T.
Rice cDNA from root
                                                                                              Oryza sativa
Eukaryota; Viridiplantae;
                                                                                                                                          Oryza sativa.
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National Institute of Agrobiological Resources
Rice Genome Research Program
2-1-2 Kannondal, Tsukuba
                                                           euphyllophytes;
Poaceae; Oryza.
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PROJECT = 'RGP'.
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Fax: 0298-38-7468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Rice callus"
/note="Vector: pBluescript II SK+; Site_1:
NotI; cDNA prepared from rice callus mRNAs
NotI; cDNA prepared from the callus mRNAs
oligo(dT) as a primer and ligating to the s
of pBluescript II SK+ phagemid
of pBluescript II SK+ phagemid
49 c 52 g 79 t 2 others
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/strain="cultivar Nipponbare,
/db_xref="taxon:4530"
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Pred. No. 3.5e+04;
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hyta; Magnoliophyta; Liliopsida; Poales;
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/organism="Oryza sativa" /strain="Nipponbare, sub\_species Japonica"

Location/Qualifiers

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                             D27177
398 bp mRNA
CELK004D5R yuji Kohara unpublished
clone yk4d5 3', mRNA sequence.
D27177
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D27177.1 GI:521441
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10; Conserv
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
1 (bases 1 to 423)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          National Institute of Genetics Yata 1111, Mishima, Shizuoka 411, Tel: 0559-75-0771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene Library Lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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Similarity 100.
10; Conservative
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Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kohara, Y., Mitsuki, H., Nishigaki, A., Motohashi, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                ykohara@ddbj.nig.ac.j.
Location/Qualifiers
                                                                                                                                                                                                                                                                                  /organism="Caenorhabditis elegans"
/strain="CB189 him-8(e1489)"
/db_xref="taxon:6239"
/clone="yk14d2"
/clone_lib="Yuji Kohara unpublished cDNA"
/note="dev_stage=varied, sex=Hermaphrodite male,
tissue_type=whole animal"
a 52 c 104 g 107 t
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/clone="R"
/clone_lib="Rice root"
/clone_lib="Rice root"
/note="Prepared from seedling root. "
/note="Prepared from seedling root."
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Prismatches 0;
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Cz
1 (bases 1 to 398)
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l Similarity 100.0%;
10; Conservative 0
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National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411,
Tel: 0559-75-0771
Fax: 0559-75-6240
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 471)
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D27179
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Yata 1111, Mishima, Shizuoka 411,
Tel: 0559-75-0771
Fax: 0559-75-6240
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Unpublished (1994)
                                                                                                                                                                                                                                 Contact: Yuji Kohara
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                      Tabara,H.
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                                                                                                     ykohara@ddbj.nig.ac.j.
Location/Qualifiers
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42 c 88 g 105 t 1 others
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/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
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Pred. No. 3e+04;
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RESULT 1
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                                               UZ/544 417 bp mRNA
CELK013A7R Yuji Kohara unpublished cDNA
clone yk13a7 3', mRNA sequence.
DZ7544
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D27544.1
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CELK012B4R Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA
clone yk12b4 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                    National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 0559-75-0771
Fax: 0559-75-6240
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Unpublished (1994)
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Caenorhabditis elegans
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Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                    /Clone_lib="Yuji Kohara unpublished cDNA"
/note="dev_stage=varied, sex=Hermaphrodite male,
tissue_type=whole animal"
73 c 89 g 155 t
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tissue_type=whole animal"
70 c 99 g 118 t
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National Institute of
Yata 1111, Mishima, Sh
Tel: 0559-75-0771
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Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 403)
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National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411,
Tel: 0559-75-0771
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Unpublished (1994)
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                                                                                                                                                                                             ykohara@ddbj.nig.ac.j.
Location/Qualifiers
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/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
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/clone_lib="Yuji Kohara unpublished cDNA"
/note="dev_stage=varied, sex=Hermaphrodite matissue_type=whole animal"
2 a 85 c 75 g 144 t 1 others
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tissue_type=whole animal"
                                                                                            /organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
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Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea;
                                                                                     D27882 470 bp mRNA EST 20-NOV-1995 CELK005GXR Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA czione yk5g10 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                Email: ykohara@ddbj.nig.ac.j.
Location/Qualifiers
1. .387
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vata 1111, Mishima, Shizuoka 411, Yata 1210, Mishima, Shizuoka 411, Tel: 0559-75-0771
Fax: 0559-75-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Toward an expression map 
Unpublished (1994)
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda;
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                                                      D27882.1 GI:522637
                                                                                                                                                                                                                                    h 100.0%;
Similarity 100.0%;
10; Conservative 0
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                                                                                                                                                                                                                                                                                                          /organism="Caenorhabditis elegans"
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/note="dev_stage=varied, sex-Hermaphrodite male,
tissue_type=whole animal"
1 others
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Pred. No. 3e+
0; Mismatches
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Pred. No. 3e+04;
; Mismatches 0;
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 Rhabditia; Rhabditida;
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 BASE COUNT
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AUTHORS
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SOURCE
ORGANISM
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JOURNAL
COMMENT
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D27887/c
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TTTTTTGAAG 182
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National Institute of Genetics
Yata 1111, Mishima, Shizuoka 41
Tel: 0559-75-0771
Fax: 0559-75-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
1 (bases 1 to 403)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D27887 403 bp mRNA EST 20-NOV-1995
CELK005G2F Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA
clone yk5g2 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411,
Tel: 0559-75-0771
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                                                                                                                                                                                                                                                                                                                                                 Contact: Yuji Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kohara, Y., Mitsuki, H., Nishigaki, A., Motohashi, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ykohara@ddbj.nig.ac.j.
Location/Qualifiers
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                                                                                                                                                                                         ykohara@ddbj.nig.ac.j.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         an expression map ished (1994)
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63 c 76 g 110 t
                                                                                                        /organism="Caenorhabditis elegans"
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/db_xref="taxon:6239"
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96 c 99 g 126 t 3 others
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Pred. No. 2.8
0; Mismatches
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                                                                                                                                                                                                                                                                                  411,
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2.8e+04;
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Title: Perfect score:

US-08-956-518A-85 10 1 TCTCCTTAAG 10

Scoring table: Sequence:

IDENTITY\_NUC

- L'abase :

N\_Geneseq\_36:\*

311585 segs, 125096042 residues

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No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, a derived by analysis of the total score distribution.

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OM nucleic - nucleic search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 1998 Comp

Compugen Ltd

September 18, 1999, 00:33:26;

26; Search time 425.19 Seconds (without alignments)
5.884 Million cell updates/sec

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Best Local
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30-AUG-1989, 103127.
23-FEB-1988; US-160416.
(GEHO) Gen. Hospital Corp.
Seed B, Allen J, Aruffo A, Camerini D, L, Simmons D, Stamenhovic I, Stengelin S; WPJ: 89-250302/35.
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Rapid immuno:selection cloning - used to clone genes encoding cell surface antigens associated with mammalian T lymphocytes. Disclosure; fig. 10; 69pp; English.
CD20.4 encodes a cell surface antigen involved in cell mediated immunity. This DNA can be expressed in a vector which transforms COS cells. The vector can isolate any protein, and clones are easy to manipulate. Sequence 1473 Bp; 434 A; 321 C; 286 G; 432 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tyrosine suppressor gene; ASV LTR; human cytomegalovirus AD169 enhancer; HIV box; immunoselection; immune deficiency diseases; vasculitis; systemic lupus erythematosus; rheumatoid arthritis; neoplasms. Location/Qualifiers
Key 94. 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rapid immuno:selection cloning - used to clone genes encoding cell surface antigens associated with mammalian T lymphocytes. Disclosure; fig. 13; 69pp; English.
CD20 encodes a cell surface antigen involved in cell mediated immunity. This DNA can be expressed in a vector which transforms COS cells. The vector can isolate any protein, and clones are easy to manipulate. Sequence 1476 Bp; 435 A; 324 C; 285 G; 432 T;
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25-FEB-1988; US-160416.
(GEHO) Gen. Hospital Corp.
Seed B, Allen J, Aruffo A, Camerini D,
Simmons D, Stamenkovic I, Stengelin S;
WPI; 89-250302/35
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1042
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/note= site of polyA+ tail in CD20.6
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Pred. No. 6.7e+02;
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א כ	10	100.0	2781	- ب	013239	Sec
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c 25	10	100.0	102	<b></b> +	N50386	Sequence of synthe
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30	10		1476	$\vdash$	021173	CD20
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C 34	10	•	102	,_	N30067	H
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New antigenic proteins from Plasmodium falciparum - new encoding nacid sequences and derived antibodies, useful in vaccines, diagnos Claim 1; page 23 and Table 18; 25pp; German.

The DNA encodes a malaria-specific P. falciparum 41kD protein (see P90419) is useful in a protective vaccine, esp. against malaria. Produced antibodies are useful reaseful on antibodies are useful on antibodies are useful as diagnos antibodies. See also N90211-25 and P90403-19.

Sequence 1982 BP; 764 A; 230 C; 287 G; 701 T;
                                                                             05-APR-1989.
27-AUG-1988;
08-SEP-1987;
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05-JUL-1989.
20-DEC-1988;
30-DEC-1987;
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Sequence of plasmid p8/3
Slasmid p8/3; vector; plas
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Knapp B, Hundt E, Enders B, Kupper H;
WPI; 89-194071/27.
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                                                             (HOFF) Hoffmann-La
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05-APR-1989.
27-AUG-1988;
08-SEP-1987;
                                                                  contg. epitope(s) of Plasmodium falciparum merozoite antigen, for use in malaria vaccines
for use in malaria vaccines
Figure 12a-12d; 67pp; German.
The genomic DNA of isolate RO-33 Ghana was largely identical to this genomic isolate of K1, whereas cDNA from M25 isolates differs
in 3 codons (see n9297). Plasmodium falciparum merozoite antigen can be coupled to an affinity peptide, or adsorbed or covalently bonded on a carrier. It, and its derivatives, are useful as immunogens anti-malaria vaccines. Antibodies directed against it are useful for
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N90733;
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for use in malaria vaccines
Figure 11a-11e; 67pp; German.
Plasmid p8/3 is used as an expression vector.
Sequence 5376 BP; 1592 A; 1152 C; 1213
                                                 passive immunisation and diagnosis.
Sequence 1599 BP; 619 A; 207 C;
                                                                                                                                                                New peptide(s)
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DNA encoding
Chloroplast;
Key
cds
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DNA is introduced into various kinds of plants to alter the nature of the chloroplast mambrane lipid phosphatidyl glycerol. It may also be used as a probe to allow cloning of enzyme genes which exist in closely related plants but which have slightly different substrate selectivity.

Sequence 1426 BP; 384 A; 322 C; 312 G; 408 T;
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20-SEP-1989.
14-MAR-1988;
14-MAR-1988;
                                                                                                                                                                                                                                                                            cDNA from Plasmodium falciparum Mimerozoite antigen
Plasmodium falciparum M25isolate;
                                      New
                                            WPI; 89-101095,
P-PSDB; P93567
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contg. epitope(s) of Plasmodium for use in malaria vaccines Figure 12a-12d; 67pp; German. It differs from genomic DNA in F
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WPI; 89-319095/44
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immunisation;
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                          falciparum merozoite antigen
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Best Local
Matches
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric antibodies against markers and therapeutic too Disclosure; pp; English
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Sequence 1254 BP; 471 A; 186 C; 229 G; 368 T;
                                                        signal_peptide
                                                                                                                    Vaccines; poultry; fowl vaccine; ss.
                                                                                                                                                         New recombinant cDNA coding disease virus (NDV)
                                                                                                   Newcastle disease virus.
                                                                                                                                                                                                                                           N81290 standard;
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WPI; 90-133521/18
                                                                                                                                                                                                      22-OCT-1990 (first entry)
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(DOWC) Dow Chemical Co
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1so Q04259-Q04265 and
nce 1717 BP; 492 A
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10; Conserv
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68. .361
                                                     Location/Qualifiers 68. .121
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TAG72; variable region ofimmunoglob
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A; 297 C;
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                                                                                                                                          Newcastle
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29-JUN-1987; 870091.
30-JUN-1986; US-880371.
(SMIK) Smith Kline Rit SA.
Espion D, Burny A, Debouck C
WPI; 88-001887/01.
                                                   removing poly adenylation signals in the gene.
Claim 22; Page 77; 144pp; English.
The insecticidal protein gene of B.t.t. was modified by site-directed mutagenesis to remove all putative polyadenylation signals and ATTTA sequences. The mutated sequence was inserted into a plant transformation vector such as pMONB93. The vector is then inserted into an Agrobacterium strain and used to transform potato, tomato and tobacco plants. Transformed plants were found to be resistant to Colorado Potato Beetle.
See also 005790-005795, 005797-005800 and 005561.
Sequence 1791 BP; 501 A; 467 C; 391 G; 432 T;
                                                                                                                                                                                                                                                                                                                                                      Encodes B.t.t insecticidal protein.
B.t.t insecticidal protein; polyade
Bacillus thuringiensis tenebrionis.
FD-20566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Poly(A) mRNA is isolated from NDV-infected BHK-21 cells used to construct complementary DNA by usual methods and this inserted into PstI-cleaved pBR322. Recombinant plasmids were cloned in E.coli M294 and selected by hybridisation with a viral RNA probe 'Clone (designated II.14(F) contg. the longest insert was sequenced: it contains the claimed 1764-base sequence which codes for 526 AA protein consisting of two polypeptides linked by a pentapeptide region where proteolytic cleavage occurs. NDV fusion protein, and immunogenic polypeptide, are useful in vaccines for protecting poultry against NDV infection, and can be used diagnostically. Sequence 1764 BP: 522 A: 415 C: 385 G; 442 T;
                                                                                                                                                                                                                                      (MONS) MONSANTO CO. Fischhoff DA, Perlak FJ; WPI; 90-269905/36.
                                                                                                                                                                                                                                                                                 20-FEB-1990; 870025.
24-FEB-1989; US-315355.
12-FEB-1990; US-476661.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Q05796 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Pages 7-9 and Fig 1(a)-1(b); 21pp; French. A DNA molecule with this sequence is claimed. It wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant DNA encoding fusion or its immunogenic polypeptide f
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l Similarity 100
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377. .1648
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362. .376
100.0%;
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Pred.
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DB 1;
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6.7e+02;
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            Length 1791;
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Example: Fig 7, 24pp; English.
Plasmid pTh alpha 1, which is based on pBR3
specifying ampicillin resistance and a struthymosin alpha 1 cloned at its 5' coding st site at its 3' end into a BamHI site.
Sequence 102 BP; 33 A; 14 C; 25'
WO9015144-A.
13-DEC-1990.
01-JUN-1990;
                                                                                                                                            exon
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N71032
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15-MAR-1991 (first entry)
Sequence contg. abaA gene of Aspergillus nidulans.
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27-NOV-1981; US-325511.
09-NOV-1983; US-550167.
(ELII ) ELI LILLY & CO.
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27-NOV-1981;
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17-MAR-1987
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15-DAN-1991.
22-FEB-1990; US-483516.
22-FEB-1990; US-483516.
(USSH) NAT INST OF HEALTH.
Waters AP, MCCutchan TF;
WPI; 91-044381/06.
P-PSDB; R10935.
                                                                                                                                                                                           Plasmodium merozoite antigen proteins and DNA sequences - useful in vaccine prodn., anti-malarial drug design, and in diagnostics Disclosure; fig 1; 31pp; English.

This sequence is contained in a recombinant DNA molecule comprising e.g. a pUC19 or vaccinia virus vector sequence and regulatory elements. This allows efficient expression of the antigen on transformation of host cells. The P.vivax antigen prod. is useful in an anti-malarial vaccine for conferring immunity against the merozoite form of the parasite and preventing infection of uninfected red blood cells. See also 010418. Sequence 1470 BP; 496 A; 279 C; 361 G; 334 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q10869 stand
Q10869;
15-APR-1991
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This DNA fragment encodes the A.nidulans abacus (abaA) gene for ing processing to remove the 2 introns. The protein encoded ing processing to remove the 2 introns. The protein encoded ing processing to remove the 2 introns. The protein encoded in the protein growth and development in filamentous further than the control of the shanger of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium vivax 66kD merozoit
Plasmodium merozoite antigens;
Plasmodium vivax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enabling the mis-scheduled expression of the aban gene, indusabortive development in the fungus. This enables increased of medically or commercially important substances which are only produced by the fungi during conidiation.

Sequence 3744 BP; 933 A; 1100 C; 793 G; 918 T;
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R-PSDB; R10047.
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(UYGE-) UNIV GEORGIA RES FO.
Timberlake W. Adams TE, Mirabito
WPI; 91-007214/01.
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l Similarity 100.
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Pred. No. 6.7
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malaria vaccine; ss.
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16-JAN-1991.
13-JUL-1990;
13-JUL-1989;
29-DEC-1989;
06-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA was isolated from a urate oxidase-producing strain of A.flavus and reverse transcribed into cDNA. A gene bank was constructed from E.coli MC 1061 containing plasmid pTZ19R containing the cDNA. Probes were synthesised based upon the amino acid sequence of A.flavus urate oxidase and these used to screen the gene bank. Five positive colonies were analysed; this is the sequence of the longest cDNA insert ("clone 9C"). See also Q10246-Q10253, Q10255.
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16-JAN-1991.
13-JUL-1990;
New protein with high urate oxidase active one protein with high urate oxidase activened transformed hyperuricaemia, etc. Claim 10; Page 50; 68pp; French.
                                                                                                     (SNFI ) SANOFI SA.
Caput D, Ferrara P, Guillemot
Loison G, Labree, Lupker J;
WPI; 91-016644/03.
                                                                                     P-PSDB; R10222
                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                        urate oxidase;
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DNA encoding it, vectors and transformed
hyperuricaemia, etc.
Claim 8; Fig 3; 68pp; French.
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Clone 9C encoding a protein with urate oxidase activity.
urate oxidase; uricase; hyperuricaemia; kidney stones; chemotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caput D, Ferrara P, Guillemot Loison G, Labree, Lupker J;
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06-FEB-1990;
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Q10245;
27-MAR-1991 (first entry)
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FR-017466.
FR-001368.
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FR-017466.
FR-001368.
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ormed cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression in 
kidney stones
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6.7e+02;
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                                                                                                                                              Legoux
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                                        and recombinant, used for treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                        stones;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and recombinant used for treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prokaryotes.
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CC mRNA was isolated from a urate oxidase-producing strain of A.flavus CC and reverse transcribed into cDNA. A gene bank was constructed from CC E.coli MC 1061 containing plasmid pTZ19R containing the cDNA. Probes CC were synthesised based upon the amino acid sequence of A.flavus CC urate oxidase and these used to screen the gene bank. Five positive CC colonies were analysed, one of which contained inserts of 1.2kb ("CC colonies were analysed, one of which contained inserts of 1.2kb ("CC colonies (substituted) bases are found to replace codons immediately downstream of the start ATG with codons typical of prokaryotic CC genes (substituted) bases are found at positions 6, 9, 21 and 42). CC The recombinant sequence was ligated to plasmid p462 to give p466. See also Q10245 and Q10247-Q10253 and Q10255. See also Q10245 and Q10247-Q10253 and Q10255. Sequence 906 BP; 219 A; 267 C; 241 G; 179 T; Ouery Match 10: Conservative 0; Mismatches 0; Indels 0; Gaps 0; ITCTCCTTAAG 10 | ITTCCTTAAG 10 | ITTCCTTAAG 511

Search completed: September 18, 1999, 00:33:28

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77

12.7 12.7

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Q03810 X26936

gC gene of RB1B cDNA encoding a

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ALIGNMENTS

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RESULT
Q02842,
ID Q0
AC Q0
AC Q0
DT 00
DE PI
KW C1
OS AC
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                                                                                                                                                        Query Match
Best Local S
Matches 7
                                                                                                                                                                                                         DNA indicating complement to RNA gene -
of Human Immunodeficiency Virus type 2 used for new vaccine
diagnostic for AIDS virus.
Claim 2; Fig.4; 12pp; Japanese.
Claim 2; Fig.4; 12pp; Japanese.
cDNA to novel HIV-2 (GH-1) has been integrated into plasmid
DC HIV-2(GH-1). Useful for diagnosis and vaccination agains
Carries 7 overlapping genes in varrious reading frames, incl
Pol and Env.
Sequence 9360 BP; 3211 A; 1944 C; 2317 G; 1888 T;
                                                                                                                                                                                                                                                                                                                                     J01289486-A.
21-NOV-1989.
16-MAY-1988;
16-MAY-1988;
                                                                                                                 1086
       01-JUN-1990 (first entry)
pKS311 Plasmid carrying mature fibrolase.
Crotalidus; fibrolase; thrombolytic; ds.
Agkistrodon contortrix contortrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA to HIV-2 RNA.
HIV; AIDS; Vaccine
                                                   Q02842 standard; DNA;
Q02842;
                                                                                                                                                                                                                                                                                                                   Toa Nenryo Kogyo KK, WPI; 90-005177/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                     cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cds
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                                                                                                                                                                                                                                                                                                         P-PSDB; R04024-30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIV-2.
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                                                                                                                                    49
                                                                                                               9 CTGCACG 55
|||||||
6 CTGCACG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIDS; Vaccine; pUC-HIV-2(GH-1)
                                                                                                                                                         . Similarity 7; Conserv
                                                                                                                 1092
                                                                                                                                                          Conservative
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JP-119024.
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 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                /label=F
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Pred. No.
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Result

Query Match

Length

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Heat-resistant RNa
Cephalosporium acr
Pseudorabies virus
Pseudorabies virus
Pseudorabies virus
Phosphinothricin r
Translation activa

Thyamidine kinase Thyamidine kinase Marek's disease vi

MPB-57 protein enc Sequence of plasmi Acetyl-CoA-carboxy Acetyl-CoA-carboxy

Chromosomal gene f
DNA homologous to
HindillyHpall frag
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Nucleotide sequenc
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1873 1084 2967 2546 2038 2038 1392 1392 1392 1392 1392

pBT23 secretion ex Sequence of pre-TG cDNA sequence enco

Nucleotide sequenc BUF-3 gene for hum DNA sequence encod Gene encodes funct pBT23 secretion ex

PelC Pectin lyase PelB Pectin lyase

Aspergillopepsin A SalI restriction f Gene encoding prot RAP2 Gene encoding

pkS311 Plasmid car cDNA insert of vec

cDNA to HIV-2

Chromosomal gene I

Scoring table: Perfect score: Sequence:

IDENTITY\_NUC

\_\_tabase

N\_Geneseq\_36:\*

seqs,

125096042

residues

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Title:

OM nucleic

,

nucleic search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen

September 17, 1999, 19:17:20;

0; Search time 425.19 Seconds (without alignments)
32.363 Million cell updates/sec

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N ZA8809415-A.

N ZA8809415-A.

PE 15-DEC-1989.

PF 15-DEC-1988; 889415.

PR (CHIR) Chiron Corp.

PA (CHIR) Chiron Corp.

PA (CHIR) Chiron Corp.

PA (CHIR) Chiron Corp.

PT also yeast expression vectors contg. DNA and recombina.

PS Example 5; Page 29; 64pp; English.

CC alpha factor leader (S.cerevislae) encoding mature fibrolase.

CC Fibrolases are thrombolytic agents, useful in treating thromboemby conditions e.g. pulmonary embolism.

"- also Q02837 and Q02838.

"- 2809 BP; 887 A; 552 C; 538 G; 832 T;

Mismatches 0; Indels

Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                         PR 222
RESULT 4
Q03206/c
ID Q03206 standard;
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RFFESSSSSSS
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Best Local S
Matches 7
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11-JUL-1990 (first entry)
CDNA insert of vector PSP 6K-13-
Respiratory distress syndrome; R
disease; pulmonary surfactant pr
                                                                                                                                                                                                                                                                    21-NOV-1989:
24-SEP-1987; 100372.
26-SEP-1985; US-791120.
15-AUG-1986; US-897183.
15-AUG-1986; US-897183.
(GENE-) Genetics Institute.
Taeush HW, Jacobs KA, Steinbrink DI
WPI; 90-036829/05.
P-PSDB; R05093
                                                                  1722
                                                                                                                                                                            Purified human pulmonary surfactant protein - useful for treating respiratory distress syndrome. Disclosure; Table 6; 15pp; English.

Protein is useful in treatment of respiratory distress syndrome membrane disease) enhancing pulmonary surfactant activity.

Protein is encoded by the cDNA insert in vector PSP 6K-I3-7.

Sequence 2026 BP; 442 A; 626 C; 532 G; 425 T; 1 Othe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2286
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                                                                  CTGCACG
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7; Conser
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ilarity 100.0%;
Conservative
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614.811
'++ag= b
                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
  DNA;
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                                                                                                                  0;
                                                                                                                            Score 7;
Pred. No.
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Matches 7
Query Match
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Matches 7; Conserv
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4-JUL-1988; FR-009031.
(INRM) Inserm Inst Nat Sante.
Tavitian A, Pizon V, Chardin P
WPI; 90-037122/05.
P-PSDB; R05070.
                                                                                                                                                                                                                                                                                                                                        003212;
003212;
                                                    DNA encoding sequences associated with human oncogenes - and derived antibodies, useful for in vitro diagnosis of cancer and for therapy.

Disclosure; Fig 3a-b; 92pp; French.
Derived peptides can fix GTP and GTP and have GTPase activity. Abs to these peptides can diagnose associated diseases - absence or exc the product indicates loss of balance between anti- and oncogenic f in the cells. The product may be used to treat conditions associate ras or rap genes.

Sequence 558 BP; 142 A; 143 C; 165 G; 108 T;
                                                                                                                                                                   (INRM) Inserm Inst Na
Tavitian A, Pizon V,
WPI; 90-037122/05.
P-PSDB; R05076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; Page 59; 92pp; French.

Derived peptides can fix GTP and GDP and have GTPase activity. Abs rais to these peptides can diagnose associated diseases - absence or excess the product indicates loss of balance between anti- and oncogenic factor in the cells. The product may be used to treat conditions associated wires or rap genes.

Sequence 117 BP; 24 A; 36 C; 34 G; 23 T;
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4-JUL-1988;
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                                                                                                                                                                                                                                                                                            Synthetic.
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Synthetic.
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10-JUL-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoding sequences associated with human oncogenes derived antibodies, useful for in vitro diagnosis
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                                                                                                                                                                                                                                                                                                                 encoding
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rm Inst Nat
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                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                        cancer;
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           12.7%;
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Score 7; DB 1
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. Be+03;
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Q03247;
WO9000191-A.
11-JAN-1990.
27-JUN-1989; UO2809.
01-JUL-1988; US-214085
                                                                                                                                                                                       11-JUL-1990 (first entry) Sall restriction fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bovine chymosin, t-PA;
may be produced.
Sequence 1766 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aspartic proteinase deficient filamentous fungi prepn. by pref. using a gene replacement vector, useful as hosts increased prodn. of heterlogous polypeptide(s). Disclosure; Fig 3; 64pp; English. Mutating the aspergillopepsin gene, a strain defficient in proteinase may be synthesised. The absence of such proteol improves the production of heterologous gene products, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENE-) Genencor Inc.
Berka R, Hayenga K, Lawlis
WPI; 90-037128/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9000192-A.
11-JAN-1990.
01-JUL-1989; U02891.
01-JUL-1988; US-214237.
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Aspartic proteins
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1573.
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238. .385
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65. .1635
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                                                                                                                                                pre-glycoprotein
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Best Local S
Matches 7
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26-JUN-1989; GB-014666.
(CIBA) Ciba Geigy AG.
Heim J. Meyhack B. Visser J
WPI; 90-031714/05.
                                                                                           DNA coding for pectin lyase(s) PLA, PLB, PLC, PLE or PLF - used to produce pectin lyase(s) in pure form for constructing hybrid vectors expressing foreign genes. Claim 5; Fig 12; 63pp; English. Useful in production of hybrid vectors expressing the pectin lyase gene and/or hybrid vectors expressing foreign genes eg. interferon within a filamentous fungal expression system esp. Aspergillus nige sequence 3168 BP; 823 A; 780 C; 720 G; 845 T;
  1823
                                                                                                                                                                                                                                                                                                                                                                                                                                 Q03246
Q03246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolating rabies preglycoprotein G, and associatin segment of a methylotrophic yeast strain and a ter methylotrophic strain, allows the protein to be se P. pastoris culture (pref. ATCC 20880). The inactive virus protein is useful in a vaccine measure for at risk individuals and animals. Sequence 2122 BP; 634 A; 458 C; 487 G; 5
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PelC Pectin lyase PLC recombinant
Pectin lyase; PLC; expression syst
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Prodn. of rables glyco-protein G
by culturing P.pastoris contg. DN
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Disclosure; Table 1; 82pp; English.
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Similarity 100.0%;
7; Conservative (
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Pred. No. 7.7
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system;
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train and a terminator fr
rotein to be selectively
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7.7e+03;
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Best Local :
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26-JUL-1989; JP-185428.

27-JUL-1988; JP-185428.

08-SEP-1988; JP-223399.

08-MITP) Mitsubishi Petroch KK.

(MITP) Mitsubishi Petroch KK.

Kohama K, Kobayashi M, Kurusu Y, Yukawa H;

Kohama K, Kobayashi M, Kurusu Y, Yukawa H;

WPI; 90-031347/05.

New DNA fragments which stabilise plasmids in and derived recombinant vectors which are ret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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26-JUN-1989; GB-014666.
(CIBA) Ciba Geigy AG.
Heim J. Meyhack B. Visser J
WPI; 90-031714/05.
without selection pressure.

Claim 6; Page 23; 27pp; English.

Claim 6; Page 23; 27pp; English.

Plasmid pBF503 contains DNA fragment present in Brevibacterium stationis if o 12144, contains gene which stabilises plasmids in the bacteria, allowing maintainance with no selection pressure.

Tryptophan synthetase gene with associated promotor/operator system has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA coding for pectin lyase(s) PLA, PLB, PLC, PLE or PLF used to produce pectin lyase(s) in pure form for constructing hybrid vectors expressing foreign genes.

Claim 4: Fig 11: 63pp; English.

Useful in production of hybrid vectors expressing the pectin lyase gene and/or hybrid vectors expressing foreign genes eg. Interferon within a filamentous fungal expression system esp. Aspergillus niger. Sequence 2774 BP; 653 A; 785 C; 673 G; 663 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JUL-1990 (first entry)

Gene encodes function of maintaining a plasmid bacteria of the genus Brevibacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PBY503; tryptophan synthetase; coryneform;
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12-JUJ-1990 (first entry)
PelB Pectin lyase PLB recombinant DNA molecule
PelB Pectin lyase PLB ression system; interfer
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Matches 7
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Best Local Similarity
Matches 7; Conser
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using Escherichia coli system including tryptophan promotor and
E.coli alkaline phosphatase signal peptide gene.
Disclosure; Fig 4; 23pp; English.
An E.coli strain transformed with the vector is useful for producing
hEGF in large pure quantities, with glycerol and/or glucose as a C-so
The hEGF is useful as an anti-cancer agent.
Sequence 354 BP; 97 A; 73 C; 82 G; 102 T;
                          10-MAR-1993 (revised)
31-MAY-1989 (first entry)
Sequence of pre-TGF-betal c
Transforming growth factor
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Sequence
                                                                       Q02814 standard;
Q02814;
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Q03235;
12-JUL-1990 (fir
                     inhibition.
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                                                                                                                                                                                                                                                                                                                      Yano J, Murai M;
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15-JUL-1988; JP-177685.
(NNSH) Nippon Shinyaku
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92. .154
Location/Qualifiers 842. .2011
                                                                                                                                                                                                                                                                                                                                                                                                       /label=hEGF
327. .350
                                                                                cDNA;
                                                                                                                                                                                                                                                                                                                                                                                  /label-trp A
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                            cDNA.
r beta-3 (TGF beta
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                                                                                                                                                                                                                                                                                                                                                                                                                  gene.
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0; Mismatches
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Pred. No. 7.8
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                            tumour cells; growth
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RESULT COLORS OF THE PROPERTY 
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Best Local
Matches
(GETH) Genentech Inc.

Dernyck RM, Goeddel DV;

WPI; 90-007474/01

P-PSDB; R04080.

Nucleotide sequence encoding transforming growth factor beta-3 -used as a probe, or to produce TGF beta 3; for inhibition of growth of normal and neoplastic cells, eg A549.

This sequence encodes porcine transforming growth factor-beta 3 (TGF-beta 3) polypeptide. The nucleic acid sequence encoding this subtype is useful as a probe or to produce TGF-beta 3 for both normal and neoplastic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence encoding transforming growth factor beta-3 -used as a probe, or to produce TGF beta 3, for growth inhibition of certain normal and neoplastic cells, eg A549.

Disclosure; Fig. 1b; 61pp; English.

Sequence encodes the 390 amino acid (AA) precursor transforming growth factor beta 1 (pre-TGF-beta 1) polypeptide. The 5' untranslated region of the TGF-beta 1 mRNA is 841 bases long, is purine rich and has a region of potential secondary structure. The TATA-like sequence in the 3' untranslated region of the gene is presumably a polyadenylation signal. Mature TGF-beta 1 comprises the C-terminal 112 AA's of pre-TGF-beta 1 and is cleaved at the Arg-Arg dipeptide preceding its NH2 terminus. The nucleic acid encoding the second subtype of TGF-beta (TGF-beta 3) is useful as a probe or to produce TGF-beta 3 for inhibition of growth of normal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO8912101-A.
14-DEC-1989.
08-JUN-1988;
08-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                                    31-MAY-1989 (first entry)
cDNA sequence encoding porcine TGF-beta
Transforming growth factor beta-3 (TGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q02819;
Q02819;
                                                                                                                                                                                                                                                                      14-DEC-1989.
08-JUN-1988; W01945.
08-JUN-1988; WO-U01945.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probe or to produce neoplastic cells.
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Dernyck RM, Goeddel DV;
WPI; 90-007474/01.
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31-MAY-1989
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llarity 100.0%;
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/label=pre-TGF }
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37. .113
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21-JUL-1989; 113414.
26-JUL-1988; JP-184538
(FARH) Hoechst Japan I
(FARH), Kato M;
                                     14-FEB-1990.
05-AUG-1989; 114505.
09-AUG-1988; JP-197144.
(FARH) Hoechst Japan Ltd.
Hashimoto T, Takahashi M;
WPI; 90-046218/07.
                                                                                                                                            Nucleotide sequence coding for hybrid human/bovine Human protein C: bovine protein C: Gla domain; bloo blood coagulation disorders; blood fibrinolsis acception of the control of the cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 11-14; 22pp; English.

This sequence encodes a protein which differs from human protein C at positions 156 and 157 (Lys-Arg is substituted by Asn-Ser). This creates a single uncleaved chain. The mutant product shows anti-coa activity when activated by the thrombin-thrombomodulin complex. It a lower activation rate and longer duration of activity compared withe native protein.

Sequence 1389 BP; 289 A; 419 C; 433 G; 248 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human protein C mutant with residues 156 has reduced activation rate and extended anti-coagulant.
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WPI; 90-031241/05.
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JP-184538.
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                                                                                                                                                                        blood anticoagulant; acceleration.
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                                                                                                                                                                                                                                                                       PT having Gla domain replaced by the bovine Gla to increase calcium PT binding activity and improve activation
PS Claim 3; Page 14; 17pp; English.

CC Also claimed are its encoded human protein C, the gene structure conty.

CC Also claimed are its encoded human protein are for of comman protein C having gamma-carboxylated glutamic acid residues (Gla CC domain) has been replaced by the Gla domain of bovine protein C or by an equivilent of this bovine protein sequence w.r.t. its calcium binding CC activity, and/or its enhanced protein C activity. PCS4 was constructed CC from pCS1. DNA coding for part of protein C as removed from pCS4 by CC sail digestion at a site just upstream of the leader sequence-coding CC sequence and again at a site corresp. to the 45th (Val) and 46th (Asp) CC sequence these Sail sites and introduced into E. coli K12/HB101. The transformants harbouring a plasmid in an appropriate orientation, named CC pCS8, were screened and cultivated. pHSG293 was also constructed which casymmetric cohesive ends as pCs8 by digestion. The pCS8 was digested CC with BSTX1 and the 2 kb fragment was lighted with BstX1 digested which same asymmetric cohesive ends as pCs8 by digestion. The pCS8 was digested CC with BSTX1 and the 2 kb fragment was lighted with BstX1 digested pHSG293. The lighted bNA was packaged in vitro in a lambda phage packaging mixt. and transfected into E. coli K12/Om206. The DNA was isolated and introduced into CHO cells which were cultured to produce the hybbid corporation C. activated protein C inhibits blood coagulation of accelerates blood fibrinolysis and is used for treating blood coagulation disorders. SQ Sequence 1383 BP; 288 A; 413 C; 442 G; 240 T;
                                                                                                                             Query Match
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Matches 7; Conserv
432 CTGCACG 438
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                                                                                                                         12.7%; Score 7; DB 1; Length 1383; 100.0%; Pred. No. 7.8e+03; tive 0; Mismatches 0; Indels
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32

Search completed: September 18, 1999, 00:33:26
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nucleic search, using sw model
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D15131 328 bp mRNA EST 20-JUL-1998 RICC0129A Rice callus Oryza sativa cDNA clone R, mRNA sequence. D15131 g286323 D15131.1 GI:286323 EST.
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D15980
D21672
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                                                        ALIGNMENTS
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D22924 RICC1794A R
D24072 RICR1057A R
D24444 RICR1932A R
D24493 RICR2912A R
D25754 HUMGS04121
D31273 HUML13202 H
D34553 CELK00BB2R
D35356 CELK00DDYF
D35439 CELK00ZGZF
D36191 CELK00ZGZF
D38092 RICR1916A R
D39092 RICR1916A R
D39092 RICR1916A R

6 MUSBO45A la
5 BNAESTE756
0 EST00201 H1
0 EST00222 H1
4 EST00333 H1
9 WEST00316 M
7 WEST00305 M
8 WEST00305 M

Description

D15131 RICC0129A D15980 RICC1808A D21672 MUS81D09 π

M79639 WEST00176 M M797637 WEST00304 M M79768 WEST00307 M M79768 WEST001102 E T00987 WEST011102 E T00997 WEST01718 E T01374 WEST02795 E T01374 WEST02795 E T01374 WEST02795 E T01374 WEST02795 E T05220 WEST02370 F T05217 EST04416 Fe T05573 EST04416 Fe T06573 EST04491 Fe T06602 EST04491 Fe T06602 EST04491 Fe T06603 EST04491 Fe T06604 EST06172 In T10525 horosomological months T10526 NIB1349 Nor T18018 036023 Cbsp T18018 036023 Cbsp

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RICC1808A Rice callus Oryza sativa cDNA clone R,
D15980
9287175
9287175
FCT
  Japan 305
Tel: 0298-38-7441
Fax: 0298-38-7468
Email: tsasaki@abr.affrc.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                     1 (bases 1 to 435)
Sasaki, T. and Minobe, Y.
Rice cDNA from callus
Unpublished (1994)
                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                   Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 328)
Sasaki,T. and Minobe,Y.
Rice cDNA from callus
                                                                               Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
2-1-2 Kannondai, Tsukuba
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: tsasaki@abr.affrc.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 0298-38-7441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1994)
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NotI; cDNA prepared from rice callus mRNAs
oligo(dT) as a primer and ligating to the S
of pBluescript II SK+ phagemid."
a 100 c 101 g 51 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="oryza sativa"
/strain="cultivar Nipponbare,
/db_xref="taxon:4530"
/clone="R"
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a SalI-NotI site
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10; Conserv
                                                                                                                                                                                                                                                                                                                                                    Contact: Kazunori Shimada
Department of Medical Genetics, Division of
Research Institute for Microbial Diseases, C
3-1, Yamadaoka, Suita, Osaka, 565, Japan
Tel: 06-879-8325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 405)

Nishiguchi,S., Joh,T., Horie,K., Zou,Z., Yasunaga,T. and Shimada,K. A survey of genes expressed in undifferentiated mouse embryonal carcinoma F9 cells: characterization of low-abundance mRNAs J. Biochem. 116, 128-139 (1994)
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MUS81D09 mouse
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llarity 100.0%;
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                                                                                                                                                                                          /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="81D09"
/clone_11b="mouse embryon
a 74 c 117 g 84
148
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1 97 c 117 g 112 t 1 others
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/strain="cultivar Nipponbare, sub_species Japonica"
/db_xref="taxon:4530"
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Osaka University
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221 TCTCCTTAAG 212
                                                                                               1 (bases 1 to 347)
Minobe,Y. and Sasaki,T.
Rice cDNA from root
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                     D24072 347 bp
RICR1057A Rice root
                             Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
                                                                                                                                                                                                                     Oryza sativa
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                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
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National Institute of Agrobiological Resources
Rice Genome Research Program
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Sasaki, T. and Minobe, Y.
Rice cDNA from callus
Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; Lillopsida; Poales;
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D22924
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     [baraki
                   2-1-2 Kannondai, Tsukuba
                                                                                                                                                                      Poaceae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Rice callus"
/rote="Vector: pBluescript II SK+; Site_1: SalI; Site_2:
NotI; cDNA prepared from rice callus mRNAs by using
NotI; cDNA prepared from rice callus mRNAs by using
oligo(dT) as a primer and ligating to the SalI-NotI site
of pBluescript II SK+ phagemid.
a 122 c 117 g 61 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryza sativa"
/strain="cultivar Nipponbare, sub_species Japonica"
/db_xref_"taxon:4530"
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Pred. No. 4.3e+03;
Mismatches 0;
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108 TCTCCTTAAG
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                         TCTCCTTAAG
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                                                  10;
                                                                                                                                                                                                                                                       Tel: 0298-38-7441
Fax: 0298-38-7468
Email: tsasaki@ab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity 100 10; Conservative
                                                                                                                                                                                                                                          Email: tsasaki@abr.affrc.go.jp
PROJECT ='RGP'.
                                                                                                                                                                                                                                                                                                                               Contact: Takuji Sasaki
National Institute of Agrobi
Rice Genome Research Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa
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Minobe, Y. and Sasaki, T.
Rice cDNA from root
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.
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Fax: 0298-38-7468
                                                              Similarity
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r ='RGP'.
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                                                                                                                       /clone_lib="Rice root"
/note="Prepared from seedling
80 c 106 g 113 t
                                                                                                                                                                           /organism="Oryza sativa"
/strain="Nipponbare, sub_species
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Rice root"
/note="Prepared from seedling root.
60 c 90 g 95 t
                                                                                                                                                                /clone="R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism-"Oryza sativa"
/strain-"Nipponbare, sub_species Japonica"
/db_xref-"taxon:4530"
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Pred. No. 4
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4.3e+03;
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                                                                                                             y root.
2 others
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                                                                                                                                                                                                                                                                                                                                                                                108 TCTCCTTAAG
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                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 205)
Okubo,K., Yoshii,J., Yokouchi,H., Kameyama,M. and Matsubara,K.
Global analysis of gene expression in colon mucosa: a large scale random cDNA sequencing analysis
   Contact: Okubo, K., Itoh, K., Institute for Molecular and Osaka University
3-1 Yamada-Oka, Suita, Osaka 5
                                                                                                                                                                                                                                                                                  HUMGS04121 Human colon mucosa Homo sapiens cDNA clone cm1888 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 0298-38-7468
Email: minobe@rtcs0.riken.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Yuzo Minobe
National Institute of Agrobiological Resources
Rice Genome Research Program
2-1-2 Kannondai Tsukuba
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Minobe,Y. and Sasaki,T.
Rice cDNA from root
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales;
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RICR2912A Rice root (
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Poaceae; Oryza.
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Yamada-oka, Suita, Osaka 565, Japan
                                                                                                                                                                                                                                                                          sequence
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/note="Prepared from seedling root. "
54 c 81 g 85 t 2 others
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/strain="Nipponbare, sub_species Japonica"
/db_xref="taxon:4530"
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                          Yoshii, J., Yokouchi, H.
Cellular Biology
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                                       and Matsubara, K.
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414 bp mRNA
CELK008B2R Yuji Kohara unpublished cDNA
clone yk8b2 3', mRNA sequence.
clone yk8b2
D34553
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10; Conserv
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D31273.1
                                                                                                                                                                                                                                                                                                 Email: yusuke@ims.u-tokyo.ac.jp
Insert Length: 596 Std Error:
High quality sequence stop: 157.
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Fax: 81-3-5449-5433
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 310)
Sudo, K., Chinen, K. and Nakamura, Y.
                                                                                                                                                                                                                                                                                                                                                                               University of Tokyo
                                                                                                                                                                                                                                                                                                                                                                                         Contact: Yusuke Nakamura
Institute of Medical Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="cm1888"
/clone_lib="Human colon mucosa"
/note="Adult male, tissue_type = cc
a 44 c 51 g 52 t 5
                                                                                                                                                                                                                         /clone_lib="Human fetal lung"
86 c 78 g 78 t
                                                                                                                                                                                                                                                organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI:644153
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                                                                                                                                                           100.0%;
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                                                                                                                                              Score 10; DB 20;
Pred. No. 4.3e+03;
; Mismatches 0;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                 Tokyo 108,
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hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from a human fetal lung cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
                    EST 05-AUG-1994
Caenorhabditis elegan
                                                                                                                                                                                                                          1 others
                                                                                                                                                                       Length 310;
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5 others
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                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia;
                                                                                                                                                0,
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                    elegans cDNA
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KEYWORDS
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D35356/c
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KEYWORDS
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Best Local s
Matches 10
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TCTCCTTAAG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                             D35356 315 bp mRNA CELK001DYF Yuji Kohara unpublished clone ykld11 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda;
                                                                                                                               Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411,
Tel: 0559-75-0771
                                                                                                                                                                                             Contact: Yuji Kohara
                                                                                                                                                                                                                             Toward an expression map of the C.elegans genome Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                   D35356
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Eukaryota; Metazoa; Nematoda;
Rhabditina; Rhabditoidea; Rhal
1 (bases 1 to 414)
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EST.
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Unpublished (1994)
                                                                                                                                                                                                                                                                         Kohara,Y., Mitsuki,H., Nishigaki,A., Motohashi,T.,
                                                                                                                                                                                                                                                                                              Rhabditina; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                 D35356.1 GI:525357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ykohara@ddbj.nig.ac.j.
Location/Qualifiers
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                                                                                                                                                                                                                                                             abara, H.
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                                                                            ykohara@ddbj.nig.ac.j.
Location/Qualifiers
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/note="dev_stage=varied, sex=Hermaphrodite male,
tissue_type=whole animal"
92 c 109 g 112 t 2 others
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
/clone="yk1d11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
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Pred. No. 4.4e+03;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                           Dda; Secernentea; Rhabditia; Rhabditida;
Rhabditidae; Peloderinae; Caenorhabditis.
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Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                                                             Japan
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                                                                                                                                                                                                                                                                           Sugimoto, A. and
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RESULT 1
D36191/c
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SOURCE
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D35439/c
                                           ACCESSION
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Best Local 9
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Best Local
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                                                                                                                                                                352 TCTCCTTAAG
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g525409
D36191.1
EST.
                                             D36191 330 bp mRNA CELK002GZF Yuji Kohara unpublished clone yk2g12 5', mRNA sequence. D36191
                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 0559-75-0771
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Caenorhabditis elegans
Eukaryota; Metazoa; Nem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D35439 360 bp mRNA EST 08-AUG-1994 CELK020E5F Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA clone yk20e5 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene Library Lab
                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ykohara@ddbj.nig.ac.j.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Yuji Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rabara,H.
Toward an expression map of the C.elegans genome
Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhabditina, Rhabditoidea; Rhabditidae; Pelo
1 (bases 1 to 380)
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                                                                                                                                                                                                                                                                                                             /organism="Caenorhabditis elegans"
/strain="CB1499 him-8(e1489)"
/db_xref="rtaxon:6239"
/clone="yk20e5"
/clone="Tuji Kohara unpublished cDNA"
/clone="Tuji Kohara usex-Hermaphrodite
/note="dev_stage=varied, sex-Hermaphrodite
tissue_type=whole animal"
a 77 c 79 g 90 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Yuji Kohara unpublished cDNA"
/note="dev_stage="varied", sex=Hermaphrodite male,
tissue_type=whole animal",
101 c 68 g 62 t 2 others
              GI:525409
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Pred. No. 4.3e+03;
Pred. no. 4.3e+03;
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Pred. No. 4.3e+03;
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                                                                       CDNA
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Peloderinae; Caenorhabditis.
                                                                    EST 08-AUG-1994
Caenorhabditis elegans
                                                                                                                                                                                                                                                   Length 360;
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                                                                                                                                                                                                                                                                                                                                              male,
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KEYWORDS
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AUTHORS
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D38872
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Best Local
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                                                                                                                                                                                                                                                                                                          Oryza sativa

Gukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Poaceae; Oryza.

1 (bases 1 to 444)
Sasaki, T., Miyao, A. and Yamamoto, K.
Rice cDNA from callus 1995
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g568037
D38872.1
                                                                                                                                                                                                                                  Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D38872 444 bp mRNA EST 11-NC RICC1810A Rice callus Oryza sativa cDNA, mRNA sequence. D38872
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Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
1 (bases 1 to 330)
Rohara, Y., Mitsuki, H., Nishigaki, A., Motohashi, T., Sugimoto, A. and
                                                                                                                                                    Japan 305
Tel: 0298-38-7441
Fax: 0298-38-7468
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ykohara@ddbj.nig.ac.j.
Location/Qualifiers
1. .330
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                                                                                               tsasaki@abr.affrc.go.jp.
Location/Qualifiers
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/organism="Oryza sativa"
/strain="cultivar Nipponbare, sub_species Japonica"
/db_xref="taxon:4530"
/clone_lib="Rice callus"
/note="Vector: pBluescript II SK+; Site_1: SalI; Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Yuji Kohara unpublished cDNA"
/note="dev_stage=varied, sex=Hermaphrodite male,
tissue_type=whole animal"
89 c 75 g 72 t 15 others
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/strain="CB1489 him.8(e1489)"
/db_xref="taxon:6239"
/clone="yk2g12"
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Search completed: September 17, 1999, 21:27:55 Job time: 14259 sec
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RICR1916A Rice
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Fax: 0298-38-7468
Email: tsasakiebtr.affrc.go.jp.
Location/Qualifiers
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Sasaki,T., Miyao,A. and Yamamoto,K.
Rice cDNA from callus 1995
                                                                                                                                                                                                                                                                                                                                                                                                       National Institute of Agrobiological Resources Rice Genome Research Program
                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Takuji Sasaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1995)
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ilarity 100.0%;
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/note="Prepared from seedling
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/strain="Nipponbare, sub_species Japonica"
/db_xref="taxon:4530"
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                                 Direct Submission
Submitted (04-MAY-1998) Kletzin A., Institut fuer Mikrobiologie und Genetik, Technische Universitaet Darmstadt, Schnittspahnstrasse 10, Darmstadt, 64297, GERMANY
2 (Dases 1 to 5598)
The succinate dehydrogenase from the extremely thermophilic archaeon Acidianus ambivalens
                       Kletzin, A.
                                                                                                 Kletzin, A.
                                                                                                                                    Acidianus ambivalens.
Acidianus ambivalens
                                                                                                                                                       2Fe-2S-ferredoxin; 4Fe-4S-ferredoxin; flavoprotein; iron-sulfur protein; nagD gene; ORF1; ORF2; ORF3; sdhA gene; sdhABCD operon; sdhB gene; sdhC gene; sdhD gene; succinate dehydrogenase.
                                                                                                                                                                                                                                      ORF1 and
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Acidianus ambivalens
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                                                               /translation="MEKLSYDAIVIGGGLAGLMAAHEIAVSGYKVAVISKVFPTRSHS
SSAEGGIAAVIEGNSDPNDNPDYMTVDTIKGGDFLVDPDAAELLSQKSGEIVRIMESW
GTLFNRQPDGRVAVRYEGGGTFVPTRVGDKLEMALLHIEGRVSGLDIDEYNEWFAL
DLIRDKRVVGVVAMEKKSMTVVFFKARAIVMATGGMGHLYAHSTNAVINTGDGYAMA
LRAGAALKDEFFVQHETALVESDILISEAARGEGAILINNKGERFMARYAFRRLDLA
LRAGAALKDEFFVQHETALVESDILISEAARGEGAILINNKGERFMARYAFRRLDLA
                       PRDITSRAIITEIREGRGFPGGYVGLDLRHLGEDYIKERLALAYEAAKNFAGVDATQE
PIFVRPAQHYYMGGIDVDITGQNPDLVGLFAAGEAACVSVHGANRLGSNSLLETLVFG
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/translation="MLDYDLIISDVDGVIVREGEPIWENIFAIRKLKEEGKKIILVTN
NGGTSRVLLSGOLNYLGLEITPNDIITSGLSAAIYMKRNTKVKGVYVIGEEGLVEEMK
NFNFRYLSTEEVEENNPDAVVLGLDRLATYDKLSTGMRCVARGSMFIVTNMDRLWPSK
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/translation="MDSEKLTRKYYSKLISLPSARILLFIDVIEGAIIAFRGLEIGIL
FFYSFLIYSVSLLAILGKRIRTALTLISIFSA"
{	t RETGRAVAKFLSEHKEEDSNSLDKEAEKVVDDAYKFVKSESGVHFGEILNKLRNVMWE}
                                                                                                                                                                                                                                                                                                    /evidence=experimental
/product="succinate dehydrogenase, subunit A"
/protein_id="CAA06780.1"
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/note="flavoprotein"
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/protein_id="CAA06778.1"
/db_xref="pi:e1313720"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(<1. .229)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="hypothetical protein"
/protein_id="CAA06779.1"
/db_xref="PID:e1313721"
                                                                                                                                                                                                       'db_xref-"SPTREMBL:073937"
                                                                                                                                                                                                                            'db_xref="PID:g3378540"
'db_xref="GI:3378540"
                                                                                                                                                                                                                                                                                  'db_xref="PID:e1313722"
                                                                                                                                                                                                                                                                                                                                                                                    transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                               'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'gene="sdhA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'db_xref="GI:3378539"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="nagD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db_xref="G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        db_xref="PID:g3378537"
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'transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="ORF1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'db_xref-"taxon:2283"
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'isolate="Lei 10"
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/product "succinate dehydrogenase, subunit B"
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SKLAQEVLRKKGIIQ"
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GFLDEYNEKAHVALNLRNLSTVERMGMDKMYTPCSVCLQSHRLAAYKYNENKDLRKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3045. .3989
/gene="sdhB"
                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(5231.
/note="ORF1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIKDLIVDWTDFYNRMFKVKPRLYPSKEVLEGKAEHRLKPEDQRELWKFEQCIWCGLC
VSACPSVKNDPEFLGPAAHAKGYRFLADPRDTIFDERLKILIDSAWRCTYCYQCFNVC
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MMGKVHLRLDGDLYVHIISKIPFNWKDRVKDLKIKGSIEDAAGGLMWIKTTPEDMYSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="succinate do
/protein_id="CAA06783
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RTALERKESRGAHYRTDYPERDDINWLKHTIAYLKGETVEITYKPVRITRWKPEPRVY
                                                                                                             'db_xref="PID:g3378544"
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'db_xref="GI:3378543"
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protein_id="CAA06782.1"
db_xref="PID:e1313724"
db_xref="PID:g3378542"
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                                                               b_xref-"GI:3378544"
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xref-"SPTREMBL:073941"
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translation-"DNIPYPLIKVIKNAKSKDVIKMIEYIGKIRGGGGTDISRSVISA

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SOURCE
ORGANISM
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AUTHORS
TITLE
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AB008831
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takeo,M., Fujii,T., Takenaka,K. and Maeda,Y.
Cloning and sequencing of a gene cluster for the meta-cleavage
pathway of aniline degradation in Acinetobacter sp. strain YAA
J. Ferment. Bioeng. 85, 514-517 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (13-NOV-1997) to the DDBJ/EMBL/GenBank databases. Masahiro Takeo, Himeji Institute of Technology. Department of Applied Chemistry, 2167 Shosha, Himeji, Hyogo 671-22, Japan (E-mail:takeo@chem.eng.himeji-tech.ac.jp, Tel:0792-67-4893, Fax:0792-67-4891)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acetoaldehyde dehydrogenase; 2-oxopent-4-dienoate hydratase; 2-hydroxymuconic semialdehyde hydrolase; 2-hydroxymuconic semialdehyde dehydrogenase; catechol 2,3-dioxygenase; small ferredoxin-like protein; aniline dioxygenase reductase component; aniline dioxygenase beta-subunit; aniline dioxygenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Microbiology 143
9717776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Acinetobacter sp. (strain:YAA) DNA.
Acinetobacter sp.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AB008831 10498 bp DNA BCT 05-JUN-1998 Acinetobacter sp. genes for aniline dioxygenase subunits and reductase component, partial and complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fujii,T., Takeo,M. and Maeda,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Acinetobacter sp. strain YAA
Microbiology 143 (Pt 1), 93-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Moraxellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lasmid-encoded genes specifying aniline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     axellaceae; Acinetobacter. (bases 1 to 10498)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CEDIKEGHVKGVSEVIILTDGEDKIAETTVRRSLKDANATLISVMIRGDNADLRRVSD
TYLVVYKLDQNDLLKVVEA"
a 849 c 1203 g 1547 t
                             /organism="Acinetobacter sp."
/strain="YAA"
                                                                                                                                                                                                                                         /gene="atdA3"
                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                          ʻgene≖"atdA3"
                                                                                                                                                                                                                                                                                                                                      'db_xref="taxon:472"
                                                                                                                                                                                                                        codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 10; DB 1;
Pred. No. 2.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oxidation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 5598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="aniline dioxyge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="aniline dioxyge
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1902. .2828
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PGLITKESFAGSVSDDNGDTVESSAEKDVTVNFMLNGIKNSVMCSEDDFILNEIIKAG
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                                                                                                                                                                                                                                     NEYTTTKAMR"
                                                                                                                                                                                                                                                             CGLCKVTVREGDYECGKMSRVHAPPEALAQGEVLACRIYPLSDLIIECRPRQSAAGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  {	t NSLKIKRLGTFGLGVFGSASYIDDIVDEFGKDALRDKSDLIKTGIGFSYKPHDFVFGL}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="munukdlsikiydpsavnlayygeikgysdyfwnlsnigepald
HKINMFLTKEARLLDQQCFDEWLTLFLEDGCYWIPGSMPAASPASEATYEFHDIRRLK
DRIVRLQTGFAYSQIPVSKINRILGAPEVWAVPGSSEGFLVRTSFIVFESRDGKSQVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PQNWDRDFVFFAGGSGITPVISIIKTALNRHKNRIKLFYANSSESSIIFHKELKDLCL
                                                                                                                                                                                                                                                                                                                                                                                /product="small ferredoxin-like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MRCVLKHSSSYDNANWDNVKAFLALYRAKDYEAAAESLGVDGST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGWYGYVIIKDNDELKIKMKQINLNDCLSPQGNNSFFL"
                                                                                               'transl_table=11
                                                                                                                                                                                                                                                                                translation-"MGESYQITEQCSGQRFPCKAGQSVLKAMEQQGLECAPVGCRGGG
                                                                                                                                                                                                                                                                                                                                                       db_xref="PID:d1024433"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVSIPFVLVNQFSDVLIAFRKIYPEFTFDISSDARFVDLEREGFDFAIRLARPISNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "translation="MNTLKFRVIDKIAETKESFSFVLKPLDGVLAEHSPGKYLPIKIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene≖"atdA5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene≖'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WLISRLDMKSDWQVVLGNMLSAKSKEMEVS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .1895
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1551 1 "
                                                     ,3-dioxygenase"
5.1"
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Query Match
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GPCVHVCPFDTEEEAIELANSLPYGLASAIWSBHITRAHRVAGGIEAGIIWVNSWFLR
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LEQVDLVGNSFGGGLALALAIEHPQRRRLVLMGSVGVSFPITKGLDEVWGYEPSIENN
RRLMDVFAYNKNLLIDELAEMRYQASVRPGFQESFAAMFPAPRQPGLDNLASPEEDIR
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4187. .5647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'db_xref-"PID:g2627155"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="2-hydroxymuconic semialdehyde dehydrogenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="atdC"
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      100.0%;
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   Score 10;
DB 1;
Length 10498;
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AUTHORS
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KEYWORDS
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AB016431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tennodai 1-1-1, Tsukuba, College of Medical Technology.
Tennodai 1-1-1, Tsukuba, Ibaraki 305, Japan
(E-mail:tohta@sakura.cc.tsukuba.ac.jp, Tel:+81-298-53-3454,
7, (2:1-28-53-3454)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (21-UUL-1998) to the DDBJ/EMBL/GenBank databases. Ohta, University of Tsukuba, College of Medical Technology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohta, T., Kuroda, M. and Hayashi, H. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus (strain:912) DNA. Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AB016431.1 GI:4126670 CzrB; czrA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus.
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IEHDLLHLNIHHMTIQLETPNHKHDESIICSGTHSHSHNHHAHHHAHVH" complement(1703. .2023)/gene="Czra"
                                                      SILIVFEAIKRFFVPSEVQSKEMLIISIIGLIVNIVVAFFMFKGGDTSHNLNMRGAFL
HVIGDLLGSVGAITAAILIWAFGWTIADPIASILVSVIILKSAWGITKSSINILMEGT
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complement(671..716)
complement(724..1701)
                                                                                                                                                                                                                                                                                                                     complement(724. .1701)
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                                                                                                                                                                                                                                                                                 /function="Zinc resistance"
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                                                                                                                                                                                                                                                                                                                                                                                                                                     FTDLFIAFKKGNYLKSVLIGLVSIAMIIVLSLLTSLLYKLFSPVSEMIMNS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(<1.
                                                                                                                                                                                                                                                                                                                                                            'gene="czrB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MFTYFKSAFKNAKPQLLITLIYALIAFAVIAVVYLLANFQLAKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Staphylococcus aureus"
/strain="912"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transl_table=11
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// Mismatches 0;
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                                                         AUTHORS
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               Smith,D.R., Doucette-Stamm,L.A., Deloughery,C., Lee,H.-M.,
Dubois,J., Aldredge,T., Bashirzadeh,R., Blakely,D., Cook,R.,
Gilbert,K., Harrison,D., Hoang,L., Keagle,P., Lumm,W., Pothier,B.,
                                                                                                                                                                                                                      AE000810 10446 bp DNA BCT 16-APR-1998 Methanobacterium thermoautotrophicum from bases 172512 to 182957 (section 16 of 148) of the complete genome.
AE000810 AE000666
                                                       Smith, D.R.,
                                                                                                                             Methanobacterium thermoautotrophicum. Methanobacterium thermoautotrophicum
                                                                                                                                                                                      AE000810.1
                                                                                           Methanobacterium
                                                                                                            Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                     (bases 1 to 10446)
th,D.R., Doucette-Stamm,L.A.,
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 Spadafora, R., Vicare, R., Wang, Y.,
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ANIKHYVMVSTYDSRRQAFDDSGDLKPYTIAKHYADDYLRRSGLNYTILHPGALINAA
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HENGQYGKSECWYIIDAEEDAEIVIGTLAESREEVANHVQHGTIESILRYIKVKPGEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(2034..2039)
complement(2064..2069)
complement(2087..2092)
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/db_xref="PID:g4126675"
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/db_xref="PID:d1037674"
/db_xref="PID:g4126673"
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/transl_table=11
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                                                                                       /db_xref="PID:g2621280"
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2682. .3452
                                                                                                                                            /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAB84736.1"
/db_xref="PID:g2621278"
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/strain="delta H"
                                                                                                                                                                                                                                                                          .858. .2625
'gene="MTH232"
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db_xref="GI:2621279"
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053. .1781
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                                                                                                                                                                                                                                      note="function Code:14.01 - imilar to, sp:LN:YD72_METJA
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                                                                                                                                                                                                                                                                                                                MTH232"
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Submitted (10-AUG-1997) Genomics and Technology Development, Genome Therapuetics Corporation, 100 Beaver Street, Waltham, MA Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics J. Bacteriol. 179 (22), 7135-7155 (1997) Gibson,R., Jiwani,N., Caruso,A., Bush,D., Safer,H., Patwell,D., Prabhakar,S., McDougall,S., Shimer,G., Goyal,A., Pietrovski,S., Church,G.M., Daniels,C.J., Mao,J.-i., Rice,P., Nolling,J. and

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/translation-"MDTKNKIIIGLFIVILGLSVVTYENYITNSQNVFVGEKHVLLLC ADPGEPROGGAVDMAFIITMNEGNITNYTAVYPHNVAHPTAQSPASLRAQGVSRWLL HDALWENDTERGARLAQSETVEYNTGIKTDTVVTPQAVDGILQSIGPVYVEGOGYVS GNSIQFLREEQQQGSSRGVAIQSLMRAIFNATKDRSKYLAMVNAGLQQYQQGNIVVVP

/note="Function Code:14.01 - Unknown, Conserved protein; similar to, pir:LN:B64471 AC:B64471, p()=3.1E-32, pid=37%"

/translation="MYGSEGAMRIVAGUGENRNMERAASLADFEVDLVHSEEEFIEE LRRGAANVRGSLPAANIMAELKKGGPLNRASWIEVGANGFLLAPVGIDEGRTVDDRF KLAVSASEFLRKTGEEFRVGVISGGERGDLGRSEFVDRSIHEGEEFLTSMIKDKV KVAV HILLIEEAVADGCNVIIAPDGITGNLIFRSLVLVGTARSYGAVALGFDGIFVDTSRSQ

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similar to, pir:LN:A64438 AC:A64438, p()=8.3E-46, pid=48%"
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IMVGINTVLADDPRLTVHRVDAAFGDNFVLVHVHSMARTPPFERVSINDEAFTVIGVSE
SAPPERVAELAKRAETVVAGTRRVDLHILLERLHGMGTERLMLEGGSTLNYSMLTGGL
VDEVRVCIAPMIVGGRDARTLVDGEGIDEMADAIRLELKRSYTLGEDLIVEYTVKG"
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GNRRALELASLNPGFICPTMGFHPVDASKARQDLIGEVVSQIESNIDLIVAVGETGMD
FHHTRDEEGRRRQEETFRVFVELAAEHEMPLVVHARDAEERALETVLEYRVPEVIFHC
/codon_start=1
                                                /note="Function Code:9.10 · Metabolism of Cofactors and Vitamins, Porphyrin and chlorophyll metabolism; simila: to., pir:LN:564721 AC:584721, p()=1E-97, pid=24%"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MYFMLEDIYERIVRIREEGCRECLKVVCRMDDFQFNQLMSRLDL
QIEITSRYSPFVRPALDPMISTELGVYRGDDBNIGRLLGYPECCIRSFSRNTRYALDG
EHLAEVSELDIPEGKCALIMPSGFIPCSLRCQEAWERKLIGFADRDEFRRILELEDEL
MMRLPHFHLAYDEYFEKIYLE"
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Vitamins, Riboflavin metabolism (B2); similar to,
Vitamins, Riboflavin metabolism (B2); similar to,
Vitamins, Riboflavin metabolism (B2); similar to,
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/gene="MTH234"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Function Code:14.01 - Unknown, Conserved protein; similar to, pir:LN:E64497 AC:E64497, p()=8.6E-44, pid=36%"
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VYSRGVLDLKTRELLTLAALTVLRADDQLKSHVRGALNAGCSKDEIIEVMIQMAVYAG
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'protein_id="AAB84742.1"
'db_xref="PID:92621284"
'db_xref="GI:2621284"
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/protein_id="AAB84741.1"
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/protein_id="AAB84740.1"
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to, sp:LN:DC4C_ACICA AC:P20370, p()=1.2E-12, pid=28%"
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/protein_id="AAB84739.1"
/db_xref="PID:g2621281"
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Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics J. Bacteriol. 179 (22), 7135-7155 (1997)
                                                                                                                                                                                                     Smith, D.R., Doucette Stamm, L.A., Deloughery, C., Lee, H.-M., Dubois, J., Aldredge, T., Bashirzadeh, R., Blakely, D., Cook, R., Gilbert, K., Harrison, D., Hoang, L., Keagle, P., Lumm, W., Pothier, B., Qiu, D., Spadafora, R., Vicare, R., Wang, Y., Wierzbowski, J., Qiu, D., Spadafora, R., Vicare, R., Wang, Y., Wierzbowski, J., Gibson, R., Jiwani, N., Caruso, A., Bush, D., Safer, H., Patwell, D., Prabhakar, S., McCougall, S., Shimer, G., Goyal, A., Pietrovski, S., Necougall, S., Shimer, G., Goyal, S., Shimer, G., Shimer, G., Shimer, G., Shimer, G., Shimer, G., Shimer, G., Goyal, S., Shimer, G., Shimer
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Methanobacterium thermoautotrophicum
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                                                                                                                                                                                 Church, G.M., Daniels, C.J., Mao, J.-i., Rice, P.,
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metabolism; similar to, pir:LN:B64382 AC:B64382,
p()=7.3E-70, pid=31%"
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GRYPETVAVDIGDVISTGGGSIAAIFYFLGVRPIYESGALIGTEIIPLESLGRPRIDV
VISDFHNFRGAIPATWDVIDNTIKRIVNLNESSEMNYVRKHYLAMKAGIYAELVAAGM
NTSEADANADRLARTRIFGLPPGADPHGAGVDRILMSRDDWTPEQLAETYLSYYSYAY
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DALVDVASPDVWRRIADTFLFDSSVRSQFDPSALQMIARYVRQAHTRGLVSLSQEELV
AISEMLGEKSGSDGNDQGTTTTPHGGTTGGSATSGGRTGTGSPGLSPGVSGAISMDSQ
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SLSNILLAMRAAGHSTGNGNLTEEYIYELINRAGRNPRNMTQTELRKLVDAGCITIPV
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PLFYFLQTSLDDY INSTRQQGLRGLEY YMLSMF EMQGR I EP IL IGGSR I SGPDPLTGV
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FKNDLKTVDIFFIFTRPGYPTTGMSYGTEFDALVDLQAIAASLKPGARIFVLGPVKPN
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/protein_id="AAB84743.1"
/db_xref="pID:g2621285"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MNYDKSQGGENMKRFLLIALILLISVPSVSAADNNTTSNTTES"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGVNVTNLPAYGPVAAPALSRENIKRTLLEVLRLSGAVNLTANDTKLVPGMQDFLYH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .10365)
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bases 571179 to 587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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/translation="MLYKIKDCFSVIEMPELLSPAGDFSSLMAALRSGADAVYIGLEG
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LDPDLIREEIENAIIRAGLGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTLTGIRGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Function Code:4.01 - Nucleotide Metabolism, Purine
metabolism; similar to, sp:LN:PURL_METJA AC:Q57657,
p()=6.2E-121, pid=52%"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GISTFNGNDILTHRGMGLYCDYFNPEKLEELKGNYGIGHYRYSTTGESRIENSQPFWS
EFQGGKIAIAHNGDIINSMELREELEEEGHNFYSTTDSEYICHLLSREYDEKPNNIYS
IKRYSEQLYGSYSLYYLLNQDLYVYRDPYGIKPLAFARKGSTQIYASETYAFDYIGAE
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/gene="MTH646"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(1363. .2787)
/gene="MTH646"
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EDRVRPGDLVYRRVKRPDS"
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DLEVSASEAVRSYLLSPADLCMIEHIPELVDAGVHALKIEGRGRPADYVATVTGVYRE
ALDRYLSGEWRFEERWLSELRKVFNRGFSTGFYFSEPENGSSGNISEYIKEDIGEVVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(103. .1338)
/gene="MTH645"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Function Code:14.00 - Unknown, ; similar to, pir.LN:S61081 AC:S61081:S60817, p()=0.0098, pid=10%"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(2803. .3645)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEALYREHPANADVVVPVPDSSIPAAIGYSRASGIPYGEGLIKNRYVGRTFIMPTQEE
RETAVKLKMNPIRSELEGKRIVLIDDSIVRGTTSRALIDIIRDAGAEEIHLRIGCPPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HVRDVQPGEILHLNRGKSYWVANAPNTRRAHCMFEYVYFARPDSVIDGRNVYRVRLNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="amidophosphoribosyltransferase"
/protein_id="AAB85151.1"
/db_xref="pib:92621728"
/db_xref="GI:2621728"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(103. .1338)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Methanobacterium thermoautotrophicum"
/Strain="delta H"
/db_xref="taxon:2166"
/clone="MTH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="MTH647"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDGDYPTPLPSDISEYEAMRSCSR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KSPCYYGIAMATKKELIASTRNVEEIRRIIGVDSLGYLSIESLVECIGIKKGFLCTGC
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/db_xref="PID:g2621727"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ′product≖"collagenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="Function Code:10.12 - Metabolism of Macromolecules,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="MTH645"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . .16189
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                                                                                                                                                                                                                                                                                                                                                                                         transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="MTH647"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MLGESEVRDKCGIVGIYSQDKKTGVASQIYYALYALQHRGQESA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
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LRRLDECIPELYPEIGMIGLKEAREANREIDKAARICERDGVNPDPVLGQRILDDAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Function Code:14.01 - Unknown, Conserved protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similar to,
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AE000880/c
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                                                                        AUTHORS
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MEDLINE
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Best Local
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                                                                                                                                                                                                                                 TITLE
                                                     JOURNAL
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                                                                                                                                                                                                                                                                         Smith, D.R., Doucette-Stamm, L.A., Deloughery, C., Lee, H.-M., Dubois, J., Aldredge, T., Bashirzadeh, R., Blakey, D., Cook, R., Gilbert, K., Harrison, D., Hoang, L., Keagle, P., Lumm, W., Pothler, B., Giu, D., Spadafora, R., Vicare, R., Wang, Y., Wierzbowski, J., Gibson, R., Jiwani, N., Caruso, A., Bush, D., Safer, H., Patwell, D., Spadafora, S., McDougall, S., Shimer, G., Goyal, A., Pletrovski, S., Church, G.M., Daniels, C.J., Mao, J.-i., Rice, P., Nolling, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanobacterium thermoautotrophicum
Methanobacterium thermoautotrophicum
Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
Submitted (10-AUG-1997) Genomics and Technology Development, Therapuetics Corporation, 100 Beaver Street, Waltham, MA 02154-8448, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AE000880 10072 bp DNA BCT 16-APR-1998 Methanobacterium thermoautotrophicum from bases 1008430 to 1018501 (section 86 of 148) of the complete genome.
                                                                           Direct Submission
                                                                                                Smith, D.R.
                                                                                                                                                        98037514
                                                                                                                                                                        deltaH: functional analysis and comparative J. Bacteriol. 179 (22), 7135-7155 (1997)
                                                                                                                                                                                                                           Complete genome sequence of Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                            Reeve, J.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methanobacterium
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                                                                                                                           (bases 1 to 10072)
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GGPRTVAELECKPFTALIRGSGYPGOSGFFRTCERDVTDLRTREGHCLKLTHDHRVLV
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SMELJARERGSRPEFKSGIMDLOGFECURNATLITTIAFTGSLSTIAGTSSGIEDLFAVS
ETRNILIGRSFHELHPLFKTMAGRLDKRSLEAIESRGSLRGVPGVPARIRRLFVTAHEI
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VDEVLRFPEYAGSCRDMTCPN"
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LRDMAIIHKSGGGVGFSFSRLRPRGDIVASTMGVASGPVSFMRIFDVAVDVIKQGGRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="MTH653"
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similar to,
pid=35%"
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GVTSVFTSGDVGGSPTRLEEXISDCVLHLTHTFEGGVGTRHLRIVKYRGSGHGLNRY
FFIITRRGASIFPITSISLESYISDEPADQIKGGFYRTSGNAKLLIKSTGAG-
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GGLTAILTYNGDLINDFNDDSYLVDPVTGLAGAGGSPETRNENAKHLFIRLTDFLKG
RGITSITSYLLASPFTATTTELKLSSLIDTWIVLESIRANGEYRRSLRILKSRGMNHS
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Detoxification; similar to,
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3504. .3758
                                                                                                                                                                                                            SSVAEVRFTDRGILIKGGSW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Function Code:14.01 - Unknown,
similar to, gp:GI:g1653005 LN:D90910,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MDHIIETEDIKKKYDEFLAVKGVNLRVPEGSIYGVLGPNGAGKT
TLISMLCTILRPTGGRGTVNGYDIVRDARKVRESIGIVFQSRALDDILTGREHLEMHA
ALYGVPRDVRDRRIEEVLELIALGDKADEYVKTYSGGMKRALEIGRGLIHHPRVLFLD
EPTLGLDPQTRESINRYIEKLNREEDVTVLLTTHYMEEADKLCDEVAIMSHGEIIKAD
SPGNLKRELGADTITVRVDRARGFHEILEKQDYVKEAYLMDDEVKVLVERGENLVPEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="daunorubicin resistance); Function Code:12.02 - Cell Processes, Transport of carbohydrates organic acids alcohols and lipids; similar to, gp:GI:e283950:g1707742, p()=3.3E-67, pid=31%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(1047. .1985)
/gene="MTH1093"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(1047. .1985)
/gene="MTH1093"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLGAAVREGGVEGGYKAFIYEGIIGOTVLETSIESGVSVIIDROYGELKEILVAPISR
ESMVVGKALGISTASMIQAAILLALSEIVGITMSPQCEIVSMVIALIISMGLGGLGLV
IAAETDSMEGENLIMSEIVLFIELLSGALFPITGLPAWLQGAVYINPLTYAVDALRET
ILRRSVLPLEVNLLVITIFAVJAVLIAAELENRKEQNLM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(277. .1050)
/gene="MTH1092"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="ABC transporter (ATP-binding"
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/db_xref="GI:2622194"
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                                                                                           /gene="MTH1095"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VNLAARNNYYVRAVELEHPTLEDVFIKYTGRGISEA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism-"Methanobacterium thermoautotrophicum"
/strain-"delta H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="MTH1094"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative membrane
/protein_id="AAB85581.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'gene="MTH1094"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation = "MIWMAEIEGIYTIWLREMKRFFRYRSRIVTSIVTPLLWLIIFGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'db_xref="GI:2622193"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db_xref="PID:g2622193"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    xref-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              taxon:2166"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein"
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                            Conserved protein;
p()=0.000000003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conserved protein; p()=1.4E-98,
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gene

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KENFADLIEKRGLSRNILRALGHSPEDPLNCLVEMDRSYVMKLVEVVDIVGIKGGE"
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TGAGNVINDYEDHEIDA INRPERPIPSGRISRGVAGYYSIILFALASLMGEYLGLLPG
LYVYSSSLLMYYYAWRLKKRCLVGNITISFLTGLSFVFGGIVLGEVRASILLGFYAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(5137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(5137. .5982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Function Code:14.01 - Unknown, Conserved protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MRAISVHELREMEGDFFLLDVRKITDRERFHIEGSEHIWVGDLPDNLDLIPEKDVVIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="conserved protein"
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'protein_id="AAB85587.1"
'db_xref="PID:g2622199"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="MTH1098"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MLSDDKAALIVTGDSLSERALENLMDVIDDRVELEVVNVLEKPW
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                                                                                                                                             note="Function Code:14.01 - Unknown, Conserved protein; imilar to, gp:GI:g1653859 LN:D90917, p()=2.7E-17, id=19%"
                                                                                                                                                                                                                                                                                                                                                            |TMAREIVKDMEDVEGDRAEGATTLPITHGMRISGVLAASFMLIASLTSPSLYLLG|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene="MTH1098"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="conserved protein"
protein_id="AAB85586.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="MTH1097"
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                                                                                                                                                                                                                 122. :6862
gene="MTH1099"
                                                                                                                                                                                                                                                                  gene="MTH1099"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="Function Code:14.01 - Unknown, Conserved protein; imilar to, gp:GI:g1653922 LN:D90917, p()=0.0000055,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="MTH1096"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="MTH1096"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db_xref="GI:2622196"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db_xref="PID:g2622196"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _xref="PID:g2622198"
_xref="GI:2622198"
                                                                                                                                                                                                                                                                                                                                    PVLLLAVAVFLRAAIMILRGQDRATASRVSRMIKVGMALTFIAFAAGSGTITA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                       FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ghim, S.-Y., Jeong, Y.-M., Choi, S.-K. and Park, S.-H. Sequence analysis of the 30 kb region (182') of the subtilis chromosome containing the cge cluster
                                                                                                                                                                                                                                                                                                                                                                             Submitted (04-JUN-1997) Applied Microbiology Research Division, KRIBB, P.O.Box 115, Yusong-Gu, Taejon 305-600, Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Park,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 30100)
Ghim, S.-Y., Jeong, Y.-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus subtilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 30100)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 S.-H., Choi, S.-K., Jeong, Y.-M. and Ghim, S.-Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30100 bp DNA BCT 16-OCT-1997 subtilis 168 region at 182 min containing the cge gene
                                                /codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                  'map="182 min"
                                                                                                                                                                                                                                                             /db_xref="taxon:1423"
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'db_xref="PID:g2529446"
                                                                                                                                                                                                                                                                                   'strain-"168'
                                                                                                                                          gene="yokB"
                                                                                                                                                                                      gene-
                                                                                                                    function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:2529445
```

CDS gene

gene

"yokB"

Bacillus

gene

SdC

0,

Mismatches

0;

Gaps

0;

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                                                                                                                                                                                                                                                              /product="conserved prot/
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transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene-"MTH1100"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="MTH1100"
                                                                                                                                                                                                                                        1b_xref="GI:262
100.0%;
  Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                                  protein"
2.2e+03;
                           DB 1;
                        Length 10072;
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gene
       CDS
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                                                                                                                                                                                                                                                                                                                           /transl_table=11
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/SEEDYMEYKCLIMQLKKNKKYSSFSF"
complement(3022 .3303)
/gene="yokh"
complement(3022. .3303)
                                                                                                                                                                                                                   'gene="yokg"
                                                                                                                                                                                                                                                       'gene≖"yokG"
                                                                                                                                                                                                                                                                                   translation="mieifkdtgathdlvyhskintfywdvefdivlsdskelnkcyf"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein_id="AAB81141.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transl_table=11
product="Yoke"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="yokD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene-"yokE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "translation="MENEVVFFCRKCNHHLFAKNPMINTLKVISEMDCPNCGEEGYHN
ILLSHIGDSEKEKENYNWK"
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'db_xref="GI:2529447"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'product="YokC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               function-"unknown"
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                                                                                                                                                                                      /transl_table=11
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                                                                                                                                                                                                                                                                                                                    'gene≖"
                                                                                                                                                                                                                                                                                gene="yokK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product-"YokJ"
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gene-"yokJ"
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'transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
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                                                                                                                                                                                                                                                                                                                                     .6083
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                                                                                                                                                                                    YokK"
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SLYHSOKTGAFYALVTGKQGEFEDYETVDGGKGYVTGKKYREFKLNSOTEGLVADDEY
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DGENIDNGQAVNQNFKIVSWEQIAQHLGEMPDLHKQVNPRKLKDRSDG®Complement(6154. .7107)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note-"OrfE5; a potential ORF adjacent to the DNA replication terminator TerV of B. subtilis; it includes the right attachment site for phage SPbeta (4145-4160)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          omplement(4140. .4565)
gene="orfE5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="Orf181 at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           omplement(4140. .4565)
gene="orfE5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein_id="AAB81146.1"
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db_xref="GI:2529454"
translation="MEPYQRYEELF
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JSKORINDYVGGFKSNMNIGTAMTFADAIGCSIEELYVWNFKERROLTK"
3339. . 3926
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AF015775
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                                                                                                                                                                                                                                          FEATURES
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TITLE
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                                                                                                                                                                                                                                                                                                   JOURNAL
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                                                                                                             gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF015775 29950 bp DNA BCT 04-OCT-1997
Bacillus subtillis YodA (yodA), YodB (yodB), YodC (yodC), YodD
(yodD), ABC-transporter (yodE), permease (yodF), proteinase (ctpA),
YodH (yodH), YodI (yodI), carboxypeptidase (yodF), proteinase (ctpA),
YodH (yodH), YodO (yodO), YodF (yodF), YodM (yodM), YodN
(yodN), YodO (yodO), YodF (yodF), acetylornitine deacetylase
(argE), butirate-acetoacetate CoA transferase (yodR), butyrate
acetoacetate-CoA transferase (yodS), YodT (yodT), CgeE (cgeE), CgeD
(cgeD), CgeC (cgeC), CgeA (cgeA), CgeB (cgeB), YzxA (yzxA),
DDF-glucose epimerase (yodU), YodV (yodV), and YodW (yodW) genes,
AF015775
AF015775
                                                                                                                                                                                                                                                                                                      Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 29950)
Wambutt,R., Wedler,H., Lapidus,A., Sorokin,A. and Ehrlich,D.
Sequence analysis of the Bacillus subtilis chromosome region
between the odhAB and sspC loci cloned in a yeast artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roels, S. and Losick, R. Adjacent and divergently oriented operons under the control of the Approximation regulatory protein GerE in Bacillus subtilis J. Bacteriol. 177 (21), 6263-6275 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
[bases 20424 to 24585]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 29950)
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                                                                                                                                                                                                                                ed (23-JUL-1997) Laboratoire de Genetique Microbienne,
de Vilvert, Jouy-en-Josas cedex 78352, France
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                              R., Lapidus, A.,
                                                                                                             /organism="Bacillus subtilis"
/db_xref="taxon:1423"
493. .940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="gene
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                                                                        "yodA"
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                                                                                                                                                                                                                                                                                                                                                              Sorokin, A. and Ehrlich, D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 30100;
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                                                                                                                                                                                            complement(3026.
/gene="yodE"
                                                                                                                                                                                                                                                                                                                GSVLENGMPRFFKRLSEGVFDEKDLVVRTRELKDFIDEAAETHOFNRGRVIAVGYSNG
ANLAASLLEHYKDVLKGAILHHPMVPIRGIELPDMAGLPVFIGAGKYDPLCTKEESEE
LYRYLRDSGASASVYWQDGGHQLTQHEAEQAREWYKEAIV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="G1:2415385"
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                                                                                                                                                                                                                                                    /gene="yodE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QFQKQFDISERYVPVMLISIGKAVKPAHQSNRLPLSKVSTWL"
                                                                                                                                                                                                                                                                                         complement (3026.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAB72061.1"
/db_xref="PID:g2415393"
/db_xref="GI:2415393"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/transl_table=11
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LMVSITENGDADWSFGLGEAQFLNGKL"
product="ABC-transporter"
                                                                                               citation-[2]
                                                                                                                                                    note="similar to B.subtilis hypothetical ABC transporter
                                                                                                                                                                                                                                                                                                                                                                                                            translation="MKHIYEKGTSDNVLLLLHGTGGNEHDLLSLGRFIDPDAHLLGVR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'product="YodD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                citation=[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="similar to
inase CRK1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note*"similar to E.coli oxygen-insensitive NAD(P)H
iltroreductase NfnB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
/product="YodA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1
trans1_table=11
product="yodc"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             citation=[2
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'db_xref="PID:g2415384"
'db_xref="GI:2415384"
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translation="MGNTMCPKMESAFSLLGKRWNGLIIHVLMDGPKREKEITETIPM
SGKMLAERLKELEQNEIVERQVLPETFVKVIVTLTEKGTALQAVFQEMQAWADQFCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note = "similar to B. subtilis YckH protein"
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b_xref="PID:92415385"
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                                                                                                                                                                                                                          .3937)
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gene CDS

1.8e+03; thes 0; DB 1;

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Length 29950; Indels

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/translation="MSRYLEMLSLEGVAGAHPGGLAFSKAVLQKAAPSPDQPILDAGC
GTGQTAAYLGHLLYPVTVVDKDPIMLEKAKKRFANEGLAIPAYQAELEHLPFSSESFS
CVLSESVLSFSRLTSSLQEISRYLKPSGMLIGIEAALKKPMPPAEKKQMMDFYGFTCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEKERKVTKPTVVLVNDGTASAAEIMAAALHESSNVPLIGETTFGKGTVQTAKEYDDG
STVKLTVAKWLTADGEWIHKKGIKPQVKAELPDYAKLPYLDADKTYKSGDTGTNVKVA
QKMLKALGYKVKVNSMYDQDFVSVVKQFQKKEKLNETGILTGDTTTKLMIELQKKLSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(5810. .5836)
/gene="yodf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MKRQLKLFFIVLITAVVASALTLFITGNSSILGQKSASTGDSKF
DKLNKAYEQIKSDYYQKTDDDKLVDGAIKGMIQSLDDPYSTYMDQEQAKSFDETISAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(5840.
/gene="ctpA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GFWGLAANMIAVVILNPLFVKNAGSNPVIEGLFGKKQDANPNQKGA'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DTLVKEAPQMLTIPSEGPKGIPWFITASIVSALALFMWAHAATGVFTAKSADAVRKNS
MFLPLYNIVLILVIFLGFTAFLVLPEDTNPRLALLHLIQTSYGGVAQGFAYATIALAS
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                                                                                                                                                                         /protein_id="AAB72055.1"
/db_xref="PID:g2415387"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NDTOMEKAIETLKKEM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKKGTKVKLELNRAGVGNIDLSIKRDTIPVETVYSEMKDNNIGEIQITSFSETTAKEL
TDAIDSLEKKGAKGYILDLRGNPGGLMEQAITMSNLFIDKGKNIMQVEYKNGSKEVMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEGIGAQVEEKDGEILIVSPIKGSPAEKAGIKPRDQIIKVNGKSVKGMNVNEAVALIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="proteinase"
/protein_id="AAB72063.1"
/db_xref="PID:g2415395"
/db_xref="GI:2415395"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               carboxy-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VKFVVIISFILVALYTEFSGIKGPTYTAIIKDILVWVIMLFMVVSLPLIHFNGWTPMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HFYFGNONGDPGTIMTFFPFOGSGOGTVGKGOAGRVYFSVPSGSLSFWKERLEKSGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIPCSIMAIGASNLFANNLYRDLIHPNVSQSKLTLVTRSMVFVVIGLALLFGMLFPTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MQGNLTALLITAIIVLTVVCIGFLAGRDKSSRTSVEEWSVGGRR
FGGLLVWFLVGADLYTAYTFLGLTSTAFTGGSVAFFAIPYSVLAYFIAYFFLPKLWKV
AKIHKLTTLADYARERFNSKLLASLVAIVGVLMLIPY_CLQLSGIQDTLQVAGTGYIN
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PQATIQLLTESFGYTKVAEEDQIVRLASSAAVGGVIDVHLHPEKRGVGGYGTVHHVAF
                                                                                                                                                                                                                                                                                                                            citation=[2]
                                                                                                                                                                                                                                                                                                                                                   note-"similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="similar to Synechocystis sp. PCC6803 arboxy-terminal processing proteinase precursor"
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protein_id="AAB72054.1"
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'db_xref="GI:2415394"
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                                                                                                                                                                                                                                                                                                     codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _xref="PID:g24153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QLLGVSGMVQIFPAIAVSLFWKNQTKEATVIGLLAGLAVTFIVYITQSAHGIYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (5846. .7246)
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                                                                                                                                                                                                                                                                                                                                                 E.coli biotin biosynthesis protein BioC"
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AUTHORS
TITLE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL MEDLINE
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JOURNAL
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X78854
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1113, 41080 Sevilla, SPAIN
2 (bases 1 to 2259)
Floriano, B., Herrero, A. and Flores, E.
Analysis of expression of the argc an
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J. Bacteriol. 176 (20), 6397-6401 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
10; Conserv
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GELAGWIIQHSCADRVFFCNSGAEANEAAIKLARKYAHTVLDIEGDIYVAAAILIEPLG
TLATITATGQAKYQKYFDFLVPGFHYVNYNDISAVEAAISELDEGDIYVAAILIEPLG
GEGGVRPGDVEYFQKLRQICDDTGILLMFDEVQVGMGRSGKLMGYEYLGVEPDIFTSA
                                                                     AGPKVVRFVPPLIVTEAEINTALKLLEKALATVTA'
                                                                                            KGLGGGIPIGAMMSKKFCDVFQPGEHASTFGGNPFACGVALAVCQTLERENILQNVQD
RGEQLRSGLRAIAAKYPHHLTEVRGWGLINGLELAADIPLTAADVVKAAINEGLLLVP
                                                                                                                                                                                                                                                                                                                  /product="N-acetylornithine aminotransferase"
/protein_id="CAA55410.1"
/db_xref="PID:g580729"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="wild type genomic in cosmid pDUCA"
/clone="pCSB335-2"
125. >1711
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                                                                                                                                                                                                                                     'db_xref="SWISS-PROT: P54752"
/translation="MSLQTLIEQAINPPESGSAASSPFSTDSFDASVMSTYGREPLAL
                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
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/db_xref="PID:g2415388"
/db_xref="GI:2415388"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (29-JAN-1992) to the DDBJ/EMBL/GenBank databases. Junichi Sekiguchi, Textile Science and Technology, Shinshu University, Department of Applied Biology; 3-15-1 Tokida, Ueda-shi, Nagano 386, Japan (E-mail:)sekigu@giptc.shinshu-u.ac.jp, Tel:0268-21-5344, Fax:0268-21-5331)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lipoprotein; major autolysin.
Bacillus subtilis (strain:1685) DNA.
Bacillus subtilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kuroda,A., Rashid,M.H. and Sekiguchi,J.
Molecular cloning and sequencing of the upstream region of the
major Bacillus subtilis autolysin gene: a modifier protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (29-Jan-1992) to DDBJ by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autolysin gene
J. Bacteriol. 173 (22), 7304-7312 (1991)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Junichi Sekiguchi
Department of Applied Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exhibiting sequence homology to the major autolysin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecular cloning and sequencing of a major Bacillus subtilis
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                                                                                                                                                                                                                                                      organism="Bacillus subtilis"
'strain="168S"
                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
    product="lipoprotein"
protein_id="BAA01223.1"
                                                             codon_start=1
                                                                                                                                                                                                                                 db_xref="taxon:1423"
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KYSKMPSVLVETAFITNASDASKLKQAVYKDKAAQAIHDGTVSYYR"
1 939 c 1020 g 1489 t
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AIGNGLLEKEVNLDIAKRVNTKLNASGALPVLSRSNDTFYSLQERVNKAASAQADLFL
                                                                                                                                                                                                                                                                                                                                            /translation="LRSYIKVLTMCFLGLILFVPTALADNSVKRVGGSNRYGTAVQIS
KQMYSTASTAVIVGGSSYADAISAAPLAYQKNAPLLYINSDKLSYETKTRLKEMQTKN
VIIVGGTPAVSSNYANQIKSLGISIKRIAGSNRYDTAARVAKAMGATSKAVILNGFLY
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$LSPTGFYKVTGDNVAVTDRFAGASRYETATLASNSQWKNPNTVILVNRDIFIDALPV
IPLAKKLNAPVLFTQPDTLTKTTERQIAKFNPDNILIIGGARSISKDVENKLKSYGAV
KRISGKNRYVLSENIAKQWGSYDKAIVVTGRVFQDALAIAPYAAAHGYPILLTEKDKL
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KQYLGTVNFSIESTKYIRPVNENIPFEDYLKGVIPNEMPASWSLEALKAQTVAARTYS
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VWTNGTKYADVLIGASLASKKNSQILFVKQDSVPAAAKSITKDKATYAYDFIGSTSSI
                                                                                                                                                                                                                                                                                                                                                                                                                                             'product="N-acetylmuramoy1-L-alanine amidase"
'protein_id="BAA01225.1"
'protein_id="BAA01225.1"
'db_xref="pip:d1001695"
'db_xref="pip:d1001695"
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/translation="MKKFIALLFFILLLSGCGVNSQKSQGEDVSPDSNIETKEGTYVG
LADTHTIEVTVDNEPVSLDITEESTSDLDKFNSGDKVTITYEKNDEGQLLLKDIERAN
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/db_xref="PID:g216256"
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/product="li
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Bacillus subtilis N-acetylmuramoyl-L-alanine amidase (cwlB) gene,
complete cds.
                                                          BACENZYMEI 2277 bp DNA
Bacillus subtilis 168 enzyme I of the PEP:phototransferase system gene, 3' end, and spore photoproduct lyase gene, complete cds.
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Bacillus subtills (strain 1685) DNA.
Bacillus subtills
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Bacillus/Staphylococus group; Bacillus.
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Molecualr cloning and sequecing of a major Bacillus subtilis
 PEP:phototransferase;
                  L08809.1 GI:289267
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AIGNGLLEKEVNLDIAKRVNTKLNASGALPVLSRSNDTFYSLQERVNKAASAQADLFL
SIHANANDSSSPNGSETYYDTTYQAANSKRLAEQIQPKLAANLGTRDRGVKTAAFYVI
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VOITVGGTPAVSSNTANQIKSLGISIKRIAGSNRYDTAARVAKAMGATSKAVILNGFLY
ADAPAVIPYAAKNOYPILFTMKTSIKSATTSVIKDKOISSTVVVGGTGSISNTYVKL
PSPTRISGSNRYELAANIVOKLNLSTSTVYVSNGFSVPDSIAGATLAAKKKOSLILTN
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/db_xref="GI:142806"
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/strain="168S"
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442 c 508 g 671 t
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Bacillus/Staphylococcus group; Bacillus
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HFGQSDLGKLRFVTKFHHVDHLLDAKHNGKTRFRFSINADYVIKNFEPGTSPLDKRIE
AAVKVAKAGYPLGFIVAPIYIHEGWEEGYRHLFEKLDAALPQDVRHDITFELIQHRFT
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FAKEVDFFSIGTNDLIQYTMAADRMNERVSYLYQPYNPAILRLITLYIEAAHKEGKWV
GMCGEMAGDEIAIPILLGLGLDEFSMSATSILPARTQISKLSKQEAESFKEKILSMST
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IYETYHPFAEDDAVFASYEEAKSLYKELFDIDPYE"
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/strain="W168"
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Submitted (15-APR-1996) Christopher M. Thomas, School of Biological Sciences, University of Birmingham, Edgbaston, Birmingham B15 2TT, UK
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A putative serine protease helps to ensure stable inheritance of cryptic plasmid pPOD2000 from Bacillus subtilis Unpublished (1996)
2. (bases 1 to 8397)
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/gene="rep"
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plasmids"
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/note="ORF3"
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MDNEFHGQFCLKCCKEMTGEV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:1423"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Bacillus subtilis"
/plasmid="pPOD2000"
                                                                                  codon_start=1
                                                                                                                                                'note="replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note "ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _xref="GI:1305509"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (822. .917)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .1381)
.1580)
                                                                                                                                                                                                                                                                                                       .2706)
                                                                                                                                                                                                                                                                                                                                                                     .1592)
                                                                                                                                                initiator protein; similar to proteins from other gram posit
                                                                                                                                                                                                                                                                         SgS
                                                                                                                                                                                                                                                                                                                                        RBS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           rep_origin
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                                                                                                                                                                                                                                                                                                                                 complement(5088. .5297)
/note-"single strand replication origin; this is the site that lagging strand replication is initiated on the plasmid during rolling circle replication"
5930. .5937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(4527.
/gene="rapA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YCVKGKSYAEKYDDSMFVDLFNVLHELYVTVSPSVEVNOKFDQLLYSRGYPYLEDLAL
EAGRFYNDIERLDDSVFFYKKMIQVQKLIQRGDFEYDV"
complement(3417...3424)
/gene="rapab"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="GI:135514"
/db_xref=
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/standard_name="transcription terminator"
complement(3293. .3424)
/gene="raphb"
/transl_table=11
/transl_table=11
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/protein_id="AAA99154.1"
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/db_xref="GI:1305515"
/translation="MDNQETWHSIKSLERELQIPDTTLRRYIRQHGHHLNIKKNGKSY
/VANESIPLIKKIRGLYVEGKSIENIETTLTNEGHPITITIDNHTESTALTLNESIED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(4587. .4625)
/note="ComAP recognition site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="RapAB"
/protein_1d="RAPA99152.1"
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/db_xref="GI:1305513"
/translation="MTFKKIMAAVLILAVTVAPVYGLATQDNSVSVASRNAT"
/complement(3399. .4535)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(3399. .4517)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(2701.
/gene="rep"
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/gene="rep"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVRIEEDDDAVANETFEVMARWHVGIKNYIIQ"
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Suayfckvælcskcakraslkiashkkliveeanreykpswieltltvenvogdblko
Titdmmkamirkfoykvyktsvloyfreraleitknheontyhehehvllpvkrsyetgk
Ryikoaewtslwkramkldyfpivhvorvkgkkgidaegiekevrkemeeokaileis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="RapA"
/protein_id="AAA99153.1"
/db_xref="PID:91305514"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to the rapA gene product (formerly gsiA) on
the Bacillus chromosome and rap40 and rap60 gene products
from plasmids pTA1040 and pTA1060, respectively"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="rapA"
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/db_xref="PID:g1305512"
                                                                                                                                                                                                     codon_start=1
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AUTHORS
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                                                                                                                                                                                                                                                                                                        1 TGTGTGTCAG 10
                                                                                                                                                                           BSUB0004 213190 bp DNA BCT 26-NOV-1997 Bacillus subtilis complete genome (section 4 of 21): from 600701 to
                                                                                                                                                                                                                                                                                                                                                   10; Conservative
   1 (bases 1 to 213190)
Kunst, F., Ogasawara, N.,
                                              Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillaceae;
                                                                      Bacillus subtilis
                                                                                   Bacillus subtilis.
                                                                                                                   299107.1
                                                                                                                                                    Z99107 AL009126
                                                                                                                     GI:2632866
                                                                                                                                                                                                                                                                                                                                                                                                            complement(7404. 8237)
/gene="parA"
/note="similar to subtilisin and other serine proteases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6450. ..._
/gene="parC"
6473. .6478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(7392...7412)
complement(7404...8302)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Translation="MFKKKLLKSFYVFLASILFSSVLFSSAQATESDTQKKVDAINK
SSFYNVETNEIMLSKDLAKSFYDFSDSELKEINKFQNLTQGEIDYILKLSNYDLDEI
DVDENVAHANWYWYIPVYAGIIVAGGIIFSALYFSHKEKQNLINKCYKQKGKPVIDSR
DSAGLKGTTKSGSAKKAGGYKFECKKK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="proposed to be involved in plasmid stability (post segregational killing) by forming an active complex with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=1
/product="ParB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(6793. .7356)
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complement(6793. .7366)
/gene="par8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="pID:g1305516"
/db_xref="G1:1305516"
/translation="MKLKKLINLORLSIIIPFSLVIASALLLIQVSFNNKBIQSLSQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAA99156.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="proposed to be a regulator of ParA and ParB at post
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein_id="AAA99155.1"
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529. .6534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _xref="PID:g1305517"
_xref="GI:1305517"
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                                                                                                                                                                                                                                                                                                                                                                 Score 10;
Pred. No.
Moszer, I., Albertini, A.M., Alloni, G.,
                                                                                                                                                                                                                                                                                                                                                                 2.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                Length 8397;
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AUTHORS
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MEDLINE
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Submitted (18-NOV-1997) I. Moszer, A. Danchin, Institut Pasteur, Regulation de l'Expression Genetique, 28 rue du Docteur Roux, 7572 Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr, padanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Purnelle, B., Rapoport, G., Rey, M., Reynolds, S., Rieger, M., Rivolta, C., Rocha, E., Roche, B., Rose, M., Saddie, Y., Sato, T., Scanlan, E., Schleich, S., Schroeter, R., Scoffone, F., Sekiguchi, J., Sekowska, A., Seror, S. J., Serror, P., Shin, B.S., Soldo, B., Sekowska, A., Seror, S. J., Serror, P., Shin, B.S., Soldo, B., Sorokin, A., Tacconi, E., Takagi, T., Takahashi, H., Takemaru, K., Takeuchi, M., Tamako, S., Yandenbol, M., Terpstra, P., Tognoni, A., Tosato, V., Uchiyama, S., Vandenbol, M., Vannier, F., Vassarotti, A., Viari, A., Wambutt, R., Wedler, E., Wedler, H., Weitzenegger, T., Winters, P., Wipat, A., Yamanoto, H., Yamane, K., Yasamoto, K., Yata, K., Vashida, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The complete genome sequence of the gram-positive bacterium Bacillus subtilis Nature 390 (6657), 249-256 (1997)
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Edantel, R.A., Denizot, F.Devine, K.M., Dusterhoft, A., Ehrlich, S.D. Emmerson, P.T., Entian, K.D., Errington, J., Fabret, C., Ferrari, E., Foulger, D., Fritz, C., Fujita, M., Fujita, Y., Fuma, S., Galizzi, A., Galleron, N., Ghim, S.Y., Glaser, P., Goffeau, A., Golightly, E.J., Grandi, G., Guiseppi, G., Guy, B.J., Haga, K., Haiech, J., Harwood, C.F. Henaut, A., Hilbert, H., Holsappel, S., Hosono, S., Hullo, M.F., Transa M., Tital
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Lardinois,S., Lauder,J., Lazarevic,V., Lee,S.M., Levine,A., Liu,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Itaya,M., Jones,L., Joris,B., Karamata,D., Kasahara,Y.,
Klaerr-Blanchard,M., Klein,C., Kobayashi,Y., Koetter,P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Borriss,R., Bourster,L., Brans,A., Braun,M., Brignell,S.C. Bron,S., Brouillet,S., Bruschi,C.V., Caldwell,B., Capuano,
                                                                                                                                                                                                                                        /gene="ydfT"
                                                                                                                                                                                                                                complement(755. .1186)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IYVDQYKDHISVPMDKE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MIELEVVIRTVASFGLLLIAERILGKQTISQMTIFDFIAAITLG
AIAAGLAYNTSIKPHNMAISFSIFVLTIFLISFLSIKNRKLRKFFAGDPTVLIQNGKI
LESNMRKMRYTLDYLNQQLREKEIFNIEEVLFAILETNGQLTVLRKPQFRHVTKQDLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IAVNQEQRLPIELIMDGEIIENNLKQNRLTESWLLEELRKRDIKVKETVYAVLLGNGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="CAB12373.1"
/db_xref="PID:e1182533"
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codon_start=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'codon_start=1
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                                                                                   function-"unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene='
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                                                                                                                                                                                                                                                                                                                                                                                              .1186)
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                          Dusterhoft, A., Ehrlich, S.D.,
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u_Docteur Roux, 75724
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                                                                                                     Cummings, N.J.,
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CDS
                                                                             terminator
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DFYQDEYNI IIVEMPGYYEEELTIRLLSKTQLLIKGTITPVFPAEMEVLRERYYGEI
ERIIQLDEAASTHLLQIQLLNGLLHISYPRQVETVAFNKGL"
complement(1199. 11441)
/gene="ydga"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="SPTREMBL:P96699"
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GDLSPTSSLLNTGNIDSDVSDQDQIGNPSAPISNQI"
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TGILEIAGALAMTAGIWNRYAAIGAGVLFVVLMAGAIHAHMFRARQSVIMAIQAMICL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(1455. .1727)
                                                                             3074.
                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MKSKGVESRKRLLKAAANEFSVRGFHDAKVSEIVKKAGFTQPSF
YLYFQSKEAIFAELITDFHSRVRKLTESLLLENGLNTEDVSKRVLLAVETVFQFLDED
KDLTKIGFFLNPEAKQMKKDLAMVLKENLEAEQRLGYFHSELDMETVAECLVGMIEHL
                                     /gene="ydgD"
3117. .3590
                                                                                                                                                         'db_xref="SPTREMBL:P96702"
                                                                                                                                                                              'db_xref="GI:2632872"
                                                                                                                                                                                                                                       /transl_table=11
/protein_id="CAB12378.1"
                                                                                                                                                                                                                                                                                                                       'gene="ydgD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein_id="CAB12377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="similar to hypothetical proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "GDTSPTESVMENFLNDPDVNDQTSIGNSDTSNVNAPPIAPPPILD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'db_xref="SPTREMBL:P96700"
'translation="MPSTVINLYYLKINSISGNGSITIGEAAYNSPINNQKSQGTNSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="PID:g2632869"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="PID:e1182535"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein_id="CAB12375.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="similar to hypothetical proteins from B. subtilis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="ydqA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="PID:g2632868"
/db_xref="GI:2632868"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein_id="CAB12376.1"
                                                                                                                                                                                                                                                                                              function="unknown"
                                                                                                                                                                                               _xref="PID:e1182538"
_xref="PID:g2632872"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   xref="SPTREMBL:P96701"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      xref="PID:e1182536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  on="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                     KDPASLAAEVVNLLIYGMLPKGNDVR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              I:2632870"
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                                                                                                                                  REFERENCE
                                                                                                                                                                                                                SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                         DEFINITION
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                                                                                                                                                                                                                                                                             /ERSION
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Best Local s
Matches 10
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299108.1
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Db 210334 TGTGTGTCAG 210343
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1 (bases 1 to 208430)
2 (consist, F., Ogasawara, N., Moszer, I., Albertini, A.M., Alloni, G., Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Borriss, R., Boursier, L., Brans, A., Braun, M., Brignell, S.C., Borriss, R., Brouillet, S., Bruschi, C.V., Caldwell, B., Capuano, V., Carter, N.M., Choi, S.K., Codani, J.J., Connerton, I.F., Cummings, N.J., Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Ehrlich, S.D., Emmerson, P.T., Entian, K.D., Errington, J., Fabret, C., Ferrari, E., Foulger, D., Fritz, C., Fujita, M., Fujita, Y., Fuma, S., Galizzi, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BSUB0005 208430
Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                              Bacillus subtilis. Bacillus subtilis
                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillaceae;
Bacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="ATP-binding transport protein"
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/db_xref="piD:92652874"
/db_xref="GI:2632874"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="sptrembl:p96703"
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/translation="maftledwieeeffeafrgmsvonfakonitsgtwtekeafekse
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/kglaolalotiderarelgaerlalhvfahnetavylyokmgyamtnirmrkolo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(5428. .7089)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QLSGGEKLKARLAKGLSEDADLLLLDEPTNHLDEKSLQFLTQQLKHYNGTVTLVSHDR
YFLDEAATKTWSLEDQTLTEFKGNYSGYMKFREKKRLTQQREYEKQQKMVERTEAQMN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QYSGTLLAVSHDRYFLEKTTNSKLVISNNGIEKQLNDVPSERNEREELRLKLETERQE
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LGFTAAQWTEPIKHMSMGERVKIKLMAYILEEKDVLILDEPTNHLDLPSREQLEETLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SWISS-PROT:P39115"
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Pred. No. 1.2e+03;
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Regulation de l'Expression Genetique, 28 rue du Do
Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 3
98044033
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Nature 390 (6657), 249-256 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                complement(1345. .2052)
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                                                                                                                                                                                                                                                                                       'note-"similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             " LAFLLPSDQKLREWHS
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                                                                                                                                                                                                                                                                                                                                                                              'gene="yfnB"
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                                                                                                                                                                                                                                                                                                                                   function-"unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="yfnC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               function="unknown"
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                                                                                                                                                                                                                                                                                       to hypothetical proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yasumoto,K., Yata,K.,
ikawa,H. and
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u Docteur Roux, 75724
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3779, 5216
                                                                            6113. .6136
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                                                                                                          KMAEKALEEE"
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/gene="yfnA"
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complement(2110. .2133)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FNYVFERIPQFSAEHTLIIGDSLTADIKGGQLAGLDTCWMNPDMKPNVPEIIPTYEIR
KLEELYHILNIENTVSC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mkryrtllfdyddtildfqaaealalrllfedqnipltndmkaq
yktingglwrafeegkmtrdevyntresallkeygyeadgallegkyrrfleeghqli
dgafdlisnlqqqfdlyivtngyshtqykrlrdsglfpffkdifysedtgfqkpmkey
gene="yfms"
245. .8159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="similar to methyl-accepting chemotaxis protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="CAB12564.1"
/db_xref="PID:e1182725"
/db_xref="PID:g2633059"
/db_xref="GI:2633059"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VIVLRKKHPEIKASFRVPFVPVVPIISAGICLWFMYSLPGVTWLSFVIWIAVGTLVYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(2110. .3529)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="yfmS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="CAB12563.1
/db_xref="pID:e1182724"
/db_xref="pID:92633058"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="similar to benzaldehyde dehydrogenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "gene-"yfmt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             function-"unknown"
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terminator

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Page 19
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CDS 5245. 8134

/function="unknown"
/function="unknown"
/function="siniar to ABC transporter (ATP-binding protein)"
/codon_start=1
/rransi_tble=11
/protein_id="CAB12566.1"
/db_xref="pli=id=187727"
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Title: Perfect score: Sequence:

US-08-956-518A-87

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Matches 10
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10-JUN-1988; US-204645.

20-APR-1989; US-341080.

(GEHO-) General Hospital Corp

Fisher RA, Schooley RT, Hirsch M.

WPT; 90-007302/01.

P-PSDB; R04032.
Combinations of soluble T4 protein and anti-retroviral agent having synergistic activity in treatment and prevention of AIDS, ARC and HIV infection.

ARC and HIV infection.

Disclosure; fig 2; 100pp; English.

Soluble T4 constructs may be produced by truncating this sequence, remove the transmembrane and intracytoplasmic domains whilst retain the extracellular region responsible for HIV binding. The sol. T4 combined with an anti-viral agent such as AZT.

See also Q03005.

Sequence 6151 BP; 1493 A; 1589 C; 1586 G; 1483 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 zy-MAY-1990 (first entry)
Full length T4 cDNA of plasmid pBG38
Soluble T4; pBG381; anti-retroviral
MG8911860-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Soluble T4 constructs may be produced by truncating this sequence, remove the transmembrane and intracytoplasmic domains whilst retain the extracellular region responsible for HIV binding. The sol. T4 combined with an anti-viral agent such as AZT. See also Q03006.

Sequence 7377 BP; 1760 A; 1954 C; 1902 G; 1761 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GEHO-) General Hospital
(BIOJ) Biogen Inc.
Fisher RA, Schooley RT,
WPI; 90-007302/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q03005
Q03005;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-MAY-1990 (first entry)
Full length T4 cDNA of plasmid p170-2.
Soluble T4; p170-2; anti-retroviral agent; AIDS; ARC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARC and HIV infection. Disclosure; h.
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20-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO8911860-A.
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US-341080.
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y in treatment and prevention of AIDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BIOJ) Biogen
MS, Johnson VA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ,SW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agent; AIDS; ARC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , 7.6e+02;
ches 0;
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, Walker
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Full length T4 Full length T4

Description

Encodes Mammalian Plasmid p170.2 enc SV40 initial promo Human Bone Morphog

Sequence of SV4 Region between Plasmid pEMp1-tPA Sequence of SV40 e

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                                     Ş
                                                                                                                                                                        PT Transient expression system for recombinant proteins -
PT comprising enharyotic host cell transfected with vector
PT encoding trans-activating protein and expression vector
PS Disclosure; 44 pp English.

CC Expression vector pF8SCIS contains the SV40 enhancer and promoter, the
Intron and splice acceptor site, the cDNA encoding factor VIII and the
cytomegalovirus splice donor site and a portion of the intron, the Ig
intron and splice acceptor site, the cDNA encoding factor VIII and the
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intron and splice acceptor site, the cDNA encoding factor VIII and the
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DNA sequence of portion of plasmid pF8SCIS containing SV40 enhapromoter, cytomegalovirus splice donor site and Ig intron plasmid pF8SCIS; cytomegalovirus; SV40; enhancer; promoter; stabilising sequence; splice donor intron sequence; Ig region; splice acceptor sequence; human embryonic kidney cells (293);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAR-1989.
22-SEP-1988; 308784.
25-SEP-1987; US-101712.
(GETH) Genentech Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytomegalovirus; SV40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N90696 standard; DNA; 595 BP
N90696;
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                                     TGTGTGTCAG 10
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ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Stabilising sequence which includes cytomegalovirus donor and intron sequence, variable region intron and splice acceptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="PstI-ClaI converter"
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Pred. No. 6e+
); Mismatches
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Pred. No. 7.4e+02;
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                                                                                                  6e+02;
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                                                                                                                 Length 595;
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Best Local (
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17-MAY-1989, U02130.
24-MAY-1988; US-198451.
(TEXA) Univ of Texas Sys
Waxham MN;
WPI; 89-370727/50.
1513
                                                                                                                                                                                                   P-PSDB; p93666
HN specific degenerate oligonucleotide probe - cells producing HN to use prod. in vaccine devectlain 1; Page 25; 40pp; English.

Nucleotide sequence encoding HN protein of mump: to generate a large amounts of purified peptide sequence 1900 BP; 569 A; 433 C; 365 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rapid detection of specific human papilloma virus genotypes + by hybridisation of DNA digest with new labelled nucleic acid probes Claim 34; page 44; 81pp; English.
Obtd. by cutting HPV11 with BamH1 and NdeI. The patent describes probes (DNA or RNA) and their complements capable of detecting one or a combination of HPV types 6, 11, 16, 18, 31, 33 and 35.
Sequence 591 BP; 148 A; 91 C; 121 G; 231 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N92624
N92624;
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George AL, Groff DE;
WPI; 89-324314/44.
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04-APR-1989; U001318.
04-APR-1988; US-177404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-MAY-1990 (first entry)
Nucleotide sequence encoding mumps virus HN protein.
Haemagglutinin-neuraminidase; mumps; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cervical cancer
Human papilloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mumps virus.
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210 TGTGTGTCAG
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                                                                                      l Similarity
10; Conserv
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10; Conserv
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91. .1836
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Pred. No.
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Pred. No.
                                                                                         Mismatches
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d peptides
365 G;
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                                                                                                            DB 1; I
6.7e+02;
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                                                                                                                                                                                                                                                                                                    development
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                                                                                                                                    Length 1900;
                                                                                                                                                                                                        virus, from a 533 T;
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Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                          Including soluble T4-like (sT4) polypeptide number 8 (sT4#8)
HIV; soluble T4-like polypeptide 8; immunotherapeutic; prophylactic;
plasmid pBG393; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preventing, treating or detecting AIDS

Disclosure; ; 207pp; English.

It is the nucleotide sequence of the plasmid pBG396. The sequence was isolated from 2 libraries: a landa gt cDNA library derived from T cell tumour line REX and a landa gtl0 cDNA library derived from peripheral blood lymphocyes (PBL). For screening, a series of chemically synthesised antisense oligonucleotide DNA probes based on the known T4 protein sequence was used. The polypeptide encoded is useful in immunotherapeutic, prophylactic and diagnostic compsns. It can be used to purify HIV from a sample.

Sequence 5518 BP; 1334 A; 1424 C; 1403 G; 1357 T;
                                       DNA sequences coding for soluble T4-like polypeptide(s) - used in immuno:therapeutic and immunosuppressive compsns. and for preventing, treating or detecting AIDS Disclosure; ; 207pp; English.

It is the nucleotide sequence of region encoding the first 182 AA of t mature T4 sequence of plasmid pBG39. It does not contain the addition non-T4 6 amino acids at the C-terminus following AA 182. The sequence was isolated from 2 libraries: a lamda gt cDNA library derived from Teall tumour line REX and a lamda gt.0 cDNA library derived from peripheral blood lymphocytes (PBL). For screening, a series of chemica synthesised antisense oligonucleotide DNA probes based on the Known T4 protein sequence was used. The polypeptide encoded is useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1990 (first entry)
Nucleotide sequence of plasmid pi
polypeptide number 12 (s74#12)
HIV; soluble T4-like polypeptide
plasmid pBG396; diagnostic.
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N90647;
                                                                                                                                                                                                                             (BIOJ) Biogen Inc. Fisher RA, Gilbert W, WPI; 89-085519/11.
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Fisher RA, Gilbert W,
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07-JAN-1988; US-141649,
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07-JAN-1988; US-141649,
                                                                                                                                                                                                                                                                                                       09-MAR-1989
            Immunotherapeutic, prophylactic and diagnostic to purify HIV from a sample.
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(sT4#12)
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Α,
                                                                                                                                                                                                                                           VL, Flavell RA,
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Pred. No.
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 1437
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 1413
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                                                                                                                                                                                                                                           Maraganore JM,
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<u>ن</u>
                              compsns. It can
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 1365
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the additional
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1 Others;
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                                                         chemically
known T4
                              be used
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Best Local
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Best Local :
  DNA sequences coding for soluble T4-like used in immuno:therapeutic and immunosupp preventing, treating or detecting AIDS Fig 19; 207pp; English.
It is the nucleotide sequence of the plas was isolated from 2 libraries: a lamda gt
                                                                                                                                                                                                                                                                                                                                                                                                         Tt is the nucleotide sequence of the plasmid pBG395. The sequence was isolated from 2 libraries: a lamda gt cDNA library derived from T cell tumour line REX and a lamda gtl0 cDNA library derived from peripheral blood lymphocyes (PBL). For screening, a series of chemically synthesised antisense oligonucleotide DNA probes based on the known T4 protein sequence was used. The polypeptide encoded is useful in immunotherapeutic, prophylactic and diagnostic compsns. It can be used to purify HTV from a sample.

Sequence 5413 BP; 1309 A; 1401 C; 1365 G; 1338 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plasmid pBG395; diagnostic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BIOJ) Biogen Inc.
Fisher RA, Gilbert
WPI; 89-085519/11.
                                                                       (BIOJ) Biogen Inc.
Fisher RA, Gilbert W,
WPI; 89-085519/11.
                                                                                                           01-SEP-1988;
07-JAN-1988;
                                                                                                                                                                                                        01-FEB-1991 (first Nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-SEP-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence
                                                                                                                                   09-MAR-1989
                                                                                                                                                         Homo
                                                                                                                                                                    plasmid pBG394;
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                                                                                                                                                                                                                                         N90646 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA sequences coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-MAR-1989
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                                                                                                                                                                                           ncluding soluble
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                                                                                                                                                              worlde sequence of region encoding uding soluble T4-like (ST4) polypep soluble T4-like polypeptide 9; imm nid pBG394; diagnostic.
                                                                                                                                                         sapiens.
                                                                                                                                                                                                                                                                                                                           TGTGTGTCAG
                                                                                                                                                                                                                                                                                                    TGTGTGTCAG
                                                                                                                                                                                                                                                                                                                                                  l Similarity
10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e sequence of region encoding first 131 AA of plasmid pBG395
soluble T4-like (sT4) polypeptide number 10 (sT4#10)
ble T4-like polypeptide 10; immunotherapeutic; prophylactic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                          U02940.
US-141649.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-141649,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                    35
                                                                                                                                                                                                                                          DNA;
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                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                           100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for soluble T4-like polypeptide(s)
                                                                                  Sato
                                                                                                                                                                                                                                          5365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-094322
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Pred. No.
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Pred.
                                  t immunosuppressive compsns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Flavell
                                                                                    Flavell
                                                                                                                                                                                polypeptide
9; immunotl
                                                                                                                                                                                                                                                                                                                                                  Mismatches
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the plasmid pBG394.
lamda gt cDNA libra:
                                                                                                                                                                                                                                                                                                                                                            No.
                                                                                                                                                                                immunotheraputic;
                                                                                                                                                                                           first 113 AA of plasmid ptide number 9 (sT4#9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RA, Maraganore
                                                                                  RA, Maraganore
                                                                                                                                                                                                                                                                                                                                                             7.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                          Bg
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RESULT
Q04555
ID Q0
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DT 02
DE P1
KW T4
KW ar
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Best Loc
Matches
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Best Local s
Matches 10
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             02-OCT-1990 (first entry)
Plasmid p170.2 encoding T4
T4 protein; immunotoxin; P;
angiogenin; fusion protein
                                                                                                                                           1589
                                                                                                                                                                                                                                                                                                                          Amino acid hydrogenase activating protein -
isolated from mammal brain and activates tyrosine hydrogenase
and tryptophan hydrogenase
Disclosure; p; Japanese.
Probable error in specification at posn 168. C residue should
G (to give Met codon ATG instead of ATC).
Encodes a protein characterised by Mr of 27KD (by SDS-PAGE),
electric point of 4.6 and an N-terminal amino acid sequence by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J02111796-A.
24-APR-1990.
21-OCT-1988;
                                                                         Q04555 standard;
                                                                                                                                                                                                                                                      Protein activates Tyr hydrogenase and Trp hydroge of calcium ions and calmodulin-dependent protein Useful as a pharmaceutical analysis reagent. See also 004691 and 004692.

Sequence 1834 BP; 546 A; 454 C; 471 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-OCT-1988; JP-264097.
(TOFU) Toa Nenryo Kogyo
WPI; 90-169110/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; R05084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polya_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalian amino acid deh
tyrosine dehydrogenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell tumour line REX and a lamda gt10 cDNA library derived from peripheral blood lymphocyes (PBL). For screening, a series of chemically synthesised antisense oligonucleotide DNA probes based on the known T4 protein sequence was used. The polypeptide encoded is useful in immunotherapeutic, prophylactic and diagnostic compsns. It can be used to purify HIV from a sample.

Sequence 5365 BP; 1300 A; 1380 C; 1355 G; 1330 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Encodes Mammalian amino
Mammalian amino acid del
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-OCT-1990 (first entry)
                                                                                                                                                                                                        Local
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                                                                                                                                                                                       Similarity 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
10: Conser
             fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
166. .1006
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10
                                                                         cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1671. .1676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA; 1834 BP
                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ino acid dehydrogenase activating fact
  dehydrogenase activating protein-eta;
se; tryptophan dehydrogenase; ss.
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                                 T4 protein.
            Pseudomona in; ds.
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Pred. No. 6.7
); Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                      endotoxin
                                                                                                                                                                                                   DB 1; 1
6.7e+02;
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                                                                                                                                                                                                                                                                                                    hydrogenase in the
                                                                                                                                                                                                                                                     G;
                      A
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                                                                                                                                                                                                                                                                                                                                                                   residue should read
                                                                                                                                                                                                              Length 1834;
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                                                                                                                                                                                                                                                     363
                                                                                                                                                                                                                                                                                         phosphatase
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                                                                                                                                                                                                                                                                                                                            sequence beginning
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RESULT
N81632
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CC The T4 CDNA of p170.2 is almost identical to that reported by P.J.

CC Maddon et al [Cell, 42, pp 93-104 (1985)]. The Maddon sequence was

CC revised in 1988 to correct a DNA sequencing error at the codon for AA 3

CC (corrected from Asp to Lys; see M12807 in GenBank). The DNA may be

CC truncated (to remove transmembrane and intracellular regions) and/or

CC modified by SDM, pref. so the prod. extends from AAs 3-183 of the

CC mature protein. This DNA can then be ligated to a toxin DNA esp.

CC anglogenin, or a fragment of Pseudomonas exotoxin A conty. the

CC anglogenin, or a fragment of Pseudomonas exotoxin A conty. the

CC inserted into an expression vector and used to produce recombinant fusion

CC inserted into an expression vector and used to produce recombinant fusion

CC protein which is useful for preventing or treating AIDS, ARC, and HIV

CC infections. The T4 protein is an HIV receptor which binds to the virus

CC or to infected cells carrying gp110/160 marker antigen, so provides v.

CC specific targetting with minimal damage to non-target cells.

SQ Sequence 7316 BP; 1736 A; 1945 C; 1894 G; 1741 T;
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                          04-JUL-1988
23-DEC-1986, JP-305467.
23-DEC-1986, JP-305467.
(GREC) Green Cross Corp.
WPI, 88-224895/32.
                                                                                                                                                                                                                                                          N81632 stand
N81632;
O8-NOV-1990
Claim 3; page 2; 15pp; Japanese. This sequence is inserted into an enhuman immunoglobulin heavy chain enuseful for the prodon of proteins, hepatitis-B. See also N81631.

Sequence 828 BP; 220 A; 188 C
                                                                                                 Expression vector used for protein of immunoglobulin H-chain enhancer
                                                                                                                                                                                                            08-NOV-1-370 SV40 initial promoter region.

Immunoglobulin H-Chain enhancer;

Immunoglobulin enhancer;

Surface antigen; ss.
                                                                                                                                                                                                     hepatitis-B surface antigen;
J63160587-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BIOJ) Biogen Inc.
Meade HM, Lobb RR, Gates
MPI; 90-163876/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              esp. Pseudomonas endotoxin A, for transport related conditions, and new DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; R04910.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       old_sequence
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                                                                                                                                                                                                                                                                                                                                                           TGTGTGTCAG
                                                                                                                                                                                                                                                                                     standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note-"differs replace (1958.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product=T4 protein replace (1457. .145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="differs
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Pred.
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                       an expression vector alongside
in enhancer gene and the constru
ins, eg interferon, urokinase or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from M12807"
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                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                             SV40; interferon; urokinase;
  Ç
                                                                                              region.
                                                                                                                                                                                                                                                                                                                                                                                                                           NO:
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sequences
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  191
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7.5e+02;

    comprises combination
and SV40 initial promot

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olling AIDS
                                         construct is
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RESULT
N80632
ID N8
AC N8
DT 08
DE H1
KW B0
KW bo

밁 δ

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RESULT
N81970,
ID N8
AC NE
DT 12
DE P1
KW 71
KW 71
KW 71
KW 61
OS Hc
FT m:
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Best Local Similarity
Matches 10; Conser
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                                                                                                                                                                                                                                                                                                                       given in N80622.

The partial sequence is compiled from lambda U2OS-39 and several other hBMP-2 class I cDNA recombinants.

This human cDNA hBMP-2 class I contains an opem reading frame of 1188 bp., encoding a protein of 396 amino acids. The protein is preceded by a 5 untranslated region of 342 bp with stop codons in all frames. The 13 bp region preceding this 5' untranslated region represents a linker used in the cDNA cloning procedures.

See also N80619-N80636 and N81963-64.

Sequence 1606 BP; 399 A; 430 C; 423 G; 354 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bone morphogenic proteins - obtd. using recombinant DNA and used for inducing cartilage and bone formation.

Disclosure; 7pp; English.

The HindIII-SacI bovine genomic bBMP-2 fragment described in N8062 is subcloned into M13, labelled and used as probe to screen polyadenylated RNAs from various cells and tissue sources. Sequence analysis of the strongly hybridising clones hBMP-2 class (-BMP-2) indicated that they have extensive homology with the sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-OCT-1990 (first entry)

Human Bone Morphogenic Protein-2 class I cDNA.

Bone morphogenic protein; hBMP-2 class I; prob

bone formation; osteogenic cpds.; prodontal d
                                                                12-OCT-1990 (first entry)
Plasmid pEMpl-tPA.
Tissue plasminogen activator; myocardial infarction; thrombosis; embolism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENE-) Genetics Inst
Wozney JM, Rosen VA;
WPI; 88-021565/03.
P-PSDB; P80619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO8800205-A.
14-JAN-1988.
30-JUN-1987; U01537.
26-MAR-1987; US-031346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N80632 standard; DNA; 1606
                                                                                                                                     N81970 standard;
                             misc_rna
                                                      Homo sapiens
                                                                                                                                                                                                         14
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ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10
                            Location/Qualifiers 7. .1748
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/*tag= a
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    /*tag= a
/label=tPA_cDNA
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Pred. No. 6.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prodontal disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.2e+02;
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                                                                                                                                                                                                                                                                                      Length 1606
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    WO8800242-A.
14-JAN-1988.
25-JUN-1986; US-879038.
(DAMO-) Damon Biotech Inc.
Gillies SD;
WPI; 88-021592/03.
prodn. of human tissue plasminogen activator - by myeloma cells, pref. in presence of epsilon amino caproic acid.

Disclosure; p; English.

The plasmid was prepd by cleaving the very long 3' UT of t-PA cE (which causes mRNA instability) 34 nucleotides downstream of st codon and inserting it into pEMpl vector. The pEMpl vector was constructed from the following components (see feature table):

(a) a 2.25 PvuII-BamHI fragment from pSV2-gpt contg. the SV40 enhancer and early region promoter, the E.coli gpt gene, the SV40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_rna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_rna
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                                                                                                                                                                                                                                                                                                                  promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label-pBR322
/note-"contg
replication"
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                                                                                                                                                                                                                                    'note="from metallothioneine
                                                                                                                                                                                                                                                                        /note="from metallothioneine
7467. .7533
                                                                                                                                                                                                                                                                                                                                                                                                                            'note="from lambda
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/note="non-coding strand"
                                                                                                                                                                                                                                                                                                                                                                     'note="lambda mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="from SV40(gpt)"
453. .6469
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                                                                                                                                                                                                                                                                                                                                                                                                                                         label-blocking_element
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                                                                                                                                                                                                                                                                                                                                                                                  abel-cap_site
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te-"from SV40"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .1708
19- b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ie-"from SV40"
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           The mammalian cell shuttle vector plasmid pSV7d contains the SV40 origin of replication and early promoter (315 bp, Pvull pos 272-StuI pos 5193 with an 8 bp deletion between nucleotides 173 and 182), a polylinker, and the SV40 poly A addition site (217 bp Bc11 pos 2775-pos 2558). The SV40 sequences were cloned into the pBR322 derivate pML between nucleotide 4210 and Nrul pos 973. The SV40 sequences are positioned such that the direction of transcription from the early promoter is in the same direction as the ampicillin gene of the vector. Three separate constructed by isolating EcoRi fragments from cDNA clones and ligating them into pSV7d previously digested with EcoRi and treated with alkaline phosphatase. The resulting clones were called pSV7d-pDGF-A103 (D1), and pSV7d-PDGF-BI (B-chain). Recombinant pDGF is
                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-OCT-1988.
22-APR-1988; 303658.
22-APR-1987; US-041299.
(CHIR-) Chiron Corp.
Helfin C-H, Betsholtz C, F
                                                                                                                                                                                                                                                                                                                                Recombinant prodn. of growth factor A-chain polypeptide -
for use in treating wounds and ulcers caused by diseases,
infections or neoplasms
Example: Fig 7: 31pp: English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
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6705 TGTGTGTCAG 6696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SV40 virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence of SV40 early promoter, polylinker and SV40 poly A addition region from pSV7d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N80979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Platelet-derived growth factor (PDGF); SV40 virus; pSV7d; wound treatnent; SV40 polylinker; SV40 poly A addition; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and polyadenylation signals;

(b) a 2.3 kb PvuII-EcoRI fragment from pBR322 conto. the ampicillinase gene and the bacterial origin of replication;

(c) a 0.3 kb PvuII-EcoRI fragment contg. an Ig heavy chain enhancer;

(d) a 0.25 kb SacI-BgIII fragment contg. the metallothioneine I romo (e) a 0.4 kb AvaII-HaeIII fragment from the 3' UT of Ig kappa light chain gene; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (f) a 0.26 kb xbaI-bstNI fragment contg. the Ig light chain promoter, TATAA sequence, and the initiation site.
The expression plasmid can be used to transform host cells esp.
J5581, ATCC CRL 9132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-SEP-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"SV40 polylinker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="SV40 early promoter" 316. .579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= d
/note="pBR322 DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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/note="base 4210 of pBR322"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1847 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scott J,
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mucosal or
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Search completed: September 18, 1999, 00:33:31 Job time: 18971 sec

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Result
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                                                    SUMMARIES
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              Description
 AB001488 Bacillus
SOURCE
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KEYWORDS
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DEFINITION
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Bacillus subtilis
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yddL;
ydeC;
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yddB, yddC, yddD,
yddB, yddN, yddO,
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ydfF, ydfR, ydfR,
                                                                                                                                                          cspC;
                    ydgH;
                                                                                                                                              rsbv; rsbw; rsbx;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      970
209100
207730
215640
1707
                                                                                                                                                          ddlA; dinB;
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87500
2985
4753
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42157
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genome d
degree.
         (strain:168) DNA
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AC006052
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MPAE000027
MPU25989
AF058609
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AF009415
AF030775
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SPDEXCAP
U00017
VANQRBOL
AE001155
AE001544
AE0015701
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CJAJ2074
D37807
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AB008698
ACCAA616
ACCGYRB12
AF027868
BACCS18422
BATRPEG
BS16S138
BSUB0011
BSUB0016
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RABBCAS
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MC097
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LACPFYKLDH
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                                                                                                                                                          expZ;
                                                                       yddP;
                                                                                            ydcN;
                                                             ydeG;
                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                             sequence,
                                                                                                                                                         gsiB;
                                       tops
ydak,
ydbs,
ydco,
ydco,
yddf,
yddf,
ydes,
ydes,
                            ydgA;
                                                                                                                                                          mutT;
                                                                                                                                                                                                           BCT 13-FEB-1999
148 kb sequence of the region
                                                                                                                                                ; nap; or
A; ydaB;
                                       ydcF;
yddH;
yddS;
yddS;
ydeJ;
ydfA;
ydfL;
                                                                                                                ydbo;
                                                                                                                                                          orfR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y18422 Bacillus sp
221938 B.aphidicol
AJ001424 Bacterium
299106 Bacillus su
299114 Bacillus su
299119 Bacillus su
299119 Bacillus su
299119 Bacillus su
299119 Buchnera ap
M80817 Buchnera ap
L43551 Buchnera ap
L46769 Buchnera ap
AJ002074 Campyloba
D37807 Phormidium
D90902 Synechocyst
L75601 Ruminococcu
                                                                                                                                                                                                                                                                                                                AF008210 Buchnera
AF009415 Staphyloc
AF030775 Marine sn
AF049852 Borrelia
AF0049852 Borrelia
AF0058609 Mycoplasm
U2598 Mycoplasm
U2598 Mycoplasm
AF058609 Oryctolag
Y12526 A.hottentot
M33582 O.cuniculus
X54859 Porcine TNF
AB000899 Oryzias 1
AB003358 Xenopus 1
M10066 Chicken c-e
                                                                                                                                                                                                                                                                                                                                                                                                                                                        247210 S.pneumonia
U00017 Mycobacteri
237111 V.alginolyt
AE001155 Borrelia
AE001154 Helicobac
AE00156 Helicobac
AE001701 Thermotog
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AB008698 Acinetoba
L09246 Acinetobact
D73423 Acinetobact
AF027868 Bacillus
                                        yddī;
ydek;
ydfB;
ydfM;
                                                                                 ydan;
ydbe;
ydbe;
ydce;
ydck;
ydck;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M60178 L.lactis se
Z33072 M.capricolu
AL035310 Mycobacte
                                                                                                                                                          orfS; orfT;
                                                            ydaD;
ydbO;
ydbQ;
ydcH;
ydcH;
ydcS;
yddJ;
ydeA;
ydeA;
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                            ydaE
ydbG
ydbR
ydcI
ydcI
ydcI
ydcI
yddK
ydeB
ydeB
ydfD
ydfD
ydfO;
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JOURNAL
REFERENCE
AUTHORS
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AUTHORS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kasahara, Y., Nakai, S., Lee, S., Sadaie, Y. A 148 kbp sequence of the region between Bacillus subtilis genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (03-MAR-1997) to the DDBJ/EMBL/GenBank databases. Ogasawara, Nara Institute of Science and Technology, Graduat School of Biological Sciences 9916-5 Takayama-cho, Ikoma, N 630-01, Japan (E-mail:nogasawa6bs.alst-nara.ac.jp, Tel:07437-2-5430, Fax:07437-2-5439)
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LSDSSYIALVVHLTYAIERIKLGETIIMEQNELEELMNAKEYSSALEIAGELERAFGV
TIEBAEVGYITHLKSANRTKKTEYKAQEIELETALGTKLIAFISDKIRMDLTKNYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKGKDVQAYDMIVSTVPIPYENIDYIMVSPLLNEEDANQVKQYIKRKIPLILNKKRSS
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                                                                                                                                                                                                                                                                                                                                                                                                               FFTWMKEKNIL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                  codon_start=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note-"PROBABLE RHO-INDEPENDENT TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene-
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2273
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35 and 47 degree of the
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                                                                                                                                                                                                                                                    terminator
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                                                                                                                                                                                                                       'note-"PROBABLE
                                                                                                                                                                                                                                                                         [FTDPR]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note-"FUNCTION UNKNOWN."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5645. .6148
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                     note="PROBABLE ACETYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transl_table=11
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"ydaf" .6784

RHO-INDEPENDENT TRANSCRIPTIONAL

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REFERENCE
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AUTHORS
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ORGANISM
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                                                                                                                           Direct Submission
Submitted (09-007-1997) to the DDBJ/EMBL/GenBank databases. Maki Bubmitted (09-007-1997) to the DDBJ/EMBL/GenBank databases. Maki Hayashi, Faculty of Pharmaceutical Sciences, Chiba (Diversity, Laboratory of Membrane Biochemistry; 1-33 Yayo1-cho, Inage-ku, Chiba, Chiba 263, Japan (E-mail:makiha@p.chiba-u.ac.jp, Tel:043-290-2932, Fax:043-290-3021)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AB008030 6908 bp DNA circular BCT 13-FEB-199. Vibrio alginolyticus genes for Na-translocating NADH-quinone reductase complex, ngr operon, complete genome. AB008030 D43958 D49364 g2558472
                         Hayashi,M., Hirai,K. and Unemoto,T.

Sequencing and the alignment of structural genes in the ngr operon encoding the Na(+)-translocating NADH-quinone reductase from Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                Nqr1 subunit of Na-translocating NADH-quinone reductase complex alpha-subunit; Nqr2 subunit of Na-translocating NADH-quinone reductase complex; Nqr3 subunit of Na-translocating NADH-quinone reductase complex gamma-subunit; Nqr4 subunit of Na-translocating NADH-quinone reductase complex; Nqr5 subunit of Na-translocating NADH-quinone reductase complex; Nqr6 subunit of Na-translocating NADH-quinone reductase complex; Nqr6 subunit of Na-translocating NADH-quinone reductase complex; Nqr6 subunit of Na-translocating NADH-quinone reductase complex beta-subunit.
                                                                                                                                                                                                                                                                                                                                                       Vibrio alginolyticus DNA.
Vibrio alginolyticus
                                                                                                                                                                                                                                                                             1 (bases 1 to 6908)
Hayashi, M., Unemoto, T. and
                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AB008030,1 GI:2558472
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Pred. No. 1.2e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nakayama, Y., Hayashi, M. and Unemoto, T. Identification of six subunits constituting Na+-translocating NADH-quinone reductase from the marine Vibrio alginolyticus FEBS Lett. 422 (2), 240-242 (1998)
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Cloning of the Na(+)-translocating NADH-quinone rethe marine bacterium Vibrio alginolyticus and the beta-subunit in Escherichia coli
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Existence of Na+-translocating NADH-quinone reductase
Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                                                                                                           /gene="nqr2"
1732. .2976
/gene="nqr2"
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                                                                                                                                                                                                                         /evidence-experimental
/product="Ngr2 subunit of Na-translocating
reductase complex"
                                                                                                                                                                                                                                                                                                                                                  /note="hydrophobic membrane protein with
Ngr2 subunit of Na-NQR complex"
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GenBank Accession Number: 237111."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Vibrio alginolyticus"
/db_xref="taxon:663"
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he expression
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VERSION KEYWORDS

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/gene="ngr4"
/note="hydrophobic membrane protein with pI 9.17;
/note="hydrophobic membrane protein with pI 9.17;
Ngr4 subunit of Na-NQR complex"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="Nqr5 subunit of
reductase complex"
/protein_id="BAA22914.1"
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4376. .
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Na-NQR complex gamma-subunit"
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reductase complex beta-subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="PID:d1023785"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="hydrophobic membrane protein Ngr5 subunit of Na-NQR complex"
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/gene="ngr5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MSSAQNVKKSILAPVLDNNPIALQVLGVCSALAVTTKLETAFVM
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VSAITYYEQGETPGLGGEVENPSWRDQFIGKKLYNDDHQPAIKVVKGGAPQGSEHGVD
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                                                                                                                                                    activity, pI 4.55;
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                                                                              transl_table=11/
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                                                                                                                                                 as a cofactor,
nqrf, Nqr6 subun
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nit of Na-NQR compl
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (10-NOV-1997) to the DDBJ/EMBL/GenBank databases. Satoshi Yamamoto, Marine Biotechnology Institute, Kamaishi Laboratories; Heita 3-75-1, Kamaishi City, Iwate 026, Japan (E-mail:syamamoto@kamaishi.mbio.co.jp, Tel:81-193-26-6544, Fax:81-193-26-6584)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamoto, S., Bouvet, P.J. and Harayama, S.
Phylogenetic structures of the genus Acinetobacter sequences: comparison with the grouping by DNA-DNA Int. J. Syst. Bacteriol. 49 Pt 1, 87-95 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acinetobacter radioresistens (strain:SEIP 12.81) DNA Acinetobacter radioresistens Bacteria; Proteobacteria; gamma subdivision; Pseudomo
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/db_xref="prD:;d1039153"
/db_xref="GI:;4514433"
                                                                                                                                                                                                                                                                                                   /gene="gyrB"
:1. .>1167
                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:40216"
                                                                                                                                                                                                                                                                                                                                                                                                      organism="Acinetobacter/
strain="SEIP 12.81"
                          <sup>t</sup>translation="DNSYKVSGGLHGVGVSVVNALSSKLELTVQRAGQIHEQEYQHGV
`QYPLRVVGQTERTGTKVRFWPSAETFSQTIFNVDILARRLRELSFLNAGVRIVLCDE
                                                                                                                                                                                                                                                 'gene="gyrB"
'EC_number="5.99.1.3"
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GI:4514432

gamma subdivision; Pseudomonas

group;

based on gyrB hybridization

Sgo

gene

gene

CDS

transl\_table=11 codon\_start-

β

radioresistens'

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3856 CIGITICIAGE 3846
                                   1 CTGTTTCTAGT 11
                                                                                                Similarity
                                                                               Conservative
                                                                                                                                                                                                                     LGVEDENILLDDFGG" 6252. .6276
                                                                                                                                                                                                                                                                                                                                            /translation="MDIILGVVMFTLIVLALVLVILFAKSKLVPTGDIIISVNDDPSL
AIVTQPGGKLLSALAGAGVFVSSACGGGGSCGQCRVKVKSGGGDILPTELDHIIKGEA
REGERLACQVAMKTDMDIELPEEIFGVKKWECTVISNDNKATFIKELKLQIPDGESVP
                                                                                                                                                                                                                                                               HCALSDPLPEDNWDGYTGFIHNVLYENYLRDHEAPEDCEYYMCGPPMMNAAVIGMLKD
                                                                                                                                                                                                                                                                                  EHGIIMLNVRIATPPPNNPDVPPGIMSSYIWSLKEGDKCTISGPFGEFFAKDTDAEMV
FVGGGAGMAPMRSHIFDQLKRLHSKRKMSFWYGARSKREMFYVEDFDMLQAENDNFVW
                                                                                                                                                                                                                                                                                                                          FRAGGY IQIEAPAHHVKYADYDI PEEYREDWEKFNLFRYESKVNEET I RAYSMANY PE
                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="PID:g2558478"
/db_xref="GI:2558478"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="BAA22915.1"
/db_xref="PID:d1023786"
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Pred. No.
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1.5e+03;
                                                                                                                 Length 6908;
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group;

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RESULT 5
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ORIGIN
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AUTHORS
TITLE
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KEYWORDS
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                                       DEFINITION
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ORIGIN
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MEDLINE
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Best Local S
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                                   ACCGYRB12
Acinetobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moraxellaceae; Acinetobacter.

1 (bases 1 to 1154)
Lambert T. Gerbaud, G., Galimand, M. and Courvalin, P.
Characterization of the Acinetobacter haemolyticus aac(6
encoding an aminoglycoside 6'-N-acetyltransferase which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acinetobacter haemolyticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aac(6')-Ig gene; aminoglycoside 6'-N-acetyltransferase.
Acinetobacter haemolyticus (strain BM2685) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acinetobacter haemolyticus aminoglycoside 6'-N-acetyltransferase (aac(6')-Ig) gene, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94079352
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                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                               /product="aminoglycoside 6'-N-acetyltransferase"
/protein_id="AAA2189.1"
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/db_xref="GI:455437"
/db_xref="GI:455437"
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LLAYSDHQAIAMLEASIRFEYVNGTETSPVGFLEGIYVLPAHRRSGVATMLIRQAEVW
AKQFSCTEFASDAALDNVISHAMHRSIGFQETEKVVXFSKKID"
a 200 c 260 g 372 t
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VKVPDPKFSSQTKEKLVSSEVKPAVEQAMNKAFSEYLLENPAAAKŠIAGKIIDAARAR
DAARKAREMTRRKSALDIAGLPGKLADCQEKDPALSELFLVEGDSAGGSAKQGRNRKM
QAILPLKGKILNVERAREDRMISSAEVGTLITALGCGIGREEYNPDKLRYHKIVI"
a 230 c 302 g 318 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Acinetobacter
/strain="BM2685"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:29430"
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                  sp. gene
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                                                        300 bp
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                                                                                                                                                                                                                                                                                   Score 11;
Pred. No.
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Pred. No.
                                for DNA gyrase subunit B protein, C terminal
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                                                                                                                                                                                                                                                                                                          DB 1;
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                                                                                                                                                                                                                                                                                     .8e+03;
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                                                      04-FEB-1999
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which modifies
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       REFERENCE
AUTHORS
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                      RESULT 6
AF027868/c
LOCUS
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ACCESSION
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ORIGIN
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AUTHORS
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SOURCE
ORGANISM
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NID
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Best Local
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                             1 CTGTTTCTAGT 11
                                                                                                                                                                                                                                                                                                                                                                     CTGTTTCTAGT
                                                                                                                                                                                                          AF027868
Bacillus
AF027868
                Bacillus subtills
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
1 (bases 59208 to 59540)
                                                                                                                Bacillus subtilis.
                                                                                                                                                               AF027868.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamamoto, S. and Harayama, S.
Phylogenetic analysis of Acinetobacter strains based on nucleotide sequences of gyrB genes and on the amino acid of their products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97088999
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Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax:0193-26-6584)
2 (bases 1 to 300)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (30-SEP-1995) to the DDBJ/EMBL/GenBank databases. Satoshi Yamamoto, Marine Biothechnology Institute, Kamaishi Laboratories; 3-75-1 Heita, Kamaishi, Iwate 026, Japan (E-mail:HGD02251@niftyserve.or.jp, Tel:0193-26-6538,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (30-SEP-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D73423.1 GI:1322104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moraxellaceae; Acinetobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acinetobacter sp. (strain:SEIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases
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llarity 100.0%;
Conservative
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                                                                                                                                                                                                                               87500 bp DNA subtilis chromosome
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/product="NNA gyrase subunit B protein"
/protein_id="BARI1148.1"
/protein_id="BARI1148.1"
/db_xref="PID:d1011809"
/db_xref="PID:g1322105"
/db_xref="GI:1322105"
                                                                                                                                                                                                                                                                                                                                                                     98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="correspond to
ene (X04341, X00870)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene-"gyrB"
'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene≖'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      strain="SEIP 12.81"
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                                                                                                                                                             GI:2618993
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van Dijl, J.M. and Behnke, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 11; |
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (2),
                                                                                                                                                                                                                             region between
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1.9e+03;
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and odhAB. 15-NOV-1997

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (01-OCT-1997) Laboratoire de Genetique Microbienne, INRA, Domaine de Vilvert, Jouy-en-Josas cedex 78352, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 (bases 1 to 87500)
Lapidus,A., Galleron,N., Sorokin,A. and Ehrlich,D.
Sequence analysis of the Bacillus subtilis chromosome region
between the terC and odhAB loci cloned in a yeast artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          apidus, A., Galleron, N., Sorokin, A. and Ehrlich,
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                                                                                                                                                                                                                                         /gene="vr
                                                                                                                                                                                                                complement(1217.
/gene="yoaB"
                                                                                                                                                                                                                                                                                                                   /translation="MFPILETDRLILRQITDQDAEAIFACFSNDEVTRYYGLENMESI
EQAISMIQTFAALYQEKRGIRWGIERRDTKELIGTIGFHALAQKHRRAEIGYEIIPEH
WRNGFASEVISKVVSYGFSALGLSRIGAVVFTDNEASNRLLLKNGFQKEGVLRQYMYS
                                                                                                                                                                                                                                                                                                                                                                                    /product-"putative alanine acetyl transferase"
/protein_id-"AAB84419.1"
/db_xref="BD:;9261895"
/db_xref-"GI:2618995"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="AYETAAESLLQGGTLEQMAVDTKIAAGFSGSMRHNLITMLDLCG
LPQAFGIQSAAKLFGELRHMLHTTSVIKYPVFIQQKNYTGYKPAITHSPILSTYAFGH
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                                                                                                                                                                                              complement
                                                                                                                                                             /_____rement(1217. .2461)
/gene="yoaB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to B.subtilis P20 protein and E.coli
/product="putative transporter"
/protein_id="AAB84444 1"
/db_xref="PID:g2619020"
                                                                 /transl_table=1]
                                                                                /codon_start-1
                                                                                                                                /note="similar
2 (400 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="yoaA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAB84418.1"
/db_xref="PID:g2618994"
/db_xref="GI:2618994"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
/product="YoxB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Bacillus subtilis"
/db_xref="taxon:1423"
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                                                                                                       citation=[3]
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gene

CDS

dehydrogenase (419 /citation=[3]

note="similar to B.subtilis D-3-phosphoglycerate hydrogenase (419 aa) encoded by serA gene"

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/protein_id="aab84445.1"
/db_xref="pi0:q2619021"
/db_xref="gi0:q2619021"
/db_xref="gi0:2619021"
/db_xref="gi0:2619021"
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/translation="%KKQGYLVFDLGTGNARVAVVSVTGSVLTVEREDIEYSTETLY
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IDNRGREMEAGIPDWEDIYSSTGRLPTALFSALKLXYGLKQRQPSLMEKTASTTSISDM
VTYQLSGILTYEPSQATETLLFDVKQNTWSEEMFTFFFFFFTFTKTRAGTALGTIA
NEYASELGLSINAKVIAGGGUTQLAVKSTGAGLEDIYIVSGTTFPITKTEDHGDTKH
KAWLNCHTDQGHWLVETNPGITGLNYQKLKQIFYPNETYEVMEEEISALAKEDHACVA
ALGSYLSAEKNALTRGGFLFDAPLSAHLKRAHFYRAALEEIAFSIKMNFDILTEVTPF
complement(4036.
/gene="yoaD"
                                                                                                                                      ERDYVWVCGGGFQSKALTQYIADLLQKKVYVQEGYHQASVVGAAVICNETFQLTEEMS
ANVRVIEPKDCQIELALYEEWKQTQRFFSGSESKVLI"
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/gene="yoaC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MLDK101PKRLAWGFLGVVLFWMGDGLEQGWLSPFLIENGLTVQ
QSASIFSIYGIALAIASWFSGVCLEAFGAKRTMFMGLMFYVIGTAAFIVFGFEQLNLP
VMYVTYFVKGLGYPJFAXSFLTWVIYRTPGSKLSTAYGWWIAYCLGWPYFGAWYSSY
AIKAFGYLNTLWSSIFWVCLGAFFALFINKDRFEKKKRKRSETAEELLKGVTILFTNP
                                                                                                          complement(4036.
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                                                                   /gene="yoab"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="xylulose kir
/protein_id="AAB84445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="yoac"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
/transl_table=11
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                                       .5070)
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gene

/protein\_1d="AAB84446.1"
/db\_xref="FID:92619022"
/db\_xref="GI:2619022"
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/db\_xref="GI:2619022"
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LTGKTVGMIGFGAVGQRIAKLLTAFDCKIKYYDPYIQDDHPLYEKASLKTVFSDSDIV SVHLPRTEETLGLIDRQYFDLMKESAIFVNTSRAVVVVNREDLLFVLKEHKISGAILDV FYHEPPEESDYELISLPNVLATPHLAGATFEVEDHHVTILNKALKKWKGEKTLNIQTM 'gene="yoaE" .7427

gene CDS

'gene="yoaE"

.7427

/note="similar to B.subtilis YyaE protein (667 aa) and E.coli formate dehydrogenase (715 aa)" /product="putative formate dehydrogenase" /protein\_id="AAB84420.1" /db\_xref="pib:92618996" /db\_xref="GI:2618996". transl\_table=11 codon\_start=1 citation-

SAGIDPEETVHTKLFIFWGINAVSTNMHQITIAQKARKKGAKIVVIDVHKNQTGRLAD WFIPIKPGTDSALALGIMHILFKENLHDEAFLSEYTVGYEELREHVKQYDPEKVSTIT GVSTEDIYRLAKMYGETSPSFIRIGNGPQHHDNGGMIVRTIACLPAITGQWLHTGGGA IKHNSGILEYNTNALQRPDLLKGRTPRSFNMNQLGRVLLETDPPIRSLFIYGTNPAVV APEANKVRQGLLREDLFTVVHDLFLTETAAYADIVLPATSAFENTDFYTSYWHHYIQL /translation="mrsfatqqngifksvcsldcpdqcgllikkkdgkivkvqgdpdh
PVTAGNICNKVRNMTERIYDEKRLTTPLKRTGAKGQAIFEPISMKEAIDTITSRWKQL
IDEEGAESILPYSFYGNMGKLTAEGMDRRFFYRMGSSQLERTICSKAGSEGYKYTMGI

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Herman,L.M.F.
Direct Submission
Submitted (16-NOV-1998) L.M.F. Herman,
                                                            Herman, L. and Heyndrickx, M. Bacterial typing by REP-PCR homologous sequences Unpublished
                                                                                                                                                                                   Bacillus sporothermodurans.
                                                                                                                                                                                                                                                                                    BACS18422 2985 bp DNA BCT 23-NC Bacillus sporothermodurans partial uvrB and uvrA genes.
                                                                                                                                                                                                                      urvA gene; urvB gene
                                                                                                                                                   Bacillus
                                                                                                                                                                                                                                       Y18422.1 GI:3924674
                                                                                                                                                                                                                                                                        Y1842:
                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillaceae;
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                                                (bases 1 to 2985)
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/gene="yoaH"
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protein McpA (661 aa)"
/citation=[3]
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YVPGPNHNFLNSTFSNNEKHIKLEKTPKLFINTKDAEKHGIVDGAPVRIWNSRGECEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="PID:g2618997"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation-"MNTVMMSFASSAELLKDKENCFPEHILDMYEQAAKHDLSFTHTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="transcription antiterminator"
/protein_id="AAB84421.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="similar to H.influenzae HI0035 protein (551 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAB84447.1"
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                                                                                                                                                                                                                                                                                               Submitted (10-MAR-1993) Chi-Yung Lai, Microbiology, California-Davis, Department of Microbiology, Univer California-Davis, Davis, California, 95616-8665, USA
                                                                                                                                                                                                                                                                                                                                                                                                               Lai,C.Y., Baumann,L. and Baumann,P.
Amplification of trpEg: adaptation of Buchnera aphidicola endosymbiotic association with aphids proc. Natl. Acad. Sci. U.S.A. 91 (9), 3819-3823 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BATRPEG 4753 bp DN/B.B.aphidicola trpE and trpG components I and II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Buchnera aphidicola.
Buchnera aphidicola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9090
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                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anthranilate synthase I;
                                                                                                                                                                                                                                                                                                                                                                                                   94224833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  teria; Proteobacteria; gamma (bases 1 to 4753)
                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 4753)
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                                                             /gene="trpE"
1027. .2574
/gene="trpE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1792. .>2985
/gene="uvrA"
/product="UvrA |
1792. .2985
/codon_start=1
/rable=11
/product="anthranilate synthase,
/protein_id="CAA79931.1"
                                                                                                                                                                               /note-"This 1.7kb EcoRV fragment is cloned seport necessary contiguous with the rest of the
                                                                                                                                                                                                                               /organism="Buchnera aphidicola"
/db_xref="taxon:9"
                                                                                                                                                                                                                                                                                 Location/Qualifiers
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497 c
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1792. .>2985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Bacillus sporothermodurans"/strain="MB342"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department Animal Product
                                                                                                                                  /evidence=experimental
                                                                                                                                                  'note="one unit of a four-unit plasmid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:472880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="UvrB protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       db_xref="taxon:46224"
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Pred. No. 1.6e+03;
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               component
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   II;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TrpE gene; trpG
                                                                                                                                                                                                                                                                                                                                University of
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KEYWORDS
SOURCE
  JOURNAL FEATURES
                                                                                        REFERENCE
AUTHORS
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ACCESSION
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ORIGIN
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TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                        ORGANISM
                                              TITLE
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Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4725
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                                                                                                                                                                                                                                                                                                AJ001424.1 GI:2385346
16S ribosomal RNA; 16S rRNA
unidentified bacterium
unidentified bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                           BS16S138 970 bp mRNA BCT Bacterium sp. 16S ribosomal RNA, clone 400-138. AJ001424
                                                                     Denissova,L.Y., Bel kova,N.L., Tulokhonov,I.I., Parfenova,V.V. and Zaychikov,E.F.
                                                                                                                           Direct Submission
Submitted (07-SEP-1997) Zaychikov E.F., Laboratory of Molecular Enzymology, Limmological Institute, Ulan-Batorskaya str. 3, Irkutsk, 664033, RUSSIA
                                       Phylogenetic analysis of aquatic bacteria of the lake Baikal
                                                                                                                                                                                                                                  l (bases 1 to 970)
Zaychikov, E.F.
                                                                                                                                                                                                                                                                               Bacteria; environmental samples
                                                                                                               (bases 1 to 970)
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ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MSKNPYEIEIIQKTAPYHPDPTMIFNHLCASRPGTLLLETAEVN
KKRDL"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="anthranilate synthase, component
/protein_id="CAA79933.1"
/db_xref="PID:g472883"
/db_xref="GI:472883"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKIRNPILMLSPGPSTPKNAGCMLNLIKKVKGEIPIVGICLGHQAIVEAYGGIIGYAG
EIFHGKASLINHDGLEMFEGLPQPLPVARYHSLICNKIPKNFIINSYFNDMIMSVRNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="anthranilate synthase,
/protetal_id="CAA/7932.1"
/db_xxef="ptD:g4/72882"
db_xxef="GI:472882"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAIGYFTDLGNLDTCITIRSAYVEKQVATIQAGAGIVYNSIPENEVNESLNKAQAVIN
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'gene-"trpE"
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/db_xref="GI:472881"
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transl_table=11
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MEDLINE
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Matches 11
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                                                                                                                                                                                                                                           Borniss, R. Boursier, L. Brans, A. Braun, M. Brignell, S.C.

Borniss, R. Brouillet, S., Bruschi, C.V., Caldwell, B. Capuano, V.

Carter, N. M., Choi, S.K., Codani, J.J., Connerton, E.F., Cummings, N.J.,

Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Ehrlich, S.D.,

Emmerson, P.T., Entlan, K.D., Errington, J., Fabret, C., Ferrari, E.,

Foulger, D., Fritz, C., Fujita, M., Fujita, Y., Fuma, S., Galizzi, A.,

Galieron, N., Ghim, S. Y., Glaser, P., Goffeau, A., Golightly, E.J.,

Garandi, G., Guiseppi, G., Guy, B.J., Haga, K., Haiech, J., Harwood, C.R.,

Henaut, A., Hilbert, H., Holsappel, S., Hosono, S., Hullo, M.F.,

Itaya, M., Jones, L., Joris, B., Karamata, D., Kasahara, Y.,

Klaerr Blanchard, M., Klein, C., Kobayashi, Y., Koetter, P.,

Klaerr Blanchard, M., Klein, C., Kobayashi, Y., Koetter, P.,

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Masuda, S., Mauel, C., Medigue, C., Medina, N., Mellado, R.P.,

Jardinois, S., Lauber, J., Liu, H.,

Masuda, S., Maznevic, V., Lee, S.M., Levine, A.,

Portetelle, D., Porwollik, S., Prescott, A.M., Noone, D., O'Reilly, M.,

Ogawa, K., Ogiwara, A., Oudega, B., Park, S.H., Parcov, Pohl, T.M.,

Ogawa, K., Ogiwara, A., Oudega, B., Park, S.H., Parcov, Pohl, T.M.,

Portetelle, B., Rose, B., Rose, M., Sadate, Y., Sato, T.,

Rivolta, C., Rocha, E., Rose, M., Sedise, Y., Sato, T.,

Schowska, A., Seror, S., Schroeter, R., Scoffone, F., Sekiguchi, J.,

Schowska, A., Seror, S., Vandenbol, M., Vannier, F., Vasarotti, A.,

Yata, A., Wanbutt, R., Wedler, E., Waller, H., Welzeneger, T., Vata, K.,

Yata, A., Wander, E., Zhard, T., Tamane, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGTTTCTAGT 11
2 (bases 1 to 209100)
Kunst, F., Ogasawara, N.,
Direct Submission
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Kunst,F., Ogasawara,N., Mc
Azevedo,V., Bertero,M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BSUB0003 209100 bp DNA BCT 26-NOV-1997 Bacillus subtilis complete genome (section 3 of 21): from 402751 to
                                                                                                                                                               The complete genome sequence of the 
Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus subtilis
Bacteria, Firmicutes, Bacillus/Clostridium group; Bacillaceae;
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/product="16S ribosomal RNA
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/db_xref="taxon:2338"
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Pred. No. 1.8e+03;
; Mismatches 0;
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                           Yoshikawa, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bessieres, P., Bolotin, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 t
                                                                                                                                                                                              gram-positive bacterium
                           and Danchin, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(1292. .1849)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'function="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="taxon:1423"
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                                    unction="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               note="similar to glutamine ABC transporter (ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="yckI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="yczE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "function="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="similar to hypothetical proteins from B. subtilis"
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KEYWORDS
                           FEATURES
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                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                       Bron. S., Broullet, S., Bruschi, V., Caluwell, J., Capuanu, V., Carter, N. M., Cholis, K., Codani, J.J., Connerton, I.F., Cummings, N.J., Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Ehrlich, S.D., Ermerson, P.T., Entian, K.D., Errington, J., Fabret, C., Ferrari, E., Foulger, D., Fritz, C., Fujita, M., Fujita, Y., Fuma, S., Galizzi, A., Galleron, N., Ghim, S.Y., Glaser, P., Goffeau, A., Golightly, E.J., Grandi, G., Guseppi, G., Guy, B.J., Haga, K., Halech, J., Harwood, C.R., Henaut, A., Hilbert, H., Holsappel, S., Hosono, S., Hullo, M.F., Itaya, M., Jones, L., Joris, B., Karamata, D., Kasahara, Y., Koningstein, G., Krogh, S., Kumano, M., Kurita, K., Lapidus, A., Kilenr-Blanchard, M., Klein, C., Kobayashi, Y., Koetter, P., Koningstein, G., Krogh, S., Kumano, M., Kurita, K., Lapidus, A., Liu, H., Masuda, S., Mauel, C., Medigue, C., Medina, N., Mellado, R.P., Mizuno, M., Moest, D., Nakai, S., Noback, M., Noone, D., O'Reilly, M., Ogawa, K., Oydwara, R., Oudega, B., Park, S.H., Parro, V., Pohl, T.M., Oyawa, K., Oyawara, K., Oyawara, K., Reynolds, S., Rieger, M., Rivolta, G., Rocha, B., Roche, B., Rose, M., Sadaie, Y., Sato, T., Schous, A., Seror, S., Schroeter, R., Scoffone, F., Sekjuchi, J., Sekowska, A., Seror, S., Seror, P., Shin, B.S., Soldo, B., Sorokin, A., Tamakoshi, A., Tanaka, T., Tarpstra, P., Vassarotti, A., Vannier, F., Vassarotti, A., Vannier, F., Vasamotto, K., Yata, K., Willat, A., Yanamoto, H., Yamane, K., Yasumoto, K., Yata, K., Vannier, F., Vasamoto, K., Yata, K.,
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                                                               Submitted (18-NOV-1997) I. Moszer, A. Danchin, Institut Pasteur, Regulation de l'Expression Genetique, 28 rue du Docteur Roux, 75724 Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr, adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45
                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                      Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchin, A.
                                                                                                                                                                                                                                                                                                                                                                                                               Winters, P., Wipat, A., Yamamoto, H.,
                                                                                                                                                                                                                                                                                   Nature 390 (6657), 249-256 (1997)
                                                                                                                                                                                                                                                                                                                 Bacillus subt:
                                                                                                                                                                                                                                                                                                                                    The complete genome sequence of the gram-positive bacterium
                                                                                                                                                                                                                                                                                                                                                                                           Yoshida, K., Yoshikawa, H.F., Zumstein, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Borriss, R., Boursier, L., Brans, A., Braun, M., Brignell, S.C., Brons, Brouillet, S., Bruschi, C.V., Caldwell, B., Capuano, V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus subtilis. Bacillus subtilis
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ilarity 100.0%;
Conservative (
                                                    48
Location/Qualifiers
1. .207730
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/gene="yckJ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus/Clostridium group; Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.:
; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                    Yamane, K.,
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7350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RKVTFVKENKKWKVNQFDAVI"
                                                                                                                                                                                                                     /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                         complement(2745. .3032)
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/transl_table=11
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/gene="yoeA"
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                                                                                                                                                                         db_xref="GI:2634233
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                                                                                                                                                                                                                                                                                                                         function-"unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1359. .2434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="GI:2634232"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'db_xref="GI:2634231"
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                    .3578)
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THLPEHAASFLRRFPEVDLSVNTADTHHLIQQVLDHKVDGAFVYGPVEHAAVRQLHVS
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EQPKDKVEGQTTHFTVADRWGNVVSYTTTIEQLFGTGIMVPDYGVILNNELTDFDAIP
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                                                                                                                                                                                /db_xref="PID:e1185316"
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                                                                                                                                                                                                                                                                                                                                       /note="similar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(5627. .6484)
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/gene="yofA"
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KTROTTI IDSRERAPAGATEDMFLDENGKAIPFSERVTKGTAVGVPGTLKGLEBALDK
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TLIQKDLAKTFKLIRSKGTDAFYKGKFAKTLSDTVQDFGGSMTEKDLENYDITIDEPI
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                                                                                                                                                                                                                                                                                                  /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                'function-"unknown"
                                                                                                                                                                                                                                                                                                                                                                                        /gene="yogA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="yofA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'product="gamma-glutamyltranspeptidase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="alternate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'db_xref="PID:g2634234"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _xref="PID:g2634235"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  on-"unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "glutathione metabolism"
Score 11;
                                                                                                                                                                                                                                                                                                                              to alcohol dehydrogenase"
DB 1;
Length 207730;
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Sg

terminator

complement(8.

/gene="ytnM"

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JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
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ORGANISM
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BSUB0016/c
                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100. Matches 11; Conservative
                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Azevedo, V. Bertero, M.G. Bessleres, P., Bolotin, A., Burlis, R., Boursier, L., Brans, A., Braun, M., Brignell, S.C., Bron, S., Brouillet, S., Bruschi, C.V., Caldwell, B., Capuano, V., Carter, N.M., Choi, S.K., Codani, J.J., Connerton, I.F., Cummings, N.J., Carter, N.M., Choi, S.K., Codani, J.J., Connerton, I.F., Cummings, N.J., Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Ehrlich, S.D., Erington, J., Fabret, C., Ferrari, E., Foulger, D., Fritz, C., Fujita, M., Fujita, Y., Fabret, C., Ferrari, E., Foulger, D., Fritz, C., Fujita, M., Fujita, Y., Fama, S., Galizzi, A., Galleron, N., Ghim, S.Y., Glaser, P., Goffeau, A., Golightly, E.J., Grandi, G., Gulseppi, G., Guy, B.J., Haga, K., Haiech, J., Harwood, C.R., Henaut, A., Hilbert, H., Holsappel, S., Hosono, S., Hullo, M.F., Itaya, M., Jones, L., Joris, B., Karamata, D., Kasahara, Y., Kolingstein, G., Krogh, S., Kumano, M., Kurita, K., Lapidus, A., Lardinois, S., Lauber, J., Lazarevic, V., Lee, S.M., Levine, A., Liu, H., Masuda, S., Mauel, C., Medigue, C., Medina, N., Wellado, R.P., Mizuno, M., Moesti, D., Nakai, S., Noback, M., Noone, D., O'Reilly, M., Ogawa, K., Ogiwara, A., Oudega, B., Park, S.H., Parro, V., Pohl, T.M., Portetelle, D., Porwollik, S., Prescott, A.M., Presecan, E., Pujic, P., Purnelle, B., Rapoport, G., Rey, M., Reynolds, S., Rieger, M., Richa, E., Roche, B., Rose, M., Sadate, Y., Sato, T., Sekowska, A., Seror, S.J., Serror, P., Shin, B.S., Soldo, B., Sakowska, A., Seror, S.J., Takagl, T., Takahashi, H., Takemaru, K., Yasumoto, K., Walters, P., Wipat, A., Yanamoto, H., Yamane, K., Yasumoto, K., Yata, K., Yoshikawa, H.F., Zumstein, E., Yoshikawa, H. F., Zumstein, E., Yoshikawa, H. and Danchlin, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CTGTTTCTAGT
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                                                                                                                                                                                 Submitted (18-NOV-1997) I. Moszer, A. Danchin, Institut Pasteur, Regulation de l'Expression Genetique, 28 rue du Docteur Roux, 75724 Paris Cedex 15, FRANCE E-mail: moszerépasteur.fr, padanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45
                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus subtilis
Nature 390 (6657), 249-256 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus subtilis
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillaceae;
                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                              Kunst, F.,
                                                                                                                                                                                                                                                                                                                                                                                                           98044033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The complete genome sequence of the gram-positive bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus subtilis.
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thes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="ribR"
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                                                                                                                                                                                                                                                                                                                                                                function-"unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="hipO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           number="3.5.1.32"
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                                                                                                                                                                                                                                                                                                                            to nitrilotriacetate monooxygenase"
                              Db 189460 CTGTTTCTAGT 189450
                                                                                                                                              Matches
                                                                                                                                                                          Query Match
Best Local
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                                                                                                                                                                             Similarity
                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                    complement(6425. .7132)
                                                                                                                                                                                                                                                                                                complement(6425. .7132)
/gene="ytmM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(5649. .6428)
/gene="hisp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(4648. .5652)
/gene="ytmo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="SPTREMBL:034639"
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DILQVKYGVRHVPVVEIGRGNQYQGITEIGIEHLDLALANHAQIKEAKR"
complement (4648. 5652)
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DTEEEAEKKYREFAELIP IENAVTYLLARFYDDYDLSVVP DLEPFPDIGDVGKNAFOST
TDRIKREAKARNLTILREVAOEMAFPRTLFIGTPERVASLIETWFNAEAADGFIVGSDI
PGTLDAFVEKVIPILQERGLYRODYRGGTLRENLGLGIPQHQSVLHSSHH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(5649.
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/gene="ytnI"
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/gene="ytnI"
                                                                                                                                                                                                                                         /gene="ytmM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="CAB14912.1"
/db_xref="PID:e1185807"
/db_xref="PID:g2635418"
/db_xref="GI:2635418"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/transl_table=11
/product="histidine transport protein (ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAB14911.1"
/db_xref="PID:e1185806"
/db_xref="PID:g2635417"
                                                                                                                                                                                                          'function-"unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene-"hisP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VQKTGIIAGTKEEVAEELTRLSGTYKINDFVIFTPIKNAVEKQLSYQLLSDAVLAAKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /function="unknown"
/note="similar to hypothetical proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAB14910.1"
/db_xref="PID:e1185805"
/db_xref="PID:g2635416"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'db_xref="SPTREMBL:034900"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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                              100.0%;
Score 11; DB
Pred. No. 1.1
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BTPLCRGEN/c
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (01-MAR-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identification of a Bacillus thuringiensis gene that positively regulates transcription of the phosphatidylinosicol-specific phospholipase C gene at the onact of the stationary phase I. Bacteriol. 178 (10), 2749-2756 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus thuringiensis.
Bacillus thuringiensis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BTPLCRGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Microbienne,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ereclus, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jereclus,D., Agaisse,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLCRGEN 1707 bp DN thuringiensis plcR gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 1707)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 1707)
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                                      614
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                                                                                                                                          /transl_table=11
/protein_id="CAA63745.1"
/brotein_id="CAA63745.1"
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/db_xref="GI:1212806"
                                                                /translation="MKKLLIGSLLTLAMAWGISLGDTAFEKSQIISHNDQEVQVAADL
PFEF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMDILQGIAAKLQIPIIHFYEVLIYSDIERKKQFKDQVIMLCKQKRYKEIYNKVWNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKEEYHPEFQQFLQWQYYVAAYVLKKVDYEYCILELKKLLNQQLTGIDVYQNLYIENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="SPTREMBL:Q45782"
/translation="MQAEKLGSEIKKIRVLRGLTQKQLSENICHQSEVSRIESGAVYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function="positively regulates transcription of phosphatidylinositol-specific phospholipase C generates of the control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ne, Dept des Biotechnologies,
75724 Paris Cedex 15, FRANCE
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                                                                                                                     'db_xref="SPTREMBL:Q45783"
                                                                                                                                                                                                                                                                                                                        /gene="orf2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'db_xref="PID:g1212805"
'db_xref="GI:1212805"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'db_xref="taxon:1428"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   strain="407"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein_id="CAA63744.1"
db_xref="PID:e214719"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product="PlcR protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               :YAENGYLKKGIDLFEQILKQLEALHDNEEFDVKVRYNHAKALYLDSRYEESLYQ
\IEISCRINSMALIGQLYYQRGECLRKLEYEEAEIEDAYKKASFFFDILEMHAYK
                                      203 c
                                   321 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGO
                                   SgS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1676 CTGTTTCTAGT 1666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CTGTTTCTAGT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Buchnera aphidicola DNA.
Buchnera aphidicola
Buchnera aphidicola
Bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Buchnera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetic anlysis of an aphid endosymbiont DNA fragment homologous the rapA-rjpmH-dnaA-dnaN-gyrB region of Eubacteria Gene 113, 175-181 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dnaA gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M80817.
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(rnpA_rmpH-dnaA-dnaN-gyrB) gene, complete cds.
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PGKYNVEVEYDINNLSNKKLELNIFGQLKQTVKLPKNRDIYSGNFALQTFRGAAYSSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MELQRNFFIFAFLFVSFLLWQAWQSQSLKKNKKNEETNSFFHLN
HKKEDKNQIIIKNDVLRLVINWYGGDIEEASLLDYKTQLNSPENLKLLETKSDFVYQA
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                                                                                                                                                                                                                                                                                                                                            'gene="rnpA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="10 kDa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'product="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proteobacteria; gamma subdivision;
                                                                                                                                                                                                                                                                                                                     codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'db_xref="GI:144146"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="60 kDa"
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1.7e+03;
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                                                                                                                                                                                                            CIGITICIAGI 1424
                                                                                                                                                                                                                                                      CTGTTTCTAGT 11
                   BUHTREPA 3641 bp DNA BCT 14-AUG-1996 Buchnera aphidicola anthranilate synthase large subunit (trpE) and anthranilate synthase small subunit (trpG) gene, complete cr3551
                                                                                                                                                                                                                                                                                                                             Similarity
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a 617 c 605 g 1700 t
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KFCGIEIKIENGKFKYLSDNQEEETAEDLFEIDYFGEKIEISINYYYLLDVINNIKSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="dnaN"
3349. .4449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VIALFLINKSKSSIQIEAENNSSNAYVVMLLKR"
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                                                                                                                                                                                                                                                                                                                           100.0%;
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VERSION
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SOURCE
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Search completed: September 17, 1999, 22:01:12 Job time: 16255 sec
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AUTHORS
                                                                                                                                                                                                                                                                                                                         BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
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                                                                                                   1 CTGTTTCTAGT 11
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The tryptophan biosynthetic pathway of aphid endosymbionts (Buchnera): genetics and evolution of plasmid-associated anthranilate synthase (trpEG) within the aphididae
J. Mol. Evol. 42 (4), 414-421 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anthranilate synthase; large subunit; small subunit. Buchnera aphidicola DNA.
Buchnera aphidicola Buchnera Bacteria; Proteobacteria; gamma subdivision; Buchnera 1 (bases 1 to 3641)
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                                                                                                                                                                                                                                                                                                                         1490
                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                         Q
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a 453 c 503 g 1195 t
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1561. .2149
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LSAYQKLKKSNPSPYMFFMQDQDFTLFGASPESSLKYDEKTRKIELYPIAGTRPRGRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKRSRKIMIIDSAMRISSEHNAVKLTPLSINGMEILLVLKKIISKKIEIYRRKKNTIL
IPPNIEKOLDEDKKLFSLSVFDAFRLIIKTFENREKKSKAMFFGGLFSYDLISVFETL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDGNLDLDLDSRIELEMRTNHKELAEHLMLVDLARNDLARICKPGSRYVSDLVRVDRY
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Pred. No.
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MSP gene in pUCRS
Usp45 gene. Lactoc
Human brain Expres
Human death associ
BRCA1, human breas
BRCA1 breast and
BRCA1 gene nonsens
BRCA1 gene framesh
Human gene signatu
Mutated BRCA1 codi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence encoding Lambda gt10ch101 e Lambda gt10ch201 e Lambda gt10ch2 enc
                                                                                                                                                                                                                                                                                                                                                                                                              Human death associ
Human prostrate-sp
Gene encoding BRCA
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 용
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Matches 11
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12-SEP-1988; 114877.
15-SEP-1987; US-096579.
(GEHO-) Gen Hospital Corp.
(GEHO-) Hospital Corp.
Pfitzner UM, Pfitzner AP, G
WPI; 89-087235/12.
  exon
                              exon
                                                                                                                             N93197;
N93197;
28-JUN-1990 (first entry)
Fragment of clone lambda H
                                                                                                                                                                                                                                                                                                                                                                               to invading pathogen
Figure 3; 32pp; English.

Figure 3; 32pp; English.

It is CDNA from tobacco mosaic virus (TMV) infected tobacco plants.

It contains the sequence from two independent cDNA clones -
pNtSNNcPRIb/81 and pNtSNNcPRIb/1. Differences between the two clones a
shown in the Features Table. Expression of a recombinant DNA sequence
which includes a PR-1 promoter in a plant enhances the hypersenstivie
response of the plant to an invading pathogen.

Sequence 735 BP; 227 A; 145 C; 145 G; 218 T;
                                                          exon
                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3'utr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nicotiana tabacum cDNA for pathogenesis-related Pathogenesis-related protein; Nicotiana tabacum pNtSNNcPR1/81; pNtSNNcPR1b/1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pathogenesis-related proteins used for expression in plants
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                                                                                                                                                                                     standard; DNA; 5406 BP
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11; Conserv
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                                                                                                                             gene; vasodilator;
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hilarity 100.
Conservative
/*tag a
2538..2697
/*tag b
3967..4256
/*tag c
4375..4334
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/note="cDNA
14. .735
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498. .735
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Location/Qualifiers
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'note="cDNA from pNtSNNcPRlb/81'
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                                                                                                                            contg. kallikrein gene.
male infertility; lambda
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H. pylori cellular
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Length

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SUMMARIES

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Scoring table: Sequence: Title: Perfect score:

IDENTITY\_NUC

311585 seqs, 125096042 residues

US-08-956-518A-88 11

CIGITICIAGI

Pred.

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9n:

nucleic search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

September 18, 1999, 00:33:31;

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RESULT
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ID Q0
AC QC
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Matches 11; Conserv
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Lamda HK64a is a subclone produced from clobourne human fetal liver genomic library us clone DNA as a probe.

See also N93193-8.

Sequence 5406 BP; 974 A; 1864 C; 13
                                                                                                                                                                                                                                                                                                                                     Claim 2; Fig la; 66pp; English.

A MAEP compound having a binding affinity for a Duffy antigen of primate red blood cells, is antigenic for protein, and may be used in diagnosis, treatment and against invasion by P.vivax and P.knowlesi.

Sequence 3763 BP; 1796 A; 464 C; 611 G;
Q05632 standard;
Q05632;
17-DEC-1990 (fi:
                                                                                                                                                    2305
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Barnwell JW, Galinski MR,
WPI; 90-334616/44.
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Q06328;
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06-APR-1989; US-334270.
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Lin FK, Lu HS;
WPI; 89-009139/02.
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30-JUN-1988; 306039.
30-JUN-1987; US-068594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infection
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03-APR-1990;
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11; Conser
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Hilarity 100.
Conservative
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4838.
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Pred. No. 3.5
); Mismatches
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, preventing and diagnosing malarial
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Pred. No.
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3.5e+02;
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thes 0;
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                                                                                                                                                                                                                                                                        Length 3763;
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RESULT
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Best Local (
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17-JAN-1999; JP-005878.
(SUNR ) SUNTORY LTD.
Ohsuye K, Kitano K, Tanal
WPI; 90-25/02.
                                                                                                                                                    WO9008190-A.
26-JUL-1990.
17-JAN-1990. J00042.
17-JAN-1989. JP-0058
                                                                                                                                                                                                                                                                                             Q05630 stand
Q05630;
17-DEC-1990
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CDNA libraries were prepared from human thyroid gland poly(A in lambda gt11 and gt10. These were screened using probes de from DNA encoding similar enzymes in Xenopus laevis. Three (were isolated from the gt10 library, including gt10ch7101. Restriction analysis indicated that gt10ch7101 encoded a ditype of enzyme to one of the other two clones. The DNA can inserted into vectors for expression in E.coli or (more eff
                                                                                                                  (SUNR) SUNTORY LTD.
Ohsuye K, Kitano K, Tan
WPI; 90-254034/77
Disclosure; pp; English. cDNA libraries were prepared from human thyroid gland in lambda gt11 and gt10. These were screened using profession DNA encoding similar enzymes in Xenopus laevis. Were isolated from the gt10 library, including gt10ch Restriction analysis indicated that gt10ch7201 encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amidated
See also
Sequence
                                                                    C-terminal alpha amidating enzymes from converting C-terminal glycyl peptide(s) coding sequences.
                                                                                                                                                                                                                                                         17-DEC-1990 (first entry)
Lambda gt10ch201 encodes C-terminal alpha amidating enz
C-terminal alpha amidating enzyme; human thyroid gland;
lambda gt10ch201; ss.
                                                                                                                                                                                                                                                                                                                                                                              2813
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Key
cds
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C-terminal alpha amid
lambda gtlOchlOl; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The enzymes are useful for prodn. of physiologically amidated peptides from their C-glycyl precursors. See also Q05530 and Q05631. See also Q05630 and Q05631. Sequence 3316 Bp; 931 A; 676 C; 755 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coding sequences.
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BP; 931
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                                                                                                                                                                                                  /product=C-terminal alpha amidating enzyme
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and new
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RESULT
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CDNA libraries were prepared from human thyroid gland poly(A) RNA in lambda gtil and gtil. These were screened using probes derived from DNA encoding similar enzymes in Xenopus laevis. Three clones were isolated from the gtil library, including gtilohT2.

Restriction analysis indicated that gtilochT2 encoded a different type of enzyme to one of the other two clones. The DNA can be incompared into vectors for expression in E.coli or (more efficient content)
Q11482 standard; cDNA; 3824 BP. Q11482.
19-JUN-1991 (first entry)
Sequence encoding spike protein of IBV; spike protein; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JUL-1990.
17-JAN-1990;
17-JAN-1989;
                                                                                                               2489
                                                                                                                                                                                                                                                                                                                                                                                                                       (SUNR ) SUNTORY LTD. Ohsuye K, Kitano K, WPI; 90-254034/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q05631 standard; DNA; 2863
Q05631;
17-DEC-1990 (first entry)
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                                                                                                                                                                                                               in animal cells.
The enzymes are useful for prodn.
amidated peptides from their C-gl;
See also Q05630 and Q05632.
Sequence 2863 BP; 835 A;
                                                                                                                                                                                                                                                                                                                                                                                  C-terminal alpha amidating enzymes from converting C-terminal glycyl peptide(s)
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amidated peptides from their C-glycyl precursors.
See also Q05631 and Q05632.
Sequence 3688 BP; 1027 A; 775 C; 862 G; 1024 T;
                                                                                                                                                                                                                                                                                                                                                                        coding sequences.
                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; R96400
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JP-005878.
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12 encodes C-terminal alpha amidating
Lpha amidating enzyme; human thyroid g
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2. .2332
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                  infectious bronchitis virus
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3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                  human thyroid or protein, as
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3.5e+02;
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g probes derived
is. Three clones
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Best Local S
Matches 11
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08-CCT-1999; US-424793.

20-CCT-1989; US-424793.

(ALKU ) Akzo NV.

Sondermeijer PJ, Claessens J
from plasming prod. gene fragments. prod. gene fragments. Disclosure; Page 21; 36pp; English. Disclosure; Page 21; 36pp; English. The sequence (SEQ ID NO:1) was obtd. from a genomic library of L. lactis in lambda EMBL 3. The promoter region, and opt. the gene, fixed with a gene encoding a protein for secretion of the
                                                                                                                             02-OCT-1991;
13-MAR-1991;
22-MAR-1990;
                                                               (CIBA ) CIBA GEIGY AG.
Suri B, Schmitz A;
WPI; 91-290162/40.
P-PSDB; R14150.
Hybrid vectors for expression of polypeptide(s) -
from plasmids obtd. from Lactococcus lactis, esp.
                                                                                                                                                                                                                                                            MSP gene in pucks (DSM 5803).
Major secretion product:
                                                                                                                                                                                                                                                                                           Q13830;
                                                                                                                                                                                                 signal_peptide
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The protein encoded by this sequence is a recombinant of infectious broncitis virus (IBV) Arkansas strain.
or an antigenic fragment, e.g. S1 or S2 subunit, can k vaccine for immunising poultry against IBV infections.
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Sequence 3824 BP;
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infectious bronchitis v
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llarity 100.0%;
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1783. .3654
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151. .1767
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1768. .1782
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Mismatches 0;
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Matches 11; Conserv
                                                                         Matches
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27-MAR-1991; 200721.
30-MAR-1990; NL-000753.
(NEZU-) NEDERLANDS INST Z
WPI; 91-330695/45.
P-PSDB; R14330.
                                                                                                                                                                                                                   Lactococcus lactis DNA fragments - contg. extracellular protein signal peptide sequence bisclosure; Fig 4; 20pp; Dutch. The sequence is the KpnI/ClaI fragment from pNZ1011. Lactococci transformed with the gene may be used to produce extracellular heterologous enzymes of use in the food industry, e.g. chymosin of the contraction of the
                                                                                                                                                                     alpha-amylase.
See also Q14502.
Sequence 1592 BP;
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See also Q13831.
Sequence 1920 BP; 679 A; 344 C:
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/note= "start of transcription"
1514. .1553
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Matches
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Best Local Similarity
12-OCT-1994; U11598.
12-OCT-1993; IL-107250.
(RYCU/) RYCUS A.
(YEDA) YEDA RES & DEV CO LTD.
(XIMChi A;
WPI; 95-178528/23.
P-PSDB; R74204.
DNA whose expression mediates cytokine-induced programmed cell death - used to treat diseases or disorders associated with uncontrolled, pathological cell growth or cytokine-induced programmed cell death.
Claim 2; Fig 6; 6lpp; English.
                                                                                                                                                                WO9510630-A.
20-APR-1995.
12-OCT-1994;
12-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of most human genes of most human genes of most human genes of most human genes of sequence Tag was isolated from a human brain cDNA The Expressed Sequence Tag was isolated from a human brain cDNA library as part of a large set of ESTs which can be used as markers for human genes transcribed in vivo. They can be used to facilitate tagging of most human genes, for mapping locations of expressed genes on chromosomes, for individual or forensic identification, for mapping locations of disease-associated genes, for identification of tissue type, and for prepn. of antisense sequences, probes and constructs. EST00924 has a "poor" coding probability as evaluated using the coding-region prediction program CRM. See also Q59041-Q61440. Sequence 391 Bp; 97 A; 106 C; 115 G; 71 T;
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Death associated
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Human brain Expressed Sequence Tag EST00924.
Gene transcription product; genetic markers; tagging; in vivo; transcription; mapping; locations; chromosomes; chromosomal; s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICE Adams MD, Moreno RF, Venter CJ;
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W09316178-A.
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12-FEB-1992; US-837195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 CIGITICIAGI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CTGTTTCTAGT 11
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Pred. No. 3.4e+02;
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-vivo, facilitate
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RESULT RE
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                                                             δÃ
밁
                                                                                                                                                                                                                                                                                            pri DNA whose expression mediates cytokine-induced programmed cell price death - used to treat diseases or disorders associated with uncontrolled, pathological cell growth or cytokine-induced programmed cell death.

CC laim 2; Fig 6; 6lpp; English.

CC Laim 2; Fig 6; 6lpp; Engl
                                                                                                                                   Query Match
Best Local S
Matches 11
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Human death associated pro
Death associated protein;
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20-APR-1995.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (RYCU/) RYCUS A.
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.2-OCT-1993; IL-107250
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Pred. No. 3.5e+02;
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cytokine; cell death;
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RESULT 1
Q96296/c
       Transcriptional regulator specific for cells expressing prostate specific principles of used to express toxins, immunostimulants or anti-sense cpds., for treatment and prevention of prostatic cancer or hypertrophy for treatment and prevention of prostatic cancer or hypertrophy principles. The forest of the human provential states are specific antiper to -5824 bp. The fragment runs from a constrate specific antiper to -5824 bp. The fragment runs from a constrate specific antiper to the Hindiii site at +7 bp. The mumbering system is +1 at the transcriptional start site of PSA mRNA (Lundwall, A., 1989, Blochem. Blophys. Res. Comm. 161: 1151-59). The coding region of PSA starts at +42. An approx. 2.5 kbp fragment from about -2850 to about -5350 serves as a prostrate specific enhancer (PSE) in conjunction with a promoter to function to initiate transcription in prostrate cells. This can be isolated from the human genome as a XbaI-ApaI 2.5 kb fragment and this enhancer is antical transcription of the control of the c
antigen. There is a naturally-occurring PSA promoter spanning the segment from about '541 to +7, particularly '320 to +7 of the human PSA gene. The promoter of PSA has been reported (Riegman et al., 1989, Biochem. Biophys. Res. Comm. 159: 95). The promoter from '320 to +7 contains a TATA-box, a GC-box and hormonal response element at -170 to -156. Sequence 5836 BP; 1408 A; 1296 C; 1568 G; 1564 7
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12-JAN-1995;
13-JAN-1994;
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/note= "claimed, nts -5300 - -2800"
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/note= "claimed, nts 0 - -5322"
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/note= "nts -320 - +7"
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'note= "nts -541 - +7"
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/note= "nts +1 - +7"
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/note= "claimed, nts
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     1564 T;
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Query Match Best Local Similarity

100.0%;

Score 11; Pred. No.

DB 1; 3.6e+02;

Length 5836

RESULT T18325 ID T: AC T: DT 0: DE BI KW BI KW SI OS HC	o d z mo	3228 3228	3888888	A A A A A A A A A A A A A A A A A A A	אין אין אין אין אין אין אין אין אין אין אין אין אין	15 15 15 15 15 15 15 15 15 15 15 15 15 1	ACC DE COS	Db _
UILT 15 325/c 118325 standard; DNA; 24026 BP. 118325 standard; DNA; 24026 BP. 118325, 05-JUN-1996 (first entry) BRCA1, human breast and ovarian cancer predisposing gene. BRCA1; breast cancer; ovary cancer; predisposing gene; susceptibility gene; diagnosis; prognosis; gene therapy; ds. Homo sapiens.	Query Match 100.0%; Score 11; DB 1; Length 5712;  Best Local Similarity 100.0%; Pred. No. 3.6e+02;  Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  y 1 CTGTTTCTAGT 11	ows early 02 (C) was 1273 G;	ale breast tissue cer and normal brea hod for gene therap gene with a promotor expressing BRC typant effusions to the control of the control	ermiller PS, Page DL, Robinson-Ber treatment of pre-invasive breast ca lally expressed marker genes, also u breast cancer. ppp; English.	misc_reature 602 /*tag= c /note= "non-translatable nucleotide (see CC)" W09519369-A1. 20-UUL-1995. 17-JAN-1995; U00608. 14-JAN-1994; US-182961. 17-JAN-1995; US-373799.	peptide	RESULT 14 093027/c 193027/c ID 093027; AC 093027; DT 10-MAR-1996 (first entry) DE Gene encoding BRCA1 protein. KW BRCA1; breast cancer; diagnosis; prognosis; gene therapy; ds. OS Homo saplens saplens.	Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  1 CTGTTTCTAGT 11
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F, F, .	/*tag= u /note= n at 113 interval within 1159815023 /*tag= v 1502415424 /*tag= w	. 4 . 8 . 8	43656571 /*469	4 . 7 . 4 . 7 . 7		/*tag= f 2261. 257 /*tag= g /note= n at 25. interval within 2678. 278 /*tag= h 2789 3328	1561512 /*tag= c 15131611 /*tag= d 16122206 /*tag= e /note= n at 19. interval within 22072260	9.99.51

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2234. .22288
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Mismatches 0;
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Title: Perfect score: Sequence:

Run on: OM nucleic

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L26727 MUSF200A la M78776 EST00524 HI T08787 EST06679 In T10579 hbc233 Huma T17272 NIB615 Norm T18606 hbc2266 Hum T28224 EST32443 HU T36400 EST101330 S T36410 EST101348 S

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Description

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nucleic search, using sw model
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L26727 195 bp mRNA EST 01-MAR-1995 MUSET200A lambda unizap male testis Mus musculus cDNA clone F200, mRNA sequence.
L26727 126727 126727 GI:437510
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R04060 pk18b05.11
R04483 pk24c04.r1
R04683 pk24c04.r1
R06683 yf10b02.r1
R12759 yf58h04.r1
R12759 yf58h04.r1
T15394 yc73c03.s1
T165394 yc73c03.s1
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T77795 yc94g01.r1
T77796 yc94g01.r1
T77738 ye08d10.r1
T187738 ye08d10.r1
R11107 ym14d05.s1
R36022 yf69b06.r1
R36022 yf69b06.r1
R36022 yf69b01.s1
R36638 y944e10.s1
R57987 F7919 Fetal
R66315 y130h12.r1
R66315 y130h12.r1
R66315 y130h12.r1
R66315 y130h12.r1
R74865 MDB0185R MO
D566318 HUM219C04B
D58198 HUM355A088

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                                                                                                                            Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
                                                                                                                                                                                                                    Durbin, A.S.
EST mapping data
Unpublished (1996)
                                                                                                                                                                                                                                                                                                 Adams, M.D., Dubnick, M., Kerlavage, A.R., Moreno, R., Kelley, J.M., Utterback, T.R., Nagle, J.W., Fields, C. and Venter, J.C. Sequence identification of: 2,375 human brain genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M78776 391 bp mRNA
EST00924 Hippocampus, Stratagene (cat.
clone HHCME73, mRNA sequence.
M78776
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 195)
1 (bases 1 to 195)
Kerr.S.M., Vambrie,S., McKay,S.J. and Cooke,H.J.
Analysis of cDNA sequences from mouse testis
Mamm. Genome 5, 557-565 (1994)
95093181
                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 391)
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M78776.1 GI:273091
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                                                          Email: arkerlav@tigr.org
Seg primer: M13 Forward.
Location/Qualifiers
                                                                                                            Fax: 3018699423
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house mouse
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/note-"Vector: lambda unizap; lambda unizap
mail mouse testis"
34 c 44 g 71 t 2 others
/organism="Homo sapiens"
/db_xref="ATCC (inhost):78208"
/db_xref="GDB:D0S1760E"
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/clone="F200"
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/strain="Swiss"
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Location/Qualifiers
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#936205) Homo sapiens cDNA
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T10579
g390733
                                   T10579 250 bp mRNA EST 29 NOV-1993 hbc233 Human pancreatic islet Homo sapiens cDNA clone hbc233 5'end,
                                                                                                                                                                                                                                                                                                                                                                                                                                              The Institute for Genomic Research
932 Clopper Road, Gaithersburg, MD
Tel: 3018699056
Fax: 3018699423
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1 (bases 1 to 369)

Adams, M.D., Soares, M.B., Kerlavage, A.R., Fields, C. and Venter. Rapid CDNA sequencing (expressed sequence tags) from a directionally cloned human infant brain cDNA library Nature Genet. 4, 373-380 (1993)
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EST06679 Infant Brain,
5' end, mRNA sequence.
T08787
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Seq primer: M13 Reverse.
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/Clone_lib="Hippocampus, Stratagene (cat. #936205)"
/Clone_lib="Hippocampus, Stratagene (cat. #936205)"
/note="Vector: lambdaZAP-II; Female, 2 years; oligo-dT +
random primed cDNA synthesis; lambdaZAP-II vector, 1.0kb
average insert size."
106 c 115 g 71 t 2 others
                                                                                                                                                                                                                                                                                     /db_xref="ATCC (inhost):85285"
/db_xref="taxon:9606"
/clone="HIBBJ71"
/clone=11b="Infant Brain, Bento
119 c 97 g 92 t
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Eutheria; Primates; Catarrhini; nummer:
1 (bases 1 to 183)
1 (bases 
                                                   Department of Pharmacology
University of Colorado Health Sciences Center
Box C336, 4200 E. 9th Ave, Denver CO 80262-0236
Tel: 3032708637
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                                                                                                                                                                                             Contact: Sikela JM
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Email: g-bell@uchicago.edu
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Normalized infant
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nikki@tally.uchsc.edu
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/clone_lib="Vector: Lambda ZaPII; Site_1: Eco RI; Site_2: Xho
I; mRNA was prepared from normal adult human islets. cDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. cDNA was size fractionated to remove
to the EcoRI site. cDNA was size fractionated to remove
sequences <1000 bp in size."

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/clone="hbc233"
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Pred. No. 2.9e+03;
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Tel: 3127029116
Fax: 3127020271
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T18606.
                                                                                                                                                                                                                            Seq primer: SK primer
                                                                                                                                                                                                                                                                                                                                                   Contact: Bell GI or Takeda J
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Human pancreatic islet cDNAs
Unpublished (1995)
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hbc2266 Human
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Location/Qualifiers
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         /clone_lib="Human pancreatic islet" / note="Yector: Lambda ZAPII; Site_1: Eco RI; S I; mRNA was prepared from normal adult human I; mRNA was prepared from the Xho I i was directionally synthesized from the Xho I i to the EcoRI site. cDNA was size fractionated sequences <1000 bp in size."
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/clone_lib="Normalized infant brain, Bento Soares"
/note="Yector: BA, M13-derived; Site_1: HindII; Site_2:
NotI; The normalized infant brain library, constructed by
Bento Soares, Columbia University, was oligo-(dT) primed
and directionally cloned into an M13-derived plasmid using
total brain mRNA from a 72-day old human female afflicted
with spinal muscular atrophy. The library was normalized
as described elsewhere. "
50 t 5 others
                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="hbc2266"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 3e+03;
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Query Match Best Local S Matches 11

Similarity

100.0%;

Score 11; DB 20; Pred. No. 2.9e+03;

Length 234;

Conservative

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Mismatches

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Gaps

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CTGTTTCTAGT

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52
                                                      1 CTGTTTCTAGT 11
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1 (bases 1 to 265)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W.,
Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
FitzGerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S. M.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblon, E., Hinkley, P.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblon, E., Hinkley, P.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 3044077-1-Email: tdbinfo@tdb.tigr.org
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression
1-formation related to this EST, please contact the TIGR Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699056
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                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="ATCC (inhost):101601"
/db_xref="taxon:9606"
/clone_lib="Human Embryo"
/tissue_type="embryo"
1 52 c 43 g 101 t
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Pred. No. 2.9e+03
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RESULT

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EST101348 S.
cDNA 3' end,
                                                                                                                         Saccharomyces cerevisiae cDNAs Unpublished (1995) Other_ESTs: TC2
                                                                                                                                                                                                     Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Weinstock,K. and Venter,J.C. The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae cDNAs Unpublished (1995) Other_ESTs: TC2
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Eukaryota; Fungi; Ascomycota; Hemiascomycetes;
Saccharomycetaceae; Saccharomyces.
                                                                Contact: Weinstock, K. and Venter, J.C. The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699056
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Email: tdbinfo@tdb.tigr.org
For clone availability please contact the TIGR Database (tdbinfo@tdb.tigr.org)
                                                Fax: 3018699423
                                                                                                                                                                                                                                                   baker's yeast.
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Email: tdbinfo@tdb.tigr.org
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                                                                                                                                                                          Weinstock, K.
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                                                                                                                                                                                                                                                                                   GI:620234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4932"
/clone_lib="S. cerevisiae strain X2180-1A"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Saccharomyces/strain="X2180-1A"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: esrewarounners (221 High gality sequence stops: 221 Source: IMAGE Consortium, LINL free through LINL; contact the This clone is available royalty-free through LINL; contact the This clone is available royalty-free through LINL; contact the This clone is available royalty-free through LINL; contact the This clone is available royalty-free through LINL; contact the This clone is available royalty-free through LINL; contact the This clone is available royalty-free through LINL; contact the This clone is available royalty-free through LINL; contact the This clone is available royalty-free through LINL; contact the This clone is available royalty-free through LINL; contact the This clone is available royalty-free through LINL; contact the This clone is available royalty-free through LINL; contact the This clone is available royalty-free through LINL; contact the This clone is available royalty-free through LINL; contact the This clone is available royalty-free through LINL; contact the This clone is available royalty-free through LINL; contact the This clone is available royalty-free through LINL; contact the This clone is available royalty-free through LINL; contact the This clone is available royalty-free through LINL; contact the LINL; contact the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Rawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry, Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hillier, L., Lennon, G., Becker, M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                             quality sequence stop: 221
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   /lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: spleen; Vector: pBluescript SK-
ECORI; Site_2: XhoI; Cloned unidirectionally.
Oligo dT. Pooled spleens. Average incomplete.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XhoI"
                                                                                                                          /clone_lib="Stratagene fetal spleen (#937205)"
/tissue_type="fetal spleen"
/dev_stage="fetal"
                                                                                                                                                                                                                    /map="X; 2; 726H05; 12"
/clone="IMAGE:72249"
                                                                                                                                                                                                                                                                                                                                                     /organism⇒"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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/note="Vector: pBluescript SK-; Site_1: Ec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Saccharomyces cerevisiae"
/strain="X2180-1A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                        /db_xref-"GDB:49391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:4932"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.
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Pred. No.
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2.8e+03;
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size: 1.0 kb;
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182 CIGITICIAGE 172
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                                                                                                                                                                                                                                                                                                                                             High qality sequence stops: 216 Source: IMAGE Consortium, clone is available royalty-free through LLNL; contact th Consortium (info@image.llnl.gov) for further information. Insert Length: 704 Std Error: 0.00 Seq primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chiasoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,G., Riikin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
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yb51a04.rl Stratagene fetal spleen (#937205) Homo sapiens cDNA
clone_IMAGE:74670 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
Insert Size: 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
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Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"
                                                                                                                                                                                                        /db_xref="taxon:9606"
/clone="IMAGE:74670"
                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="GDB:496335"
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11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1707
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4444 Forest Park Parkway,
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97044478
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PORPHOBILINOGEN DEAMINASE (HUMAN), mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 418)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                quality sequence stop: 291.
                                                                                                                                                                                                                                /Clone_lib="Stratagene fetal spleen (#937205)"
/tissue_type="fetal spleen"
/dev_stage="fetal spleen"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: spleen; Vector: pBluescript SK-; Site_1:
_conl; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT: Pooled spleens. Average insert size: 1.0 kb;
Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATTCGGCACGAG
3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   'db_xref="taxon:9606"
'clone="IMAGE:74722"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism-"Homo sapiens"
db_xref="GDB:496387"
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                                                                                                       100.0%;
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                                                                                                       Score 11;
Pred. No.
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                                                                                                                               DB 20;
                                                                                                       .7e+03;
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to gb:X04217
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                                                                                                                           Length 418;
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123
                                                                           1 CIGITICIAGE 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: estéwatson.wustl.edu
Insert Size: 1280
High qality sequence stops: 321 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: polyT not found Insert Length: 1280 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: -21ml3
High quality sequer
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Fax: 314 286 1810
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="Solr.cells" (kanamycin resistant)"
/lab_host="Solr.cells" (kanamycin resistant)"
/note="Organ: ovary; Vector: Bluescript SK: Site_1: Ec
/note="Organ: ovary; Vector: Bluescript SK: Oligo
/notal ovary tissue, normal, caucasian. Average insert
/notal ovary tissue, normal, cauca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="GDB:505066"
/db_xref="taxon:9606"
/clone="IMAGE:75337"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone_lib="Stratagene ovary (#937217)"
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                                                                                                                                                          Score 11; DB 20;
Pred. No. 2.6e+03;
; Mismatches 0;
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AUTHORS
TITLE
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Contact: Genethon
Genexpress-Genethon
Genethon Centre de recherche sur
                                                                                                                                                                                                                                                                                                                                                                                            Z38728 295 bp mrNA EST 31-OCT-1994 HSCONBO82 normalized infant brain cDNA Homo sapiens cDNA clone
                                                                                                                                             Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 295)

Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,

Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,

Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,

Sebastiani-Kabaktchis,C. and Tessier,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Arabidopsis thaliana transcribed genome: the Unpublished (1996)
                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Berthomieu P., Guerrier D.,
Genetique Moleculaire d'Arabidopsis
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheopl
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                              IMAGE: molecular integration of the
                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                               Z38728.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: Giraudat@cnrs-gif.fr
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Avenue de la Terrasse,1198 Gif-sur-Yvette Cedex,France
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llarity 100.0%;
Conservative (
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culture of ecotype columbia; clone_library=AC16H; Clon
vector: Lambda ZAPII; Physiological condition: cycling
cells."
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                                                                                                                                                                                                                                                                                                                               GI:561120
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/strain="ecotype Columbia"
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/clone="TAY082"
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Pred. No. 2.7e+03;
; Mismatches 0;
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Search completed: September 17, 1999, 21:28:00 Job time: 14264 sec
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Tel: 33169472800
Fax: 33160778698
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Single read. 18 T removed at sequence 5'end
Genexpress_library_idt: C; Genexpress_sequence_idt: alc-0nb08
Seq primer: (-21)M13_universal.
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/dev_stage="3 months old"
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/note="organ; brain; Vector; lafmid BA; Site_1: HindIII;
/note="organ; brain; Vector; lafmid BA; Site_1: HindIII;
/note="organ; brain; vector; lafmid dev_stage=3 months old;
/solate=muscular atrophy patient; tissue_type="total"
// solate=muscular atrophy patient; tissue_type="total"
// solate=muscular atrophy patient; tissue_type="total"
// solate=muscular atrophy patient;
// solate=mu
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/sex="Female"
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/db_xref="taxon:9606"
/clone="c-Onb08"
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16.208 Million cell updates/sec
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Smith, D.R., Doucette-Stamm, L.A., Deloughery, C., Lee, H.-M.,

Dubois, J., Aldredge, T., Bashirzadeh, R., Blakely, D., Cook, R.,

Gilbert, K., Harrison, D., Hoang, L., Keagle, P., Lumm, W., Pothier, B.,

Glu, D., Spadafora, R., Vicare, R., Wang, Y., Wierzbowski, J.,

Gibson, R., Jiwani, N., Caruso, A., Bush, D., Safer, H., Patwell, D.,

Prabhakar, S., McDougall, S., Shimer, G., Goyal, A., Pietrovski, S.,

Church, G.M., Daniels, C.J., Mao, J.-i., Rice, P., Nolling, J. and
Reeve, J.N.

Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics
                                                                                                                                                                  Methanobacterium thermoautotrophicum.
Methanobacterium thermoautotrophicum
Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
                                                                                                                                                                                                                                                AE000815 12328 bp DNA BCT 16-APR-1998 Methanobacterium thermoautotrophicum from bases 228917 to 241244 (section 21 of 148) of the complete genome.
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D90858 E. coli geno
D90899 Synechocyst
D90900 Synechocyst
D90901 Synechocyst
D90914 Synechocyst
D90914 Synechocyst
D90914 Synechocyst
D90918 E. coli hpa[
U14003 Escherichia
X73888 E. coli gene
U58768 Escherichia
AJ130884 Flexispir
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280775 Mycobacteri
280225 Mycobacteri
X81134 M.thermoaut
X68366 M.thermofor
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U15184 Mycobacteri
AD000013 Mycobacte
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U08876 Haemophilus
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AE000815 Methanoba

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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gp:GI:g1839544 LN:S82218, p()=0.91, pid=07%"
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YSVDMGEDSGTDSARPPGAAPGHRIRGPVYYLYDDEITHGWVAWYYDVDAGQYFSEYD
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/db_xref="taxon:2166"
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translation="MWQPLRGSEGEDTRPQPARMKAGPRTITLTASDDTENLGRLTPE
                                                                                                                                                                                                       transl_table=11
                                                                                                                                                                                                                                                                                                                                                                 'gene="MTH296"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="MTH294"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'translation="MIGMNSIDIYMTLEERISSAFRMDEETWLRHANPWSVWTRLTAL
LLVAAFWSREWLGWWAIIPVTLAVLWTYLNPRIFKRPESTDSWASRSVLGERVWLNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene-
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603
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GLMDPRLGVIDPRERCWTCGARGGECPGHFGSINLARPVIHVGFADTIHKILRSTCRK
CGRYLLTGTEIEEYIRGYLKPWRKRKTSRHW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene-"MTH299"
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ILRMDNETLMKCNDEIKELVKKRRIRRGDFEGSMEELMAEIRSRLEALSGELRALSPQ LLRVTVEIDRSKPDVKITTSLDKDRMEGYLEKIKSRQLSDQSPAAPSWRDLCPVCREA PLTPFPKRRVPGRSKRNMRCSNCGAVFIYKGNGYLLSRVSNRNTRAWRLYGGKTLTEE EWTRIANGGVSNELQREIQRKRDIEERRRDIEGWLKSAAEGNVTIFREPQTPIILRKNE RAVLVLHNIDLYEPRAVRRTAGGYGGPTIRVSKNLSFRMGALNAISESRDELRRIDTG TLTLTTRMIFTGTKRTTNIDLRKVLAIQPYTNGIAVQRENKKRTEHFLNTEKTLLNI THSGRTHTVPADGAVMKAVIEGLIRKL"

/note="2528 bp direct repeat includes part of MTH297-299 (DNA-dependent RNA polymerase, subunit A' - paralog.fam. 29); 82% ID to inte"

'gene="MTH297"

regulators) ; similar to, sp:LN:RPAL\_METTH AC:P09846, p()=6.2E-48, pid=68%" /note="Function Code:10.02 - Metabolism of Macromolecules, Transcription--mRNA synthesis and modification (includes

/product="DNA-dependent
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gene-"MTH298"

Transcription--mRNA synthesis and modification (includes regulators); similar to, sp:LN:RPA1\_METTH AC:P09846, p()-6.7E-40, pid-77%"

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db\_xref="GI:262]

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gene="MTH299"

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codon\_start-

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JOURNAL
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REFERENCE
AUTHORS
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AUTHORS
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KEYWORDS
SOURCE
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AE000876/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Methanobacterium thermoautotrophicum from bases 947295 to 966282 (section 82 of 148) of the complete genome.
AE000376 AE000666
Direct Submission
Submitted (10-AUG-1997) Genomics and Technology Development, Genome
Therabuetics Corporation, 100 Beaver Street, Waltham, MA
                                                                                                                                                                                                                                                   Smith, D.R., Doucette-Stamm, L.A., Deloughery, C., Lee, H.-M., Dubols, J., Aldredge, T., Bashirzadeh, R., Blakely, D., Cook, R., Gilbert, K., Harrison, D., Hoang, L., Keagle, F., Lumm, W., Pothier, F., Qiu, D., Spadafora, R., Vicare, R., Keagle, F., Wierzbowski, J., Gibson, R., Jiwani, N., Caruso, A., Bush, D., Safer, H., Patwell, D., Prabhakar, S., McDougall, S., Shimer, G., Goyal, A., Pietrovski, S., Church, G.M., Daniels, C.J., Mao, J.-1., Rice, P., Nolling, J. and Georg, T. M., Daniels, C.J., Mao, J.-1., Rice, P., Nolling, J. and Georg, T. M.
                                                                                                                                                               Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics J. Bacteriol. 179 (22), 7135-7155 (1997)
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                                                                                                                                                                                                                                       Reeve, J
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/note="Function Code:14.00 - Unknown,
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6367. .6885
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/note-"Function Code:14.00 - Unknown,
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sp:LN:SCOT_CAEEL AC:Q09450; p()=0.98, pid=13%"
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Pred. No. 2.3e+03;
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                                                                                                                                                                                                                                VTNGLAPMNLEKLSEEPTQLYISLDAPDRDTYKELCRPQIPGAWDLLNSSLELMPSFS
CRKVLRITAVRHINMKDPEGFARMIERARPDFVEVKAYMYIGYSRRRLDIENMPLFYE
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                                                                                                                                                                                                                                                                                                   /translation="mamyleesQrkmermgyrfvgehghsavktclwtkksivnegvc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(2270. .3187)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Function Code:14.01 - Unknown, Conserved protein; similar to, sp:LN:YPUA_BACSU AC:P31847:P37951, p()=4.7E-20, pid=23%"
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LSLLLFYLAISGGLMHRSFLVLWLLGWAFGYLLMSKSFRSFILTKKSVLSFILAGA
GAFALMEFLSKVLNKŠVLSPMLRIFPALEENFYSLSLVLKNTTFWGHVGGSCYNKSG
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                                                                                                                                                               /gene="MTH1040"
3831. .4487
                                                                                                                                                                                                                                                                                                                                                                           /product="conserved protein"
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/db_xref="GI:2622143"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(2270. .3187)
/gene="MTH1039"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="G1:2622142"
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/translation="WVIMRQIIPLILIAFLYAAPVFAVSGFSVTIGEATSSNPSYKSA
VMDYFKAKTDKDLQSADIKIVTASEVNEVSRGVTGRVYSPSQILSCAMVDLSYSDGIK
VSVDTSKIRVTDEMYASALRSSGIDRGYVVVTSPVPASGEAALAGVLKSYEIAVGEQ
IPEEAKRVSVEEIYLQSRLVNETNATGDRVAELFDEVKNRTQSQNLQDPADIQRVVVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(1335. .2204)
/gene="MTH1038"
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/protein_id="AAB85533.1"
/db_xref="PID:g2622141"
/db_xref="GI:2622141"
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/note-""
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="conserved protein"
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                                                                                    /note="Function Code:14.00
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/transl_table=11
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                                                                                                                                      /gene="MTH1040"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . .18988
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                                                          /note="codon recognized: TAC"
/product="trna-Tyr"
6855. 6927
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/product="trna-Thr"
6645, 6718
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4683. .5372
/gene="MTH1041"
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                                                                                                                                                                                            /product="tRNA-pro" 6726. .6800
                                                                                                                                                                                                                                                                                           /note="61 bp direct repeat (tRNA-thr anticodon:ugu); 8 954496-954436"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="74 bp inverted repeat includes part of MTH1043
(tRNA-Thr anticodon:ugu); 84% ID to interval
678954-679026"
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                                                                                                                                                                                                                                                                                                                                                              complement(6651.
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                                                                                                                                                                                                                                                                                                                                                                                         /gene="MTH1043"
                                                                                                                           'gene="MTH1045"
                                                                                                                                                                                                                                                       'gene-"MTH1044"
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/protein_1d="AAB85538.1"
/db_xref="pib:92622146"
/db_xref="GI:2622146"
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HASKGTVKKTYRTKTKKKYTYRTKAAYKTKTKKKYRSRATYSTTSRKAYTRAISSDEL
NNLOGDEGLEKLASYINRNLMHRSGGPHTAEGVEKTGYGDCWGLSDWSARKLAANGYK
VKVVQGATSSSSRHRWLHVYSEGRWTSFEPSLVTKRYGSKHYTATCGRATRVVKTYNM
                                                                                                                                                                                                                                note-"codon recognized: CCA"
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/protein_id="AAB8557.1"
/db_xref="pID:92622145"
/db_xref="GI:2622145"
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llycolysis--Gluconeogenesis ; similar to, sp:LN:TPIS_METJA
4C:Q58923, p()=1E-63, pid=51%"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="MTH1042"
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/transl_table
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                    -"MTH1045"
.7127
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85% ID to interval
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13477.69
Y13477.69
Y13477.69
hoxE gene; hoxF gene; ORF1.
Synechococcus PCC6301.
Synechococcus PCC6301.
Bacteria; Cyanobacteria; Chroococcales; Synechococcus PCC6301.
1 (bases 1 to 2280)
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                                                                                                                                                                                                                                                                                                      Submitted (29-MAY-1997) G. Boison, Universitaet zu Koeln, Botanisches Institut, Gyrhofstr. 15, D-50931 Koeln, FRG Location/Qualifiers
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Anacystis nidulans hoxE,
Y13471
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                                                                                                                                                                                                                     /organism="Synechococcus PCC6301"
/strain="1402-1"
/db_xref="taxon:1139"
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7252. 7485
/gene="MTH1048"
                                            /gene-"hoxE"
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/note="61 bp direct repeat includes part of MTH1047
(trna-ys articodon:uuu); 85% ID to interval 954005-953945"
7.56
/codon_start=1
/transl_table=11
                                                                                                                                                        'gene•'
                                                                                         'gene=
                                                                                                              /product="DNA-dependent RNA polymerase, subunit H "
                                                                                                                                                                                                 clone_lib="lambdaGEM-11"
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/note="codon recognized:
/product="tRNA-Asp"
7056. .7127
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'product="tRNA-Lys"
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Pred. No. 2.1e+03;
Mismatches 0;
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                                    1 (bases 1 to 257000)
Tanaka,T., Kawarabayasi,Y. and Kikuchi,H.
Direct Submission
                                                                                                                                                                      Pyrococcus horikoshii (strain:OT3) DNA.
Pyrococcus horikoshii
Archaea; Euryarchaeota; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AP000002 257000 bp DNA
Pýrococcus horíkoshii OT3 genomic DNA,
(2/7).
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AB009481 AB009482 AB009483 AB009484
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CLIAELGIREGETTNDGSVSLGTVRCVGACGIAPVVVYDGDIQGRQESEAVWQQVQAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="RWGAERGRDWVRRLSAGEALDQLRRSLLNLT"
643 c 670 g 492 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESCGKCIPCRAGTVQLHELLGKLSSGQGTAIDLQQLEDLCYLVKDTSLCGLGMSAPNP
ILSTLRWFRQEYESRLIPERAIALTH"
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EGMAIAAYAVGANFGYLYVRAEYPLAIARLNQAIRQARRRGLLGNSVLDSRFSFDLEV
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   (11-JUN-1998) to
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Pred. No. 3.1e+03;
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   the DDBJ/EMBL/GenBank databases. Yutaka
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287001-544000 nt. position
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CDS
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                                                                                                                                                                                                                                                                                                                                                                         phosphoribosylglycinamide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="PH0318"
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403ma; PIR:S74842 p
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                                                                                                                              /translation-"MVVMIKLRDELGTATTDSAQKILLLGSGELGKEIAIEAQRLGVE
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TKAIMSSGKGSYFVKGPEDIPKAWEEAKTKARGSAEKIIVEEHIDFDVEVTELAVRH
FDENGEIVTTFFKYVANBWYSFRFBHDTGWTLASHPOFESSEFALHLRAVLGLEFDGEWVDF
RLFPMLIPAATHVIKAKVSGYSPRFRGLVKALSVPNATVRLFGKPEAYVGRRLGIALA
                                                                                                 WDKDVEVAKRKAEMVAHMIELRTRSSDWHDQNYEKRKHLLR"
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phosphoribosylglycinamide formyl transferase"
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.1974)

PIR:E64485 percent identity: 55.16 percent identity: 49.869 in 397aa; percent identity: 50.773 in 404aa

in

nt. position"

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Maryland, Baltimore, MD, USA.
Horikoshi, K. is at the Japan Marine Science and Technology Center, Yokosuka, Kanagawa 237-0061, Japan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oguchi,A., Aoki,K., Nakamura,Y., Robb,T.F., Hor Masuchi,Y., Shizuya,H. and Kikuchi,H. Complete sequence and gene organization of the hyper-thermophilic archaebacterium, Pyrococcus DNA Res. 5 (2), 55-76 (1998)
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                                                                                                                                                                                                                                                                                                                                                                      The other authors are at the National Institute of Technology and Evaluation, 2-49-10 Nishihara, Shibuya, Tokyo 151-0066, Japan. All the sequence with length 100 codons or more between ATG or GTG and stop codon are defined as CDS HOMOLOgy analysis is performed by Smith-Waterman algorithm against GenBank and GenPept release 103; EMBL release 52.0; SwissProt release 34.0; PR-Protein release 54.0; and OWL release 29.5.
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                                                                                                                                                                      E-mail address for comments and questions: genomeOT3@nite.go.jp
Restriction map, ORF organization, sequence alignment and more
information are available at W.W.W. site of Biotechnology Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            305-0046, Japan.

Robb, T. F. is at the Center of Marine Biotechnology, University of
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/strain="OT3"
/db_xref="taxon:53953"
                                                                                         organism≖"Pyrococcus horikoshii"
                                                                                                                                        .257000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at the University
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horikoshii OT3
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4856..6177
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GYRPKTIITYSOLECPILEETVYLASDIVLETRIINGKKYGIITKGPNENLIFELFKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (4039.
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/gene="PH0322"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MISWEIEELDREIGKIKKHSLILIHEEDASSRGKDILFYILSRK
IRSDNLVGMF51SYPLOLIIRILSRFGYDVIKYLENHELLAIVDFGSSFIGIKAIMPGV
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                                                                                                                                                                                                                                                                                                                                                             /product="219aa long hy;
/protein_id="BAA29396.1"
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LDSLLSIVQMPSGIPVATVAIDNAKNAALLALRILGIKYPEIKEKLRRYMKDMKRKVE
EKAKRLEEMGWERYLSE"
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/gene="PH0320"
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                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
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190aa; PIR:S76001 percent identity: 60.694 in 173aa;
wl:BAPURKE1 percent identity: 62.329 in 146aa"
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hosphoribosylaminoimidazole carb
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                    JOURNAL
MEDLINE
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KEYWORDS
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10; Conserv
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Actinomyces sp.
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinomycineae; Actinomycetaceae; Actinomyces.
Actinomycetales; Actinomycineae; Actinomycetaceae; Actinomyces.
1 (bases 1 to 1417)
Ramos,C.P., Foster,G. and Collins,M.D.
Phylogenetic analysis of the genus Actinomyces based on 16S rRNA
gene sequences; description of Arcanobacterium phocae sp. nov.,
gene sequences; description of Arcanobacterium phygenes
Direct Submission
Submitted (12-AUG-1994) C. Pascual, AFRC Institute of
Research, Earley Gate, Whiteknights Road, Reading RG6
                                                                                                                                                                                                                                                                                                                                                                                                                                           16S ribosomal RNA.
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phosphoribosylamide--glyc
/protein_id="BAA29397.1"
/db_xref="prD:d1030340"
/db_xref="prD:g3256714"
/db_xref="GI:3256714"
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/transl_table=11
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/protein_1d="BAA29398.1"
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RTGGGTNIHMSMGHPYGNSLWRSPMSTGRRIALEIKRGIELDELEKLVT"
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LSGEGPVLIEYNARFGDPEAINVLAVLDDNLLEIAKGIVEGSLRKAKFLNKATVVKYI
APQGYPQDPIKGIRIEVDEEGIKNEGAKIIYAAVDENLTLLGSRALAIVGVADSLEEA
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GLAKETNETWERNVETGEKWGIELEFIGGEKEVEKEVKGAELYVVKPLGLTGGKKYVKYKF
KRAMAREFWERNVIGGKKWERIEDDYOGEMKWIDEYCKFVVVKFLGLTGGKGYVKVYK
QLKDNEEAKEYAEHIIRKDGKVLIEERTDGVEFTLQVFTDGKKVIEMPLVQDYPHAYE
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7392. .8486
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/db_xref="GI:3256715"
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/gene="PH0324"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Characterization and sequence determination of the replicator region in the hairy-root-inducing plasmid pRiA4b Mol. Gen. Genet. 206, 1-8 (1987) Data kindly reviewed (23-SEP-1987) by Oka A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agrobacterium rhizogenes Agrobacterium rhizogenes
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AKLEKFRRWQLAPILLFGQELLG"
                                                                                                                                                                                                                                         complement(217. .420)
/note="put. ORF 4 (AA 1-204)"
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                                                                                                                                                                         /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Agrobacterium rhizogenes"
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339 c 506 g 299 t
                                               note="put. repA (AA 1-404)"
                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="a transjugant of cured C58 and A. rhizogenes /db_xref="taxon:359"
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1. .1417
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'translation="ILQGRIRLSRKGDFAYIGRRRAEGDLFLGYDCRIITKTIHEHIQ
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    _table=11
n_id="CAA28527.1"
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VESILEEMWMLQEEIINRLEIRDNSENNSTNAAQSEQHIQNSKPESVNELEPRSEKEQ
GAKPSEIDRARSEPIKAFPLGMILKACPTIGNYGPSGAVASWRDLMSAAVVVRSMLGV
SPSAYQDACEAMGPENAAAAMACILERANFINSPGGYLRDLTRRSELGKFSLGPMIMA
                                                                                              /db_xref="GI:39119"
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/db_xref="SWISS-PROT:P05684"
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ASAAMELLGIQSNSLAVLDALLSFHPETELRQEAGLIVFPSNAQLALRAHGMAGATLR
RHIAMLVESGLIVRKDSANGKRYARKDGAGGIERAFGFDLSPLLARSEELAMMAQQVM
ADRAAFRMAKESLTICRRDVRKLITAAMEEGAEGDWQAVEEVYVELVGRIPRAPTLAD
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/note="put.ORF 5 (AA)
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GIRTFGPSEASKLLGVGESYLRQTASEMPELNVSMSPGGRRMFSIEDIHVIRKYMDQV
GRONRRYLPHRRGGEQLQVISVMNFKGGSGKTTTAAHLAQYLAMRGYRVLAIDLDPQA
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3GAVIELDASSIEPSFVOORMRGDIDGLLTSIREGGGQVPILYMRHPSGDGRYQVAFG
BIRRLRAVSELGLEVRAVVRELTDEGVVVAGGGENURREDLTFIEKARRAHRLINGGSE
EIVIAAMSIDKSNLSKMLLLVDALPSELTDAIGAAPGVGRPSWQQLAELIEKVSSPAD
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complement(1510. .1620)
note="put. ORF 6 (AA 1-36)"
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/db_xref="PID:g39119"
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note="put. rRNA"
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/LRSIFGENVLNFPMLKTTAVSDAGLTNQTLFEVERGLFTRSTYDRALEAMNAVNDEI
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Eingqdsisahsevlromrggggltrptfeihhrdnlkllaastmwqvapvp
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                               -35_signal
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                                                                                                                                                                                 Seung H. park
Genetic Engineering Research Institute
P.O. Box 17
                                                                                                                                                                                                                                                                               1 (bases 1 to 1928)
Park, S.H., Kim, H.K. and Pack, M.Y.
Characterization and structure of the cellulase
                                                                                                                                                                                                                                                                                                                                                                                                                                                    BACCMCASE 1928 bp DNA
B.subtilis carboxymethyl cellulase (CMCase) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                    Taedok Science Town
                                                                                                                                                                                                                             Submitted (10-JUN-1991) to DDBJ by:
                                                                                                                                                                                                                                                                                                                                                              Bacillus subtilis (strain:BSE616) DNA. Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                               CMCase
                                                                                                                                                                                                                                                                                                                                                                                                             D01057.1 GI:216387
                                                                                                                                                                                                                                                                          subtilis BSE616
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10; Conservative
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                                                                                                                       042-829-4312
                                                                                                                                                     305-606
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                                                                                                                               Submitted (19-JUN-1996) Rose M., Johann Wolfgang Goethe-Universitaet Frankfurt, Institut fuer Mikrobiologie, Marie-Curie-Str. 9, Geb. N250 Frankfurt,M. GERMANY D-60439 Overlapping sequence: X87845 (bases 3016-6779).
                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                            Rose, M.
                                                                                                                                                                                                                          (bases 1 to 26170)
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82. .399
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                                                                                                                 ocation/Qualifiers
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B.subtilis DNA (26.2 kb
Z73234
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                                                                                               1 (bases 1 to 26170)
ROSE, M. and Entlan, K.D.
New genes in the 170 degrees region of the Bacillus subtilis genome encode DNA gyrase subunits, a thioredoxin, a xylanase and an amino
Microbiology 142 (Pt 11), 3097-3101 (1996)
                                                  acid transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus subtilis.
Bacillus subtilis
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Pred. No. 3.2e+03;
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/db_xref="PID:g1405444"
/db_xref="GI:1405444"
note="identical to yoxG (from acc. no. x87845)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="identical to yoxF (from acc. no. X87845)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene-"yneB"
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b_xref="PID:e249642"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          b_xref="PID:g1405446"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            roduct-"transketolase"
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complement(6669. .7097)
                                                                                                       /gene="yneK"
                                                                                                                                   complement (6669.
                                                                                                                                                                                      /db_xref="Swiss-prot:p45710"
/translation="Mismmiivssiiavlimavavmvvrikssdkpvsdkkiilppifm
/stoanlatippyfwvtgasetleaftilgvifssfeliktiskfeiknneilmkrskafvfil
/gdl/virivmksilstsidygalsgmfwilafgmivpwriamylsyrklhneilossni
                                                                                                                                                                                                                                                                                                                          /protein_id="CAA97596.1"
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LREDLVTMUITMPVKNGIKALRDILTEDPKAKVIMCTAMRQQRIVTEAIELGAKDFIV
KPFEETKVLEAVSRVMGH"
codon_start=1
                                                     /gene="yneK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5147. .6638
/gene="yneJ"
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                      note-"identical to yoxJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /function="response regulator"
/note="identical to yoxH (from acc. no. X87845)"
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db_xref="PID:g1405450"
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LLLQKRSLFHTLCFLLGFSVIFIALGYGTSFIGSLFRDYHDAIRQIGALLIILFGFI
LGVFRPEAMMKEBRIHFKHKPSGFLGSVLIGMAFAAGWTPCTGPILAAVITLAGTNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein_id="CAA97594.1
db_xref="PID:e249645"
db_xref="PID:91405449"
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db_xref="GI:1405448"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 xref="SWISS-PROT:P45706"
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f="PID:e249644"
                                                                                                                                   .7097)
                            (from acc.
                      no. X87845)"
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/transl\_table=11 /product="YneK"

/protein\_id="CAA97597.1" /db\_xref="PID:e249648"

xref="PID:g1405452"

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BS14GLUC
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-10_signal
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X67044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (22-JUN-1992) V. Lindahl, Agricultural University of Submixed, Dept of Biotechnological Sciences, PO Box 40, 1432 As,
                                                                                                                                                                                                                                                                                                                                                                                                    Lindahl, V., Aa, K. and Tronsmo, A.
Nucleotide sequence of an endo-beta-1, 4-glucanase
Bacillus subtilis CK-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus subtilis.
Bacillus subtilis
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10; Conserv
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/db_xref-"Swiss-prot:p10475"
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IDNPSVKNKVKEAVEAAKELGIYVIIDWHILNDGNPNQNKEKAKEFFKEMSSLYGNTP
                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  organism-"Bacillus subtilis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mlegwflwfilfwvimwvvllsiggffmfrkflkrlpkedgrse
LDwQDYxiensrhlwndenkQfldeltapvpelfrdaakakiagkigelalkekvaki
DQQLMIKGXILATfkrdhTflkrhlrdkkidlepyQTLlk"
                                                                                                   /product="endo-beta-1,4-glucanase"
/protein_id="CAA47429.1"
                                                                                                                                       /transl
                                                                                                                                                                                                                                                                                                      /strain="CK-
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                                                                                                                                                       codon_start=
                                                                                                                                                                                                                                                                   clone
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/db_xref="PID:g1405453"
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/db_xref="SWISS-PROT:P45711"
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                                                                                     t="PID:g39777"
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Pred. No. 2e+
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                   327-332 (1994)
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BSBGLUC2 2435 bp DNA BCT
Bacillus subtills endo-beta-1,4-glucanase gene.
X04689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MacKay,R.M., LO,A., Willick,G.; Zuker,M., Baird,S., Dove,M., Moranelli,F. and Seligy,V.

Moranelli,F. and Seligy,V.

Structure of a Bacillus subtilis endo-beta-1,4-glucanase gene Nucleic Acids Res. 14 (22), 9159-9170 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus subtilis.
Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reading frame.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               beta-glucanase; endo-beta-1,4-glucanase; glucanase; unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X04689.1 GI:39823
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                                                                                                                                                                                                                                                                            /db_xref="sptrembl:045525"
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fiktaktwirmiyriaviawvyygslsofoivwdmadlemgimalinliviallsnvay
kvykdyakorkogldpvfkaknipglknaetwedekoea"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Bacillus subtilis"
/strain="PAP115"
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YWYKAKNKGQNEDCDYAQIGCGNVTHKFVTLHKPKQGADTYLELGFKNGTLAPGASTG
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LKDANVMYALHFYAGTHGQFLRDKANYALSKGAPIFVTEWGTSDASGNGGVFLDQSRE
/note="precursor polypeptide (AA -29 to 470)"
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                                              product-"signal
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                                                                                                                               e="put. -35 region"
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Pred. No. 3.1e+03;
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                                                                                                                                                                                 Wolf,M., Geczi,A., Simon,O. and Borriss,R. genes encoding xylan and beta-glucan hydrolysing enzymes in Bacillus subtilis: characterization, mapping and construction strains deficient in lichenase, cellulase and xylanase microbiology 141 (Pt 2), 281-290 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Z29076.1 GI:509266
egglS gene; endo-1,4-beta-glucanase
Bactilus subtilis
Bactilus subtilis
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Structure of a Bacillus subtilis endo-beta-1,4-glucanase gene Nucleic Acids Res. 14 (22), 9159-9170 (1986)
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B.subtilis (168 trpC2) eglS
                                                                                                                                                                                                                                                                                   Submitted (14-DEC-1993) Borriss R., Humboldt Univ. zu Berlin, Biologie, Warschauerstrasse 43, Berlin, Deutschland, D-10243 (bases 1 to 1800)
                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                          Borriss, R.
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                                                                                                                                                                                                                                                                                                                                                                                           bases 1 to 1800)
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/note="1nverted repeat B/"
/s0 c 556 g 610
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2247. .2254
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WLKYLDSKTISWVNMNLSDKQESSALKPGASKTGGMRLSDLSASGTFVRENILGTKD
STKDIFETPSKDKPTQENGISVQYRAGDGSMNSNQIRPQLQIKNNGNTTVDLKDVTAR
YWYKAKNKGQNFDCDYAQIGCGNVTHKFVTLHKPKQGADTYLELGFKNGTLAPGASTG
NIQLRLHNDDMSNYAQSGDYSFFKSNTFKTTKKITLYDQGKLIMGTEPN"
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kgtqlunrdgkavqlkgisshglqwygeyunkdslkwilbdwgitvfraamytadggy
idnbsyknkvkeaveaakelgitviidwhilnngnpnonkekakeffremsslygntp
nviyelaneaveaveakelgitvisvirkndpdniiivgtgtwsqdvndaaddo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="i
                                                           /organism="Bacillus subtilis"
/strain="168 trpC2"
/db_xref="taxon:1423"
/gene="egls"
280. .1779
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                                                                                                                                                location/Qualifiers
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Pred. No. 3.1e+03;
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                                                                                                               DE 1 (bases 1 to 233780)

RS Kunst, F., Ogasawara, N., Moszer, I., Albertini, A., Alloni, G., Ressieres, P., Bolotin, A., Borchert, S., Bareedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Brustier, I., Brans, A., Braun, M., Brignell, S.C., Borriss, R., Boursier, I., Brans, A., Braun, M., Brignell, S.C., Bron, S., Brouillet, S., Ruschi, C.V., Caldwell, B., Capuano, V., Carter, N. M., Choi, S. K., Codani, J.J., Connexton, I.F., Cummings, N.J., Daniel, R.A., Denizot, F., Devine, K. M., Dusterhoft, A., Erricht, S.D., Emmerson, P.T., Entlan, K.D., Errington, J., Fabret, C., Ferrari, E., Foulger, D., Fritz, C., Fujita, M., Fujita, Y., Fuma, S., Galizzi, A., Galieron, N., Ghim, S.Y., Glaser, P., Goffeau, A., Golightly, E.J., Garandi, G., Guiseppi, G., Guy, B.J., Haga, K., Haiech, J., Harwood, C.R., Henaut, A., Hilbert, H., Holsappel, S., Hosono, S., Hullo, M.F., Itaya, M., Jones, L., Joris, B., Karamata, D., Kasahara, Y., Klaerr, P., Koningstein, G., Krogh, S., Kumano, M., Kurita, K., Lapidus, A., Liu, H., Lardinois, S., Lauber, J., Lazarevic, V., Lee, S.M., Levine, A., Liu, H., Masuda, S., Mauel, C., Medina, N., Mellado, R. P., Mizuno, M., Moestl, D., Nakai, S., Noback, M., Noone, D., O'Reilly, M., Ogawa, K., Ogiwara, A., Oudega, B., Park, S. H., Parro, V., Pohl, T.M., Portetelle, B., Rapoporte, G., Revy, M., Reynolds, S., Rieger, M.
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Purnelle,B., Rapoport,G., Rey,M., Reynolds,S., Rieger,M.,
Rivolta,C., Rocha,E., Roche,B., Rose,M., Sadaie,Y., Sato,'
Scanlan,E., Schleich,S., Schroeter,R., Scoffone,F., Sekig
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Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillaceae;
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KGTQLVNRDGKAVQLKGISSHGLQWYGSTVNKDSKNFKKKEFFKEMSSLYGNTP
/TOTAL TOTAL TOTAL
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NIQLRLHNDDWSNYAQSGDYSFFKSNTFKTTKKITLYDQGKLIWGTEPN"
336 c 416 g 439 t
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that published by R.M.McKay et al. (1986) NAR 14,
9159-9170 from B.subtilis PAP115 (nt452-nt2251)"
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Pred. No. 3.3e+03;
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Submitted (18-NOV-1997) I. Moszer, A. Danchin,
Regulation de l'Expression Genetique, 28 rue du
Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sekowska, A., Seror, S.J., Serror, P., Shin, B.S., Soldo, B., Sorokin, A., Tacconi, E., Takagi, T., Takahashi, H., Takemaru, K., Takeuchi, M., Tamakoshi, A., Tanaka, T., Terpstra, P., Tognoni, A., Tosatto, V., Uchiyama, S., Vandenbol, M., Vannier, F., Vassarotti, A., Viari, A., Wambutt, R., Wedler, E., Wedler, H., Weltzenegger, T., Winters, P., Wipat, A., Yamamoto, H., Yamane, K., Yasumoto, K., Yata, Institut, K., Yoshikawa, H.F., Zumstein, E., Yoshikawa, H. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature
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u_Docteur Roux, 75724
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| LICQLLPVSYAFHSSLIDPAESAYAEFLRSKSFQKPSIPIVSSLTGSCLHVMDENFFW
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
               Russt, Ogasawara, N., Moszer, I., Albertini, A.M., Alloni G., Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Boursier, L., Brans, A., Braun, M., Brignell, S.C., Broriss, R., Boursier, L., Brans, A., Braun, M., Brignell, S.C., Broriss, R., Boursier, L., Bruschi, C.V., Caldwell, B., Capuano, V., Calter, N.M., Choi, S.K., Codani, J.J., Connerton, I.F., Cummings, N.J., Carter, N.M., Choi, S.K., Codani, J.J., Connerton, I.F., Cummings, N.J., Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Ehrilch, S.D., Emmerson, P.T., Entian, K.D., Errington, J., Frabret, C., Ferrari, E., Foulger, D., Fritz, C., Fujita, M., Fujita, Y., Fuma, S., Galizzi, A., Galieron, N., Ghim, S.Y., Glaser, P., Goffeau, A., Golightly, E.J., Grandi, G., Guiseppi, G., Guy, B.J., Haga, K., Halech, J., Harwood, C.R., Henaut, A., Hilbert, H., Holsappel, S., Hosono, S., Hullo, M.F., Itaya, M., Jones, L., Joris, B., Karamata, D., Kasshara, Y., Kolting, C., Kobayashi, Y., Koetter, P., Koningstein, G., Krogh, S., Kumano, M., Kurita, K., Lapidus, A., Lardinois, S., Lauber, J., Hazarevic, V., Lee, S.M., Levine, A., Liu, H., Masuda, S., Mauel, C., Medina, N., Mellado, R.P., Mizuno, M., Moestl, D., Nakai, S., Noback, M., Noone, D., O'Reilly, M., Ogawa, K., Ogiwara, A., Oudega, B., Park, S. H., Parro, V., Pohl, T.M., Portetelle, B., Rapport, G., Rey, M., Reynollds, S., Rieger, M., Schock, B., Rose, M., Sadale, Y., Sato, T., Sekowska, A., Seror, S.J., Serror, P., Shin, B.S., Soldo, B., Seror, S.J., Serror, P., Shin, B.S., Soldo, B., Seror, S.J., Serror, P., Shin, B.S., Soldo, B., Sonoka, M., Wannier, F., Vasamoto, M., Vannier, F., Vasamoto, K., Yata, K., Yata, K., Yasamoto, K., Yata, K., Yoshikawa, H., F., Zunsteh, F., Yoshikawa, H., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ACCCACACAG 10
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Z99120.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BSUB0017 217420 bp DNA BCT 26-NOV-1997 Bacillus subtilis complete genome (section 17 of 21): from 3197001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 217420)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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9280. .10059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9280.
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GENPEVFQIDPGANGYYGYEVMDTCRPIPDSEAGDSDLSLMSYLDCCEQTFLEYQKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGANYQDTFQYLAYHTPFGGMVKGAHRTMMRKVAKVKTSGIETDFLTRVKPGLNYCQR
VGNIMGAALFLALASTIDQGRFDTPKRIGCFSYGSGCCSEFYSGITTPQGQERQRTFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IEKHLDRRYQLSMEEYELLFKGSGMVRFGTRNVKLDFEMIPGIMQSTQEKPRLFLEEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'db_xref="SWISS-PROT: P40830"
'translation="MLITCSESGIDFGKSLSTYIHEYLGLNRNCRLFEVKQACYSGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="PID:g2634097"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="GI:2634097"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus/Clostridium group; Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 10; DB 1;
Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 233780;
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MEDLINE
REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 217420)
Kunst, F., Ogasawara, N.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The complete genome sequence of the gram-positive bacterium Bacillus subtilis
Nature 390 (6657), 249-256 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Danchin, A.
                                                                                                                                           /protein_id="CAB15109.1"
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/db_xref="piD:g2635616"
/db_xref="GI:2635616"
/db_xref="SPTREMBL:005262"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MTIKANYDSAKQAYEKWGIDVEEALRQLEQVPISIHCWQGDDIE
GEFYNKGELSGGIDVTGNYPGKAQTPEELRRDLEKALSLIPCKHRVNLHAIYAETNRE
AVERDELKPDETENWYKWAKNIGIGLDFNPTIFSHEKAAGGITLSHPDDDIREFWIRF
CIAGRRIGEFYGKELGTPCLTNIWIPDGYKDIPSDRLTPRKRLKESLDRIFSEEISEQ
HNLDSIESKLFGLGSESYVVGSHEFYLAYALINHKLCLLDTGHFHPTETVSNKISSML
LYTDKLALHVSRPVRWDSDHVVVLDDELREIALEIVRNHALEKVAIGLDFFDASINRV
                        /translation="MIYTAIDVGASSGRIMVGELNEGKLDIQEIHRFANGFSQRDGHC
LWDLDHLLKQILQGLQKVKTLGYEHCTVGIDTWAVDYVILDEKGDKLREAISYRDRRT
DHFIDKLHHTLSKRAIYQKTGIQFQEVITYYQLDEEDRELLKKTDKIMKHDDYLGYCL
DHFIDKLHTGKRAIYQKTGNLDFELLEAVSVLEQQFAPLTEPGCELGKLRNEWFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(1303.
/gene="yulD"
                                                                                                                                                                                                                                                                                                                                                                                                   /gene="yulC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QMGVPVKEAWLYDIKEYEQQVLLKRKASSPIV"
DYDLPACKVMTVATHDTASAVIAAPGVNDGWAYISSGTWSLIGVENKTPIITDLALEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="yulC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(1635. .3092)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="SPTREMBL:005263"
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LDEETGRLFAYLEIEDEEKWRKMADTEVCQRWWKSMAPLMKTNSDFSPVAIDLKEVFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="CAB15108.1"
/db_xref="PID:e1184197"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAWTIGTRIMIKALLYALLLPIGYLKOLOEEGRYTERLALMEEFKTYPFGAIWDSYCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="PID:e1184196"
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/db_xref="GI:2635614"
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/strain="168"
                                                                                                                                                                                                                                                                                                                            codon_start=1
                                                                                                                                                                                                                                                                                                                                                        'note="similar to rhamnulokinase"
                                                                                                                                                                                                                                                                                                                                                                                    'function-"unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'db_xref="PID:g2635615"
'db_xref="GI:2635615"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="similar to hypothetical proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene-"yulD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="similar to L-rhamnose isomerase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene-"yulE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene≖"yulE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'db_xref="taxon:1423"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'protein_id="CAB15107.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="SPTREMBL:005264"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (1303. .1617)
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KRFLNPENMIKEIQHYCRQTRQKIPRTAGELACCIYSNLAIIYAIAIKELETTITEKPI
EQFHIIGGGARNDFLNQLTADMSGKAVYAGPIEATATGNLLMQMIAAKEVKDIKEARQ
VVRNSFPIKVFTPKDIDRSTIIQSFQQTVLKALSK"
complement(3097...3873)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KTTEKDFRGREIEVMWYKGSGSDLATMKAHNFSGLKLDDIRPLIKRDOMPDEEMYDYL
SHCMIDSKHPRPSIETLLHAFLPYKHVDHTHPDAIISICCADMSQJIAEDIYGMRFWY
VPYVRDGFTLSKMIAGOVANNHAFLPYKHVDHTHPDAIISICCADMSQJIAEDIYGMRFWY
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INDRINOHEVFGGKRYQPLPEDKRKQILAGIMPVIRGAYSEEKKMILSYDDHDDYLEF
VNSVQAPALSQIGAACPDHLYHTKRVPLYIDMWPETODVHKLADLIKSGVFTFTSEYQ
VFTRNQDGDQIFESAPRVILIFGIGHWVTGKSYAMSKYSGALVRRAIAVMKGATAL
GQFVSLHENESYHVEYWPLELYKLTLAPPEAEESRKVALITGGAGGIGSAACREFAAL
GQFVSLHENESYHVEYWPLELYKLTLAPPEAEESRKVALITGGAGGIGSAACREFAAL
GGHVIYADLNIEGAQKIAGEINDAYGKGRAMAVKMDVTKEEDVOSAFERAALAYGGID
                                                                                                                                   TLNDDVGAIYAASEDKKLYKYPDSGYPKGFDPTGRDWYKQAVAEKGQAVFSEPYTDEA
TGDIVVTISKOLKDGSGYIALDLNLDEVLTASKRIKIGKEGFAETITGNKKYIAHETI
KPGTTGSGDWINQVYSKKEGSFEYTFEGKEKKMAFTTNKLTGWKIAGTTEVSELODAS
SPVLNTAVIILCVSIVIGGILILYIIRAITKPLRKLYSTSAKISSGDLTEVIDIHSKN
                              EFGQLGESFNEMSASLRSVIGVIQTSVENVASSSEELTASAAQTSKATEHITLAIEQF
SDGNEAQSEKLETSSNHLSQMNEGISKVAQASSTITKSSIQSSEAAGSGEKLVEHTVG
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DRELISSAKGNVEELNSTLQNKLEDKVKAIDYYSETVDKDILLGKNKTLLKEKFKQYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(6137. .8125)
/gene="tlpB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IVVNNAGLATSSPFDETSLKEWNLNMNVLGTGYFLVAREAFKQMKHQNRGGSMVFVGS
KNSVYAGKNASAYSSVKALETHLARCIAAEGGEFGIRVNSVLPDAVLQGSAIWGSSWR
EERAAAYGIEPDQLEEHYRKRTALLVNIYPEDIAEAIAFFASSKAEKTTGCMITVDGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="alternate gene name: yula; similar to
sorbitol-6-phosphate 2-dehydrogenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(6109. .6124)
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IASLQDVSRLITDSGLDPASVKALEDKKVKVTAVPLSKRG"
complement(3930..5999)
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KEHKLSRSHGGAVSIQQKESEIHFSEREITNVIEKKAIAHEAAKYVKSGDRIILDAST
TAWYMAKILPDIELTVITNSMKAAIELSNKENISVISTGGILLEKSLSFAGPLAERSL
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/db_xref="PID:g2635617"
/db_xref="GI:2635617"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="methyl-accepting chemotaxis protein"
/protein_id="CAB15112.1"
/db_xref="PID:e1184201"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="SWISS-PROT:P40747"
/translation="MVKHIWDSERAAQLPKGVEELVYRSNLIGSDRTVCNWGGGNTSM
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/codon_start=1
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RGFSVVAEEVRKLAVQSADSAKEIEGLIQEIVREISTSLSMFQSVNHEVKEGLQITDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene="tlpB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="PID:g2635618"
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cloning, heterologous expression, and localization of a novel crystal protein gene from Bacillus thuringiensis serovar japon strain buibui toxic to scarabaeid insects Curr. Microbiol. 28 (1), 15-19 (1994) 94100786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene,
U04366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BTU04366 3483 bp DNA BCT 27-AUG-1994 Bacillus thuringiensis japonensis Buibui CryIII delta-endotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (15-DEC-1993) Jerald S. Feitelson, Molecular Biology
Mycogen Corporation, 4980 Carroll Canyon Road, San Diego, CA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus thuringiensis
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U04366.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feitelson, J.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hori, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sato, R., Takeuchi, K., Ogiwara, K., Minami, M., Kaji, Y., Suzuki, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus/Staphylococcus group; Bacillus.
1 (bases 1 to 3483)
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complement(8204. .10224)
/gene="mcpA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Asano, S., Ohba, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(8239. .10224)
/gene="mcpA"
SFSTLENLLRKPDFFTLLQEIRMYTSFRQNGTIEYYNYWGGQRLTLSYIYGSSFNKYS
                  KEWGYPQNDIDLFYKEQVSYTARYSDHCVQWYNAGLNKLRGTGAKQWVDYNRFRREMN
VMVLDLVALFPNYDARIYPLETNAELTREIFTDPVGSYVTGQSSTLISWYDMIPAALP
                                                   /trānslation="MSPNNQNEYEIIDALSPTSVSDNSIRYPLANDQTNTLQNMNYKD
YLKKTESTHAELSRHPGTFISAQDAVGTIDIVSTIISGLGIPVIGEVE'SILGSLIGL
LAPSNNENWOIIFMRVESLLIDKKILDSVRSRAIADLANSRIAVEYYONALEDWRKND
HSTRSAALVKERFGNAEAILRTNMGSFSQTNYETPLLPTYAQAASLHLLVMRDVQIYG
                                                                                                                                                 /product="CryIII delta-endotoxin"
/protein_id="AAA21119.1"
/db_xref="PID:g532524"
                                                                                                                                                                                                                                                                        /db_xref="taxon:1428"
/clone_lib="Library of K. Ogiwara"
/note="serotype 23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:532523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(8204. .8228)
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ASAEEQLASMEEISSSAETLANMAEELQDITKKFKIES"
                                                                                                                                                                                                                                                                                                                                                                                                                 , 1994 this sequence version replaced gi:436836.
                                                                                                                                                                                                                                                                                                                                                         'strain="Buibui"
                                                                                                                                                                                                                                                                                                                                                                           organism="Bacillus thuringiensis"
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/transl_table=11
                                                                                                                                                                                                                  transl_table=11
                                                                                                                                                                                                                                                                                                                                    'sub_species-"japonensis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  function="chemotaxis deficiency toward glucose lpha-methyl-glucoside"
                                                                                                                                     db_xref-"GI:532524"
                                                                                                                                                                                                                                      codon_start=1
                                                                                                                                                                                                                                                         .3483
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Pred. No. 1.3e+03;
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BUHARGSC/c
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Best Local Similarity
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                                                       misc_feature
                                                                                                                           -10_signal
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                                                                                                                                                                                         -35_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Buchnera aphidicola (a prokaryotic endosymbiont of aphids) contains a putative 16s rRNA operon unlinked to the 23s rRNA-encoding gene; sequence determination and promoter and terminator analysis Unpublished (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BUHARGSC 485 bp DNA BCT 26-JUL-1995
Buchnera aphidicola arginyl tRNA synthetase (args) gene, 5' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Munson, M.A., Baumann, L. and Baumann, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buchnera aphidicola DNA.
Buchnera aphidicola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         argS gene; arginyl-tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cds and 16S
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                                                       region"
382. .39
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RINGENGWTGSTGIEVVEGDVLFKDRSLRLTSAREIOTETYTYTYQQICESLLKPYT
RYKLKGFIGSSQDLEIKLIRHANQTVKNVPDNLLFPVPFVNSGGFVDRCSEQQYVDA
NLALENNGENGNMSSDSHAFSFHIDTGEIDLNENTGIWIVFKIPTINGNATLGNLEFV
EEGPLSGETLEWAQQQEQOWQDKMAKKAAASEKTYZNAKQALDRIFADYQDQKLNSGV
EMSDLLAAQNLVQSIPYVYNDALTEIDGMNYTSFTELTMLQQAWNLYDLQNAFUNG
FRNGLSWWAATSDVNVQQLSDTSVLVIDNWNSQVSQOFTVQBYKRYLLAVTAKKEGVG
DGYVIIRDGANQTETLTFNICDDDTGVLSTDQTSYITKTVEFTPSTEQVWIDMSETEG
                                                                                                                                              /note-"deduced by comparison with E. coli rrnB promoter region".
                                                                                                                                                                                                                                                                                                                                                                                                         complement(1. .>150)
/gene="argS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="host: Mindarus victoria"
complement(1. .150)
/gene="args"
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GIKTIDSGEELTYENYQSYSHRVSYITSEEIKSTGGTVLGVVPLTIGWTHSSASRNNFI
YATKISOIPINKASRTSGGAVWNFOEGLYNGGPVMKLSGSGQVINLRVAIDAKGASQ
RYRIRIRYASDRAGKFTISSRSPENPATYSASIAYTNTMSTNASLTYSTEAYAESGPI
NLGISGSSRTFDDISITKEAGAANLYIDRIEFIPVNTLFEAEEDLDVAKKAVNGLFTNE
note="deduced by comparison with E. coli rrnB promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Buchnera aphidicola"
/db_xref="taxon:9"
                               /standard_name="box A"
                                                                                                note="deduced by comparison with E. coli rrnB promoter"
                                                                                                                                                                                                                         SIAKK"
                                                                                                                                                                                                                                                                                                             product="arginyl-tRNA synthetase"
protein_id="AAA72381.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
                                                                                                                                                                                                                                                               db_xref="GI:34961
                                                                                                                                                                                                                                     translation="MNLYLEISKIIKKALIESSAPLDCNPGIKKSSPNQTSDYQVNGI
                                                                                                                                                                                                                                                                                                                                                             transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                   codon_start=1
                                                                                                                                                                                                                                                                                          1b_xref="PID:g349611"
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22-FEB-1989; US-313682.
(GEHO-) Gen Hospital Corp.
Smith JA, Raychowdhury R, NJ
WPI; 90-084851/12.
Macrophage-derived inflamatory cytokine MIP-2 used for developing screening assays, for prodn. of antibodies and in diagnosis and therapy.

Claim 5; Fig 7; 78pp; English.

MIP-2 may be used to detect idiopathic or invasive stimuli.

Antibodies raised to the cytokine may be used to measure MIP-2 activity and inhibit the production of MIP-2 used in treatment inflamation or fever.
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Key
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Q03852;
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Cloned Heymann nephritis antigen , gp330, gene used for diagnosis and in treatment of membranous glomerulonephritis, wounds and gastric ulcers. Disclosure; p; English.

The gene can be used to transform a host cell providing derivatives, free from impurities.

Sequence 2181 BP; 533 A; 541 C; 581 G; 526 T;
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19-AUG-1989;
23-AUG-1988;
22-FEB-1989;
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Q03577;
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1-SEP-1989; 003798.

2-SEP-1988; US-240078.

1-SEP-1989; US-399971.

(CHIR.) Chiron Corp., (UYRO-) Rockefeller Univ.

Wolpe SD, Cerami A, Sherry B, Olson-Tekamp PA;

WPI; 90-115959/15.
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EP-358977-A.
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Lymphotoxin gene. 6.6 kb transcript

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23-AUG-1989; U0-3621.
23-AUG-1988; US-235211.
22-FEB-1989; US-313682.
22-AUG-1989; US-996697.
(GEHO-) General Hospital Corp.
Smith JA, Raychowdhury R, Niles JJ
WPI; 90-099425/13.
Fig. 8: 20 pp; English.

The sequence is isolated from male goats and hybridises only of cattle, sheep, goats and other ruminants which contain Y-c DNA. It can be used for sex determination.

Sequence 384 BP; 113 A; 91 C; 87 G; 93 T;
                                                                                                                                                                                Caprine repeat element GRY.1a(a).

GRY.1a(a); Y-chromosome; ruminants; repeat element; sex determination;

GRY.154-A.

10-AUG-1989.

27-JAN-1989; AU0029.

27-JAN-1988; AU-006476.

(ADRI-) Advanced Riverina Holdings Ltd.

Reed KC; Lord EA; Matthaei KI; Mann DA; Beaton S; Herr CM; Matthews ME

WPI; 89-249021/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant DNA encoding and expressing Heymann's nephritis antigen its use for therapeutic and/or preventative administration. Claim 3, Fig 8, 65pp; English.

The sequence was derived from two overlapping clones of 1.4 kb and a resp. It encodes three cysteine-rich regions which are homologous to LDL receptor binding domain.

Sequence 2181 BP; 533 A; 542 C; 580 G; 526 T;
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Query Match Best Local S Matches 10

ch 100.0%; l Similarity 100.0%; 10; Conservative (

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Score 10; DB 1; 1 Pred. No. 1.1e+03; ; Mismatches 0;

Length 2589

Indels

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Gaps

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ID N90573

ID
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Best Local S
Matches 10
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W08907154-A.
10-AUG-1989; AU0029.
27-JAN-1988; AU-005476.
29-JAN-1988; AU-005476.
(ADRI-) Advanced Riverina Ho
Reed KC; Lord EA; Matthael K
WPI; 89-249021/34
                                                                                                                                                                                                                                                                                                                                                                                            N90574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               determination.

Fig. 9; 20 pp; English.

The sequence is isolated from male goats and hybridises only to the DNA of cattle, sheep, goats and other ruminants which contain Y-chromosomal DNA. It can be used for sex determination.

Sequence 448 BP; 132 A; 104 C; 103 G; 109 T;
Fig. 10; 20 pp; English.

The sequence is isolated from male goats and of cattle, sheep, goats and other ruminants w DNA so can be used for sex determination.

Sequence 2589 BP; 754 A; 522 C; 548 G
                                                                                                                     WPI; 89-249021/34.
New nucleic acid isolates hy useful in hybridisation and
                                                                                                                                                              10-AUG-1989.
27-JAN-1989; AU0029.
29-JAN-1988; AU-006476.
29-JAN-1988; AU-006476.
(ADRI-) Advanced Riverina Holdings |
Reed KC; Lord EA; Matthaei KI; Mann
WPI; 89-249021/34.
                                                                                                                                                                                                                                                                                                                              Caprine repeat
GRY.1; Y-chromo
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                                                                                                  determination.
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ilarity 100.0%;
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at elements GRY.la and
omosome; ruminants; rep
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Pred. No. 1e+03;
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Pred. No. 1e+03;
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                                        d hybridises which conta:
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AC N'
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Best Local S
Matches 10
                          Query Match 100
Best Local Similarity 100
Matches 10; Conservative
                                                                                                                                                                                                                                                                                               GB2217326-A.
25-OCT-1989
08-APR-1988; GB-008206.
08-APR-1988; 008206.
(BRBI') British Bio-Technology Ltd.
Davies JA, Johnson ID;
WPI; 89-311765/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP-314094-A.
03-MAY-1989,
26-OCT-1988; 117832.
28-OCT-1987; JP-272034.
(EISA) Eisai KK.
                                                                                                                                                                                Synthetic gene encoding tumour necrosis restriction sites at frequent intervals Disclosure, Fig. 1, 18pp, English. The sequence is the deduced TNF beta cDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - have improved antitumour activity or exhibit a cytotoxic effect on lymphotoxin-resistant cancer Figure 1; page 38; 57pp; English.
A plasmid contg. cDNA coding lymphotoxin was obtofrom mRNA of Daudi cells.
Sequence 618 BP; 110 A; 236 C; 132 G; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
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13-MAY-1990 (first entry)
Sequence of the amino acid-coding region of lymphotoxin
Lymphotoxin; lymphotoxin-resistant cancer cell; antitumo
activity.
                                                                                                                                           synthetically.
Sequence 517
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Tumour necros
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P-PSDB; P91909.
                                                                                                                                                                                                                                                                              P-PSDB; P93080.
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                                                                                                                                           105
                                                DB 1;
1e+03;
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1e+03;
                                                                                                                                                                                                                             factor beta - incorporates to facilitate manipulation
                                                                                                                                         <u>ن</u>
                                                                                                                                                                                    sequence.
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  89-324195/44
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Best Local Similarity
Matches 10; Conserv
W08909777-A.
19-OCT-1989.
07-APR-1989; U01473.
08-APR-1988; US-179587.
26-SEP-1988; US-179584.
(ARCH-) Arch Development Corp.
Sukhatme VP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   synthetic gene encoding tumour necrosis factor beta incorporat restriction sites at frequent intervals to facilitate manipulation sites at frequent intervals to facilitate manipulations of the synthetic TNF beta gene has the following restriction sites: Bashm, PvuII, NslI, RarII, KpnI, AccI, PflMI, PstI, BstXI, ScaI, and EcoRI. The claimed sequence is nucleorides 14-532. The TNF beta gene can be easily modified due to the restriction sites. The gene can be easily modified due to the into an expression system, eg mammalian cells, yeast and insect hosts. The gene is produced synthetically.

sequence 547 BP: 107 A; 206 C; 111 G; 123 T;
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25-OCT-1989.
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WPI; 89-311765/43.
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(BRBI-) British Bio-Technology
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lgr-1-contg. OC3.1 clone.
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nilarity 100.
Conservative
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regulatory proteins.
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535. .546
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); Mismatches
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1e+03;
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tXI, ScaI, BamHI
The TNF beta has
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NRESULT N93011 ID 193 191 AC N93 AC N93 HOTO CONTROL HOU CONTROL H
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Best Local S
Matches 10
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Best Local Similarity
Matches 10; Conser
27-JUN-1988; 305875.
27-JUN-1987; JP-160115.
(ELED) Denki Kagaku Kogyo K
Osawa T, Obinata M, Ishii Y
WPI; 89-009064/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-JAN-1905.
27-JUN-1988; 305875.
27-JUN-1988; JP-160115.
(ELED) Denki Kagaku Kogyo KK.
Osawa T. Obinata M. Ishii Y;
WPI; 89-009064/02.
New polypeptide with lymphotoxin activity
New polypeptide with lymphotoxin activity
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LT
                                                                       04-JAN-1989.
27-JUN-1988;
27-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This nucleotide sequence codes for the cDNA of human lymphotoxin polypeptide isolated from plasmid LT13. The lymphotoxin is useful as an antitumour agent. It is not only cytotoxic to various cancer cells but is also capable of intensifying the cytotoxic activity of certain anticancer agents or interferons. It can be produced in pure form and is stable against degradation during purification and storage. See also N93191, and P93717.

Sequence 1310 BP; 306 A; 416 C; 312 G; 276 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; P93113.

Early growth regulatory proteins of mouse and human fingers, vectors and DNA sequence encoding the protein of detecting each.

Claim 8; fig. 1.1-1.8; 55pp; English.

Claim 8; fig. 1.1-1.8; 55pp; English.

The sequence is that of the OC3.1 clone contg. the mousequence which has DNA-binding zinc fingers.

Sequence 3086 BP; 706 A; 939 C; 705 G; 736 T
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Human lymphotoxin polypeptide cDNA.
Human; lymphotoxin protein; antitumor;
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                                                                                                                                             Homo sapiens.
EP-297833-A.
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                                                                                                                                                                                             Human lymphotoxin polypeptide Human; lymphotoxin protein.
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1 Similarity 100.
10; Conservative
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Harity 100.
Conservative
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Pred. No. 1.1e+03;
Mismatches 0;
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Pred. No.
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RESULT Q03289 ID Q0 AC Q0 DT 03 DE NG KW Sy

Q03289 standa Q03289; 03-AUG-1990

standard;

DNA;

03-AUG-1990 (first entry) New synthetic human lymphotoxin Synthetic human lymphotoxin (HL)

gene

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Best Local S
Matches 10
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Best Local S
Matches 10
                                                                                                                                                                                                                           (AMGE-) Amgen Inc.
Lin FK, Lu HS,
WPI; 89-09319/02.
P-PSDB; p93722.
New recombinant kallikrein polypeptide(s) and encoding DNA useful as vasodilators and for treating male infertility.
Table IV; page 11; 43pp; English.
The monkey kallikrein gene is 93% homologous to that of the human genomic kallikrein gene. See also P92314, N93194, N93195, N93193, N93197, N93198, P93720, P93721, and P93722.
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The lymphotoxin is useful as an antitumour agent. It is not only cytostatic to various cancer cells but is also capable of intensifying the cytotoxic activity of certain anticancer agents or interferon. It can be produced in pure form and is stable against degradation during purification and storage. See also N91469, and p93717.

Sequence 453 BP; 81 A; 168 C; 95 G; 109 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - useful purity.
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New poly
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28-JUN-1990 (first entry)
Monkey recombinant kallikrein gene
Monkey; kallikrein gene; vasodilator;
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N93196 standard;
869
                                                                                                                                                                                                          Sequence
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30-JUN-1987; US-068594.
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polypeptide with lymphotoxin activity
ACCCACACAG
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/note="start
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/note="mature
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                                                                                                              1.1e+03;
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Job time: 18973 sec

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RESULT 15

N81442/c

ID N81442;
AC N81442;
DT 17-OCT-1990 (first entry)
DE Clone encoding human protein S
KW Protein S; anti-thrombolytic age
OS synthetic.
FH Key Location/Qualifi
FT cds /*tag= a
FT cds /*tag= a
FT PPBE-1988.
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Best Local Similarity 100.0%;
Matches 10; Conservative
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05-JAN-1990.
27-OCT-1987; 271513.
27-OCT-1987; JP-271513, J
(SANY) Sankyo Kk.
                                                                                                                                                                                                                                                                                                                                                                                                               N81442;
17-0CT-1990 (first entry)
Clone encoding human protein S
Protein S; anti-thrombolytic agent; antibodies; ss.
synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human lymphotoxin synthetic gene altered to leave only one restriction enzyme recognition site Disclosure; Fig 1; 13pp; Japanese. It is altered so that only one restriction enzyme site exists. It has
                                                                                                                             Recombinant DNA encoding mature human Protein S - used therapeutically as anti-thrombolytic agent and for producing antibodies for diagnostic use Disclosure; p; English
This clone encodes the complete mature human Protein S. To facilitate expression in mammalian cells it is fused to the leader sequence of bovine cDNA. See also NB1441.
Sequence 3344 BP; 1072 A; 575 C; 688 G; 1009 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the same amino acid sequence but not the same base sequence as natural HL and the addition of 30 nucleotides has eliminated the 6 bp palindromic sequence. It makes modifications of HL easier and improved lymphotoxins
2925 ACCCACACAG 2916
                                                                                                                                                                                                                                    (INTE-) Integrated Genetics.
Wydro R, Cohen E, Dackowski W, Stenflo J, Lundwall A, Dahlback B;
WPI, 88-037719/06.
P-PSDB; P81137.
                                                                                                                                                                                                                                                                                           10-FEB-1988.
24-JUL-1987; 306564.
25-JUL-1986; US-890401.
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Sequence 618 BP;
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47 ACCCACACAG 556
                1 ACCCACACAG 10
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Pred. No. 1.1e+03;
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Description

D20150 HUMGS01123

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D20150 336 bp mRNA EST 30-JUL-1996 HUMGS01123 Human promyelocyte Homo sapiens cDNA clone pm2161 3', mRNA sequence.
D20150 9501247 D20150.1 GI:501247
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Match
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T09172 T11879 T14435 T14477 T14830

T08188

5 HSCOCD082 R 1 EST001814 Su 2 EST001831 H1 3 EST001271 Su 4 EST00233 Fe CELL2B2 Chr 4 EST0233 Fe CELL2B2 Chr 4 EST0233 Fe 1 EBJ012 Feta 6 IB1444 Infan 1 IB742 Infan 1 IB781 Infan 1 IB781 Infan 1 IB781 Infan 2 EST05683 Fe 3 EST070679 In 2 EST070679 In 2 EST070683 Fe 3 EST07068 In 2 EST07069 In 3 EST07069 In 4 IB1362 Infa 3 IB1153 Infa 3 IB1153 Infa 3 IB1163 Infa 4 IB163 Infa 5 IB1362 Infa 6 IB13508 Infa 6 IB163 Infa 7 SMEST0096 S 8 CORSTO SH 9 ALOST HEAT 9 ALOST HEAT 1 IB163 Infa IB163 In

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                                                                                                                                                                                                                                                                                              Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                         g426856
D22931.1
                                                                                                                                                                                Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
                                                                                                                                                                                                                                             1 (bases 1 to 295)
Sasaki, T. and Minobe, Y.
Rice cDNA from callus
Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                    RICC1816A Rice
D22931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Okubo,K., Fukushima,A., Yoshii,J., Niiyama,T., Yoshinari,H., Arimoto,J. and Matsubara,K.
Institute for Molecular and Cellular Biology
Osaka University
3-1 Yamada-oka,Suita,Osaka 565,Japan.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 336)

Okubo, K., Fukushima, A., Yoshii, J., Nilyama, T., Kojima, Y.,
Yoshinari, H., Arimoto, J. and Matsubara, K.
Gene expression of human promyelocytic cell line HL60 before and after induction of differentiation. A new application of 3'directed cDNA sequencing
Unpublished (1993)
                                                                                                  Fax: 0298-38-7468
Email: tsasaki@abr.affrc.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                         Kannondai, Tsukuba
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    /organism="Oryza sativa"
/strain="cultivar Nipponbare,
/db.xref="taxon:4530"
/clone="R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Human promyelocyte"
/note="Female, adult, cell_line = HL60,
promyelocyte."
                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="pm2161"
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Oryza sativa cDNA clone
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. 7.9e+03;
                             sub_species Japonica"
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Tel: 0298-38-7441
Fax: 0298-38-7468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
2-1-2 Kannondai, Tsukuba
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Minobe, Y. and Sasaki, T.
Rice cDNA from root
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: tsasakl@abr.affrc.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales;
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ilarity 100.0%;
Conservative 0
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/note="Vector: pBluescript II SK+; Site_1: SalI; Site_2:
NotI; colla prepared from rice callus mRNAs by using
oligo(dT) as a primer and ligating to the SalI-NotI site
of pBluescript II SK+ phagemid.

a 89 c 112 g 37 t 7 others
                                                                                                                                                                                                                                                                                         /clone_lib="Rice root"
/note="Prepared from seedling root. " .
/no 78 c 105 g 113 t 2 others
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                                                                                                                                                                                                                                                                                                                                                                        /organism-"Oryza sativa"
/strain-"Nipponbare, sub_species Japonica"
/db_xref_"taxon:4530"
 Rice root Oryza sativa
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                 351 bp
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Pred. No. 8.2e+03;
; Mismatches 0;
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Pred. No. 7.8e+03;
Mismatches 0;
                     mRNA
EST 20-JUL-1998 cDNA clone R, mRNA sequence.
                                                                                                                                                                                                                       Length 434;
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                                                                                                                                                                                                                                 Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
(bases 1 to 360)
                                                                                                                                                                                                                                                                                                                                                              D36166 360 bp mRNA EST 08-AUG-1994 CELK029H4F Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA clone yk29h4 5', mRNA sequence.
                                                                                      Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411,
Tel: 0559-75-0771
                                                                                                                                                                         Toward an expression map of the C.elegans genome Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
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D36166.1 GI:528104
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National Institute of Agrobiological Resources
Rice Genome Research Program
2-1-2 Kannondai Tsukuba
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                               Contact: Yuji Kohara
                                                                                                                                                                                                                     Kohara, Y., Mitsuki, H., Nishigaki, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: tsasaki@abr.affrc.go.jp
PROJECT ='RGP'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minobe, Y. and Sasaki, T. Rice cDNA from root
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0298-38-7468
                                                                          0559-75-6240
                                          ykohara@ddbj.nig.ac.j.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Rice root"
/note="Prepared from seedling root. "
/no 65 c 85 g 87 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa"
/strain="Nipponbare, sub_species Japonica"
/db_xref_"taxon:4530"
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
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7.9e+03;
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g645302
F01745.1
                            HSC0CD082
c-0cd08 3'
F01745
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyliophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Poaceae; Oryza.
                                                                                                                                                                                                        10;
                                                                        F01745
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Fax: 0298-38-7468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 344)
Sasak1,T., Miyao,A. and Yamamoto,K.
Rice cDNA from callus 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RICR1067A Rice
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                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        baraki
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                                                                                                                                                                                                                                                                                                                                                                                            tsasaki@abr.affrc.go.jp.
Location/Qualifiers
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/note="dev_stage="varied, sex=Hermaphrodite
tlssue_type="whole animal"
78 c 71 g 88 t 3 others
                                        260 bp mRNA normalized infant brain cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                          /clone_lib="Rice root"
/note="Prepared from seedling root.
77 c 91 g 103 t
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/strain="Nipponbare, sub_species Japonica"
/db_xref="taxon:4530"
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Pred. No. 7.9e+03;
; Mismatches 0;
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                                                      Homo sapiens cDNA clone
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GI:645302

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                                                                                                                                                                                                                                                                 M78221 409 bp mRNA EST 26-MAY-1992 EST01814 Subtracted Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCPS22 similar to Myelin basic protein, mRNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 409)
Adams,M.D., Dubnick,M., Kerlavage,A.R., Moreno,R., Kelley,J.M., Utterback,T.R., Nagle,J.W., Fields,C. and Venter,J.C.
                                                                                                                                                                                                           M78221
g273958
                                                                                                                                                                   EST
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95277534
                                                                                                                      Homo sapiens
                                                                                                                                                                                M78221.1
                                                                                                                                                                                                                                                    sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single read. removed at sequence 5'end
Genexpress_library_idt: C; Genexpress_sequence_idt: alc-0cd08
Seq primer: (-21)M13_universal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genexpress@genethon.fr
Single read. removed at seque
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Genethon Centre de recherche sur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Sebastiani-Kabaktchis, C. and Tessier, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 260)
Auffray, C., Behar, G.,
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/dev_stage="3 months old"
/notes_organ: brain; Vector: lafmid BA; Site_1: HindIII;
/notes_organ: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type="total"
brain; total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA vector. Clone library from B.Soares, Psychiatry Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"
s 53 c 59 g 81 t
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/db_xref="taxon:9606"
/map="17 (15)"
                                                                                                                                                                                     GI:273958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 10; DB 20;
Pred. No. 7.7e+03;
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Best Local
                                                                                                                                                                        AUTHORS
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                                                     Bioinformatics
The Institute for Genomic Research
The Content Drive, Rockville,
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                                                                                                                                        EST mapping 
Unpublished
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Durbin, A.S.
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                                           9712 Medical Center Drive, Tel: 3018699056
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                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                      clone HHCMC05, mRNA sequence
Seq primer: M13 Reverse
                                                                                                      Contact: Kerlavage, AR
                                                                                                                                                                                                                Sequence identification of 2, Nature 355, 632-634 (1992)
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Fax: 3018699423
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            smail: arkerlav@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                          GI:272998
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/db_xref="APCC (inhost):78862"
/db_xref="GDB:DOS1215E"
/db_xref="taxon:9606"
/clone="HHCPS22"
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(1996)
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1 (bases 1 to 423)

Adams,M.D., Dubnick,M., Kerlavage,A.R., Moreno,R.,
Utterback,T.R., Nagle,J.W., Fields,C. and Venter,J.
Sequence identification of 2,375 human brain genes
Nature 355, 632-634 (1992)
                                                                                                                                                                                                                                                                                                                   Seq primer: M13 Forward.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                               The Institute for Genomic Research 9712 Medical Center Drive, Rockvil
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EST01271 Subtracted 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kerlavage, AR
                                       /note="vector: lambdaZAP-II; The hippocampus library (#4 above) was subtracted with a fibroblast cell line cDNA library (Stratagene cat. #936209; WIJ8 Lung fibroblast cell line; oligo-dT + random primed cDNA synthesis; lambdaZAP-II vector, 1.0kb average insert size.) by the method of Sive & St. John (Nucl. Acids Res. 16:10937, 1988)."
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/note="Vector: lambdaZAP-II; Female, 2 years; oligo
random primed cDNA synthesis; lambdaZAP-II vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:273436
                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="ATCC (inhost):78667"
/db_xref="GDB:D0S2091E"
/db_xref="taxon:9606"
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/map="16 p13.13"
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/db_xref="GDB:D16S442E"
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P-II vector, 1.0)
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RESULT 1
M85714/c
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Best Local
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                                       M85714

EST02233 Fetal brain, sclone HFBCM42, mRNA se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhahditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: arkerlav@tigr.org
Seq primer: M13 Foward.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      wESTUU425 Mixed stage, Stratagene (cat. #937006) Caenorhabditis elegans cDNA clone CEMSF05 similar to Actin, mRNA sequence. M79888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M79888 312 bp wEST00425 Mixed stage,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans expressed sequence tags identify gene families and potential disease gene homologues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhabditina; Rhabditoidea; 1
1 (bases 1 to 312)
McComble,W.R., Adams,M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M79888.1 GI:271907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McCombie,W.R., Adams,M.D., Kelley,J.M., FitzGerald,M.
Utterback,T.R., Khan,M., Dubnick,M., Kerlavage,A.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                             /clone_lib="Mixed stage, Stratagene (cat. #937006)"
/note="Vector: Uni-ZAP XR; C. elegans mixed stage cDNA
library. Strategene catalog #937006. The library is ol
                                                                                                                                                                                                                                                                                                                                                                                          /organism="Caenorhabditis elegans"
/db_xref≈"taxon:6239"
/clone="CEMSF05"
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                                                                   Stratagene
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                                                                                                                                                                                                                             Score 10;
Pred. No.
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Pred. No. 8.1e+03;
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7.8e+03;
                                                                   (cat#936206) Homo sapiens cDNA
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                                                                                                                                                                                                                                                                                                      3 others
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ORGANISM

Homo sapiens

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AUTHORS
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EST02312 Fetal brain, Stratagene (cat#936206) Homo clone HFBCN71, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                    The Institute for Genomic Research 9712 Medical Center Drive, Rockville, Tel: 3018699056
                                                                                                                                                                      Bioinformatics
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Cr
Eutheria; Primates; Catarrhini;
1 (bases 1 to 323)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams, M.D., Dubnick, M., Kerlavage, A.R., Moreno, R., Utterback, T.R., Nagle, J.W., Fields, C. and Venter, J. Sequence identification of 2,375 human brain genes
                                                                   Email: arkerlav@tigr.org
Seq primer: M13 Forward.
                                                                                                                                                                                      Contact: Kerlavage, AR
                                                                                                                                                                                                                                          Adams,M.D., Dubnick,M., Kerlavage,A.R., Moreno,R., Kelley,J.M., Utterback,T.R., Nagle,J.W., Fields,C. and Venter,J.C. Sequence identification of 2,375 human brain genes Nature 355, 632-634 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: arkerlav@tigr.org
Seq primer: Ml3 Forward.
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92168112
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                                                                                                       3018699423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="retal brain, Stratagene (cat#936206)"
/note="Vector: LambdaZAP-II; 17-18 wk gestation; fema
oligo-dT + random primed cDNA synthesis; lambdaZAP-II
vector, 1.0kb average inser size."
1 others
2 9 8 t 1 others
/organism="Homo sapiens"
/db_xref="ATCC (inhost):81368"
                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="ATCC (inhost):81291"
/db_xref="GDB:D0S407E"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
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Pred. No.
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.W., Fields, C. and Venter, J.C.
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                                                                                                                                       20850 USA
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CEL12B2 Chris Martin :
cDNA clone cm12b2 5' :
M88939
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Waterston,R., Martin,C., Craxton,M., Huynh,C., Coulson,A.,
Hillier,L., Durbin,R.K., Green,P., Shownkeen,R., Halloran,N.,
Hawkins,T., Wilson,R., Berks,M., Du,Z., Thomas,K., Thierry-Mieg,J.
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Road, Cambridge CB2 2QH, UK
Tel: (USA) (314)3627072 or (UK) (0223)248011
Fax: (USA) (314)3624137 or (UK) (0223)402008
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M88939.1 GI:275440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Box 8232,4566 Scott Ave.,St. Louis,MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A survey of expressed genes in Caenorhabditis elegans Nature Genet. 1, 114-123 (1992)
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(USA) Washington Univ. School of Medicine or (UK) MRC Laboratory of
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Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rw@nematode.wustl.edu
                                                                                                                                                                                                                                     successively picking groups of clones that didn't hybridize to previously picked clones. Vector: lambdaphage SHLX2 (Lipshitz, D.H. et al., Gene 88:25-36 (1990)) Host: MC1061"
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/note="Vector: LambdaZAP-II; 17-18 wk gestation, fema.
/note="Tector: LambdaZAP-II; 17-18 wk gestation, fema.
/note="Tector" tambdaZAP-II
/note="Tec
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/clone="cm12b2"
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′strain="Bristol N2"
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Pred. No. 7.9e+03;
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56 ACCCACAGAG 165
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1 ACCCACACAG 30
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1 (bases 1 to 376)

Khan, A.S., Wilcox, A.S., Polymeropoulos, M.H., Hopkins, J.A., Stevens, T.J., Robinson, M., Orpana, A.K. and Sikela, J.M. Single pass sequencing and physical and genetic mapping of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: nikki@tally.uchsc.edu
Seq primer: -21M13 Universal
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Pharmacology
University of Colorado Health Sciences Center
Box C236, 4200 E. 9th Ave, Denver CO 80262-0236
Tel: 3032708637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Sep 21, 1992 this sequence version replaced gi:279283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature Genet. 2, 180-185 (1992) 94258200
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/note="Yector: Lambda ZAP II; The FB library (catalog
/note="Yector: Lambda ZAP II; The FB library (catalog
#937201, Stratagene) was constructed by directional
cloning and oligo d(T)-priming in Lambda ZAP II phage
utilizing mRNA from a 17 week human fetus (total brain)."

90 c 73 g 109 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="ATCC (inhost):86789"
/db_xref="GDB-0052912E"
/db_xref="taxon:9606"
/clone="FB25F5"
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Title: Perfect score: Sequence:

US-08-956-518A-90

CCCTATGGAG

Scoring table:

IDENTITY\_NUC

tabase :

311585 seqs, .125096042 residues

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Run

8

OM nucleic

nucleic search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

September 18, 1999, 00:33:33;

3 ; Search time 425.19 Seconds
(without alignments)
5.884 Million cell updates/sec

Result No.

Score

Match

Length

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Query

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Apoptosis-regulati Protein PRO224 cDN

## ALIGNMENTS

RESULT 1
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ID Q03064 standard; D
AC Q03064;
AC Q03064;
DT 06-JUN-1990 (firs
DE HindIII-PStI fragm
DE HindIII-PStI fragm
Of human c-myc gen
KW Autonomously replit
OS Homo Sapiens.
FH Key
FT stem\_loop 76
FT stem\_loop 12
FT stem\_loop 14
FT misc\_rna 7\*
FT Tansid JP-28
PA (DAUC) Daitchi Pha.
PI Nariga H, Sato Y, S.
PI Transgenic animals
PI Ariga H, Sato Y, S.
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PI Ariga H, Sato Y, S.
PI Stem\_loop PN EP-350052-A.

PD 10-JAN-1990.

PD 10-JAN-1990.

PF 06-JUL-1988; JP-166992.

PR 10-NOV-1988; JP-284367.

PR 10-NOV-1988; JP-2844641.

PA (DAUC) Dalichi Pharmaceutical Ltd.

PA (DAUC) Dalichi Pharmaceutical y replicating sequence.

PT Transgenic animals producing peptide prods. - carrying a plasmid contg.

PT a mammalian cell derived autonomously replicating sequence.

PT a mammalian ce Query Match Best Local S Matches 10 06-JUN-1990 (first entry)
HindIII-PstI fragment contg. core of autonome of human c-myc gene upstream region.
Autonomously replicating sequence; c-myc; ss. ch 100.0%; l Similarity 100.0%; 10; Conservative 0 49. /\*tag= t .155 /\*tag= 149. .1 /\*tag= a 120. .160 Location/Qualifiers /note="Claim DNA; label-ARS າg= b .190 າg= c .101 210 ₽P 0 Score 10; DB Pred. No. 2.8); Mismatches page of autonomously 2.8e+02; DB 1; Length 210; Indels replicating sequence 0 Gaps 0

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Human brain Expres Human TLE-1 gene. Complete human c-m Vector pHEBO-DR-LU Vector pHEBO-DR-CA Sequence complemen JEV Nakayama strai

Sequence from PATK

Odorant receptor c

Clone 7.2 encoding Clone 1 encoding 1 cDNA sequence enco P40 genomic DNA. N Autonomously repli CDX, a MILA involv

Partial nucleic ac DNA encoding Gene encoding yeas Human T-cell leuke HindIII-PstI fragm Description

Toxoplasma Cellular Receptor

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N81434 Q06691 Q11140 Q11917 N92778 Q12760 Q14382

RESULT
Q030617
ID 30617
AC Q00
AC Q00 В EP-352060-A.
24-JAN-1990.
18-JUL-1989; 307250.
21-JUL-1988; JP-188187.
(TAKE) Takeda Chemical Ind KK.
Fujisawa Y. Kato K. Hatanaka M;
WPI: 90-02445704.
P-PSDB; R03724. 003061; 04-JUL-1990 (first entry) 04-JUL-1990 (first entry) Human T-cell leukemia virus type-1 gag gene; HTLV-1; vaccine; Group specific antigen. Q03061 ે standard; DNA; 1290 ВP

ဂ ဂ 0 0 529 5578 2101 2564 259 2450 2178 2178 14042 14042 14042 14044 3416 3416 3416 3233 T100880 T115928 T115929 T15929 T1287773 T287775 T287775 T28775 T28775 T28776 Human TLE-1 gene.
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CC The gag (group specific antigen) proteins can be mass-
CC produced using Saccharomyces cerevisiae transformants. The
CC HTLV-1 gag gene or part of it can be prepared from an HTLV-1
CC pro virus using appropiate restriction enzymes. A large
CC amount of gag gene or part of it can be prepared by
CC amplifying in Escherichia coli a plasmid subcloned with the
CC HTLV-1 gag gene. DNA that encodes the gag protein is then
CC inserted into an expression vector. The proteins obtained
CC can be used in a diagnostic kit or as a HTLV-1 vaccine. See
                                                                                                                                                                                                                                              Query Match
Best Local :
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9-SEP-1988; US-243733.
13-SEP-1988; US-243733.
14-DEC-1988; US-28244.
(GEHO-) Gen Hospital Corp.
Smith JA, Chang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tches
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Disclosure; 24pp; English.

Aminopeptidases are useful in extending the stability, solubility and biological activity and half-life, or in decreasing the immunogenicity. The vacuolar location presequence encoded by the gene is useful ni directing linked polypeptides through the vacuolar membrane.

Sequence 1891 BP; 606 A; 387 C; 388 G; 510 T;
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P-PSDB; R05535.
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//abel*Vacuolar localisation presequence
301. 487
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                                                                                                                                                                                                              Score 10; DE Pred. No. 3.2); Mismatches
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Pred. No.
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                                                                                                                                                                                                                                           DB 1;
3.2e+02;
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N80297,
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Query Match
Best Local S
Matches 10
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Partial nucleic acid sequence of the Japanese encephalitis virus genome encoding C, M, E and NS proteins
Japanese encephalitis virus (JEV); vaccine; flavivirus immunity; C protein; M protein; E protein; NS protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO8905353-A.
15-UUN-1989.
01-DEC-1988; U04280.
04-DEC-1987; US-2479
(DANA) Dana Farber C
Reinherz EL, Shipp M
WPI; 89-192699/26.
 mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding human common acute lymphoblastic leukaemia antigen used for obtaining pure protein for diagnosis and treatment of medical conditions.
Claim 4; fig 3; 73pp; English.
DNA encoding human common acute lymphoblastic leukaemia antigen (CALLA) (see corresp. p90393), and its fragments. Binds to anti-CALLA its (see corresp. p90393), and its fragment, to design a drug for use as a general analgesic. The DNA has functional endopeptidase activity.
Sequence 5524 BP; 1777 A; 1039 C; 1066 G; 1642 T;
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ne encoding human common acute lymphoblastic leukaemia
DNA; human common acute lymphoblastic leukaemia
analgesic; inhibits leukaemia; endopeptidase.
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N90123;
1-NOV-1989 (first ent
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10; Conserv
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4297. .4992
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3904. .4296
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2167. 3400
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MA, Richardson NE,
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Pred. No. 3.4e+02;
; Mismatches 0;
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RESULT
N81434,
ID NI
AC NI
DT 1:
DE AI
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PT Nucleic acid of Japanese encephalitis virus -
PT Nucleic acid of Japanese encephalitis virus -
PT inmunisation against the virus
PT inmunisation against the virus
PT inmunisation against the virus
PS Claim 4; Fig 5/1-5/5; 52pp; English.
CC Substantially purified nucleic acid sequence of JEV but not to the nucleic acid sequence of yellow fever virus wherein the 10 bp sequence CC of DNA corresponding to the nucleic acid sequence of JEV but not to the nucleic acid sequence do not correspond to those found in 80297. Pref. the nucleic acid sequences do not correspond to those found in yellow fever virus, west encephalitis virus. The nucleic acid may be obtd. from the virus and inserted into a vector. Specific probes can be derived from this conserved into a vector. Specific probes can be derived from the puliphide and nucleic acid and antibodies produced to the polypeptide. The CC protein immunogens or with active vectors encoding such immunogens, encephalitis protective antiviral antibodies. The vaccination induces conserved to the disease caused by other flaviriuses.

CC sequence 4992 BP; 1332 A; 1166 C; 1390 G; 1100 U; 4 Others;
  388888888
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Best Local S
Matches 10
EP-254315-A.
27-JAN-1988.
23-JUL-1987; 110696.
24-JUL-1986; JP-174036.
26-SEP-1986; JP-227455.
(DAUC ) DAIICHI SEIYAKU #
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27-OCT-1986; US-923907.
(FOUR/) Fournier MJ.
MCAda PC, Mason PW;
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Conservative
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Pred. No.
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Best Local
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Claim 9; page 10; 17pp; English.
Claim 9; page 10; 17pp; English.
This sequence, and active fragments, is contained in an expression plasmid alongside a promoter and a gene encoding a protein of interest. The plasmid is propagated in host cells for the prodn. of erest. The plasmid is propagated in host cells for the prodn. of
                                                                                                                                                                                       PPSDB; R08119.
Endothelial cell adhesion mols.
                                                                                                  Disclosure; Fig 9 (A-C); 136pp; English.
The sequence was obtained from CDX PCDM8 clone 7.2 and f portion of the 7.2 insert subcloned into the sequencing CDX is a MILA, involved in ELAMI-mediated adhesion and i the (or an) ELAMI ligand. CDX is expressed in melanomas. See also Q06686-91.
See also Q06686-91.
Sequence 2175 BP; 403 A; 643 C; 652 G; 477
                                                                                                                                                                                                                                                                                                                                                                                                         27-FEB-1991 (first entry)
27-FEB-1991 (first entry)
CDX, a MILA involved in ELAM1-mediated adhesion, from pCDM8 clone
Endothelial cell-leucocyte adhesion molecule 1; ELAM1; CDX;
molecule involved in leucocyte adhesion; MILA; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           erest. The plasmid is propagated in host cells for e.g. insulin, growth hormone, TNF and lymphokines ously replicating sequence has an affinity for a pie in and may be recovered by binding a mammalian cefragment/myc protein prod.

See also N81433.
                                                                                                                                                                                                                                             Rosa MD;
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Hession C, Lobb
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28-APR-1989; US-345151.
01-JUN-1989; US-359516.
18-DEC-1989; US-452675.
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15-NOV-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q06691;
27-FEB-1991
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WPI; 88-022976/04.
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conservative
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/product= CDX
/note= "a MILA
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Pred. No. 3.2e+02;
Mismatches 0;
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2.8e+02;
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lian cell-derived
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Cellular receptor 2 ligand gene.
Cellular receptor 2; Cr2; binding site; BS; auto-immune disease;
Epstein-Barr Virus; EBV; B lymphocyte; ligand; ss.
Synthetic.
Key
Location/Qualifiers
cds
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21-MAR-1991.
04-SEP-1990; 1
08-SEP-1989; 1
20-APR-1990; 1
Q11917 standard; DNA; 1092
Q11917;
14-AUG-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Epstein-Barr virus infection
Disclosure; Fig 1, 129pp; English.
The production of CR2 ligands including a binding site (BS) is
possible by transforming a cellular host with a recombinant DNA
mol. contg. this sequence. The ligand pref. includes a fragment
encoded by a sequence indicated in the features, or the total
CDS. The ligand pref. contains only a single BS and has an
amino acid sequence <100 (pref. <20) residues in length.
The ligand may also comprise a plurality of the segment indicated
                                                                                                                                                                        1983
                                                                                                                                                                                                                                                                                                                                                                                   The compsn. can be administered vivo by Epstein-Barr Virus. See also Q11140-42. Sequence 2208 BP; 458 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_rna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A therapeutic compsn. contg. the polypeptide is used to stimulate or inhibit B lymphocyte proliferation in pattents with B cell lymphoma. B lymphocytes and myeloma's can be stimulated in pattents with immunodeficiencies and immunoglobulin secretion by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
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Q11140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hybridoma cultures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 91-101864/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lernhardt W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-SEP-1990; U05027.
08-SEP-1989; US-404679.
20-APR-1990; US-512118.
(CALB-) CALIF INST BIOLOGIC.
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                                                                                                                                                                                                                   1 CCCTATGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                segment encoding CR-2 ligand and CR2 binding site at auto-immune disease, B-cell lymphoma and inhibit
                                                                                                                                                                     CCCTATGGAG 1992
                                                                                                                                                                                                                                                                th 100 similarity 100 10; Conservative
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939. .977
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/note= "fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     can be boosted
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Pred. No. 3.2
D; Mismatches
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                                                                                                                                                                                                                                                                                         .2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            infection
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                                                                                                                                                                                                                                                                                                          Length 2208;
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                                                                                                                                                                                                                                                                                                                                                                                   371
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Best Local S
Matches 10
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C This sequence is a structural gene of the parasite and encodes p35 antigen. Total RNA was isolated from T.gondii grown in Hep-2 cells. The poly(A) fraction was separated and converted to cDNA. EcoRI adaptors were attached prior to ligation with lambda gtil EcoRI fragments, in vitro packaging and transfection into E.coli Y1090. The resulting gene bank was screened with hyper immune rabbit anti-C T.gondii serum. Of 88 seropositive clones, 8 were sequenced and 1 crossing these (F76-see q11914) was used as a probe to isolate p35. Partial sequences from this full-length clone, e.g. nucleotides 33-527, were inserted into vector pSEM to produce the immunogenic protein as a fusion protein with beta-Gal.

See also Q11909-Q11916 and Q11918-Q11919.

Sequence 1092 BP; 216 A; 350 C; 278 G; 248 T;
                                                                                                                                                               EP-346710-A.
20-DEC-1989; 110096.
03-JUN-1989; 110096.
21-NOV-1988; US-274107,US-207678.
(MOLE-) Molecular Diagnosti.
Barnett TR, Elting JJ, Kamarck ME, K.
WPI; 89-372000/51.
P-PSDB; P93998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-DEC-1990; 123152.

08-DEC-1989; DE-940598.

(BEHW ) BEHRINGWERKE AG.

Knapp S, Ziegelmaier R, I

WPI; 91-172854/24.
Claim 1; Pages 63-64; 65pp; English.

This sequence encodes the KGCEA2 peptide sequence. When the DNA is inserted into an expression vector and a host cell transformed with this the resultant KGCEA2 antigen product is a useful tool in cancer diagnosis. Antibodies against this antigen can be used to detect its presence in animal and human patients and in conjunction with eg a toxin these can destroy a KGCEA2 - expressing cell.

Sequence 1591 BP; 460 A; 408 C; 331 G; 392 T;
                                                                                                                                                                                                                                                                                                                                                                                                    18/c
N92778
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23-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
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                                                                                                                                                    DNA's coding
                                                                                                                                                                                                                                                                                                                                            Carcinoembryonic
                                                                                                                                                                                                                                                                                                                                                           cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Toxoplasma gondii protein, nucleic acid and derived antibodies - useful as diagnostic reagents, vaccines an
                                                                                                                                    prepare probes
                                                                                                                                                                                                                                                                                                                              cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; R12351.
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                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
10; Conserv
                                                                                                                                                                                                                                                                                                                                                 (first entry)
e encoding KGCEA2 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                  for members of carcinoembryonic antigen family - used so to detect antigen or in prodn. of polypeptide(s) and
                                                                                                                                                                                                                                                                                 /*tag=
                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                           antigens (CEA's);
                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
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22. .825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= T.gondii P35 antigen
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                                                                                                                                                                                                                                                                                                   54.
                                                                                                                                                                                             Kretschmer
                                                                                                                                                                                                                                                                                                                                         antibody (anti-CEA) production;
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hes 0;
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                                                                          transformed with
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Matches Query Match

Conservative

0;

100.0%;

Score 10; Pred. No. Mismatches

3.2e+02; DB 1;

Length 1591; Indels

0;

Gaps

0,

Local 10; Similarity

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P40 genomic DNA.
T cell growth factor; AIDS; cytokine;
                         misc_rna
                                                  misc_rna
                                                                            misc_rna
                                                                                                                                           signal_peptide
                                                                                                                                                                                                       misc_signal
                                                                                                                                                                                                                          misc_signal
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                                                                                                                                                                                                                                                                  exon
WO9110738-A
                                                                                        polya_signal
                                                                                                     polya_signal
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                                                                                                                                                                                                                                                                                                                                                            Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                      Q12760;
                                                                                                                                                                                                                                                                                                                                                                                            Q12760 standard; DNA;
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|||||||||
29 CCCTATGGAG 20
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/*tag= d
/number= 4
                        /label= ATTTTA_motif
/note= " reduces stability
3543. .3547
                                                                                                                                        *tag=
.697
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                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
644. .757
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**tag**
                                                                                                                                                               /*tag= i
/note= "AP-1 binding
                                                  label- ATTITA_motif
note- " reduces stability
534. .3538
                                                                                                           label- polyd-AdC_region
note- "Z DNA; enhancer activity"
                                                                                                                                                                                       note- "interferon
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            ATTTTA_motif
     reduces stability of mRNA"
                                                                                                                                                                                        regulatory factor-1 binding
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OR-JAN-1990; US-462158.

OR (RESE) RES CORP TECHN INC.

Vansnick J. Uyttenhove C, Simpson RJ;

WPI; 91-238026/32.

P. PSDB; R13218.

Nucleic acid encoding for P40 T-cell growth factor - for patients produced acid encoding for P40 T-cell growth factor - for patients or compromised immune systems, also allows increased produced from the regulation of other cytokine(s).

Claim 1; Fig 15; 122pp; English.

Claim 1; Fig 16; 1
                                                                                                                                                                                      DNA sequences encoding 1,3-fucosyl transferase - used to develop antiinflammatory therapy by inhibition of linking activity.

S Claim 1; Fig 1; 38pp: English.

C The clone was obtd. from CDX pCDM8 clone 7.2 and from a portion of the 7.2 insert subcloned into the sequencing vector pNN11 to prepare pS0219. The sequence encodes protein 7.2, a 1,3-fucosyl transferase a surface glycoprotein which is recognised by anti-CDX antibodies and which binds to ELAM1. The portion of the sequence from nucleotide 9-2162 is identical to the portion of clone 1 (Q14383) from nucleotide 492-2645. The two inserts may represent different transcripts from the same DNA segment. The protein may be useful in the development of anti-inflammatory or other therapies.

See also Q14383.

Sequence 2175 BP; 403 A; 647 C; 648 G; 477 T;
Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 10; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local :
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Goelz SE, Hession CA;
WPI; 91-353507/48.
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08-JAN-1991; U00145
08-JAN-1990; US-462.
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Clone 7.2 encoding 1.3-fucosyl
CDX; cell adhesion; ELAM1; ss.
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27-APR-1990; WO-U02357.
26-OCT-1990; WO-U06198.
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10; Conservative
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Pred. No. 3.3
0; Mismatches
Score 10; DB 1;
Pred. No. 3.2e+02;
); Mismatches 0;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                N50275; standard; DNA; 1530 BP. N50275; N50275; (first entry) 30-NOV-1991 (first entry)
  EP-139216-A.
02-MAY-1985.
14-SEP-1984;
16-SEP-1983;
(KYOW) KYOWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The clone was obtd. from CDX pCDM8 clone 1. The sequence encodes protein 1, a 1,3-fucosyl transferase a surface glycoprotein which is recognised by anti-CDX antibodies and which binds to ELAM1. The portion of the sequence from nucleotide 492-2645 is identical to the portion of clone 7.2 (014382) from nucleotide 9-2162. The two inserts may represent different transcripts from the same DNA segment. The protein may be useful in the development of anti-inflammatory or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The clone was a factory.
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Q14383;
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                                                                                                                                                                                                                                                                                                                                                                           Sequence from pATK105 contg. the p24 coding regional gene and 5 LTR.
Antiqen: diagnosis; assay; blood transfusion; so adult T-cell leukaemia virus (ATLV).
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Goelz SE, Hession CA;
WPI; 91-353507/48.
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Clone 1 encoding 1.3-fucosyl transferase.
CDX; cell adhesion; ELAM1; ss.
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Sequence 2861
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26-OCT-1990; U06198.
27-APR-1990; WO-U02357.
26-OCT-1990; WO-U06198.
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Key
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; JP-170908.
A НАККО КОСУО КК.
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Example; Table I, Page 15-16; 37pp; Eng
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Best Local Similarity
Matches 10; Conserv
EP-113078-A.
11-JUL-1984.
06-DEC-1983; 112261.
07-DEC-1982; JP-214287.
(NICA-) JAPAN FOUND FOR CAN.
(GANK-) GAN KENKYUKAI ZH.
(JURI-) JURIDICAL FOUND.
                                                                                                                                                                                                                                                                                      misc_feature
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76. .7609
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PI Yoshida M, Sugano H;

DR WFI; 84-172336/28.

PT Viral genomic DNA complementary to RNA of human leukaemia virus -

PT useful in recombinant DNA producing therapeutic and diagnostic

PT useful in recombinant DNA producing therapeutic and diagnostic

PT proteins

CC Diagnosis of human leukaemia and/or lymphoma and virus infection is

CC made with part or all of the recombinant DNA. Virus antigenic

CC proteins can be produced. These peptides and proteins, and

CC prevention of human leukaemia.

SQ Sequence 9047 BP; 2087 A; 3164 C; 1713 G; 2083 T;

Query Match

Best Local Similarity 100.0%; Score 10; DB 1; Length 9047;

Best Local Similarity 100.0%; Score 10; DB 1; Length 9047;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps

1 CCCTATGGAG 10

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2079 CCCTATGGAG 2070

Search completed: September 18, 1999, 00:33:35

Job time: 18975 sec
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Title: Perfect score: Sequence:

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Description

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nucleic search, using sw model
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1 CCCTATGGAG 10
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D19706 257 bp mRNA EST 30-JUL-1996 HUNMGS00662 Human promyelocyte Homo sapiens cDNA clone mm08f12 3', mRNA sequence. D19706 9500022 D19706.1 GI:500022
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em_est23: *
em_est24: *
em_est25: *
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7 464 Lambda-1 833 Lambda-1 83704423 Fe 2040 Lambda 209900s Tes 2040 Lambda 209900s Tes 2040 Lambda 205782429 Hu 255782429 Hu 255782429 Hu 255734096 Hu 255749297 Hu 25574107 Hu 25574107 Ve 245754107 Ve 245754107 Ve 245754107 Ve 25574121 Nu 255

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Okubo,K., Fukushima,A., Yoshil,J., Niiyama,T., Kojima,Y., Yoshinari,H., Arimoto,J. and Matsubara,K.
Institute for Molecular and Cellular Biology
Osaka University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Okubo,K., Fukushima,A., Yoshii,J., Nilyama,T., Kojima,Y., Yoshinari,H., Arimoto,J. and Matsubara,K. Gene expression of human promyelocytic cell line HL60 before and after induction of differentiation. A new application of 3'directed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 257)
                                                                                                                                                                            Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411,
Tel: 0559-75-0771
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                                                                                                                                                                                                                                                  Contact: Yuji Kohara
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Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 360)
Kohara, Y., Mitsuki, H., Nishigaki, A., Motohashi, T.,
                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                        ykohara@ddbj.nig.ac.j.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="mm08f12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Human promyelocyte"
/note="Female, adult, cell_line =
promyelocyte."
/clone_lib="Yuji Kohara unpublished cDNA"
/note="dev_stage=varied, sex=Hermaphrodite male,
                                 /organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
/clone="yk26h5"
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RICS1711A Rice shoot Oryza sativa cDNA,
D39999
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D39999,1
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
Oryza sativa.
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    National Institute of Yata 1111, Mishima, Sh Tel: 0559-75-0771 Fax: 0559-75-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Toward an expression map of the C.elegans genome Unpublished (1994)
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Location/Qualifiers
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a 66 c 83 g 103
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/note="dev_stage=varied, sex=Hermaphrodite male,
tissue_type=whole animal;
78 c 81 g 102 t 7 others
                                                                                                                                                                                                                                                                                                                                                           /organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="rtaxon:6239"
/clone="yk27f7"
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HSC05H042 normalized infant brain cDNA Homo sapiens cDNA
c-05h04 3', mRNA sequence
                                                                                                                 Genexpress-Genethon
Genethon Centre de recherche sur le Genome
1, rue de l'Internationale, BP60 91002 EVRY
                                                                                                                                                                                                                                                                  Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B., Devignes, M.D., Mitchell, H., Mariage-Samson, R., Pietu, G., Poullot, Y., Sebastiani-Kabaktchis, C. and Tessier, A. Sebastiani-Kabaktchis, C. and Tessier, A.
                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 18)
Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  National Institute of Agrobiological Resources Rice Genome Research Program
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            Single read. removed at sequence 5'end Genexpress_library_idt: C; Genexpress_sequence_idt: Seq primer: (-21)M13_universal.
                                                                                   Tel: 33169472800
Fax: 33160778698
                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Takuji Sasaki
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                                                            Email: genexpress@genethon.fr
                                                                                                                                                                      Contact: Genethon
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0298-38-7468
1: tsasaki@abr.affrc.go.jp.
Location/Qualifiers
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/note="Etiolated shoot (8 days
61 c 62 g 79 t
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/strain="Nipponbare, sub_species
/db_xref="taxon:4530"
Location/Qualifiers
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                                                                                                                                                                                                                                     Sci. Vie 318 (2), 263-272 (1995)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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5 others
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IS CDNA clone
                               alc-05h04
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                                                                                                                                                                      FEATURES
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SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 312)

Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B., Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y., Sebastiani-Kabaktchis, C. and Tessier, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F03038 312 bp mRNA EST 02-FEB-1995 HSC1KD092 normalized infant brain cDNA Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genethon Centre de recherche sur
1, rue de l'Internationale, BP60 9
Tel: 33169472800
Fax: 33160778698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genexpress-Genethon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Genethon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F03038.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single read. removed at sequence 5'end
Genexpress_library_idt: C; Genexpress_sequence_idt: alc-lkd09
Seq primer: (-21)Mi3_universal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genexpress@genethon.fr
Single read. removed at sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        its expression
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1 48 c 30 g 47 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lafmid BA vector. Clone library from B.Soares, Dept. Columbia University, USA. Normalization_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Site_2: NotI; sex=Female; dev_stage=3 months old; Isolate=muscular atrophy pattent; tissue_type=total brain; total mRNA was oligo-(dI) primed and directions cloned 5' -> 3' into the HindII -> NotI sites of the cloned 5' -> 3' into the HindIII -> NotI sites of the cloned 5' -> 3' into the HindIII -> NotI sites of the cloned 5' -> 3' into the HindIII -> NotI sites of the cloned 5' -> 3' into the HindIII -> NotI sites of the cloned 5' -> 3' into the HindIII -> NotI sites of the cloned 5' -> 3' into the HindIII -> NotI sites of the cloned 5' -> 3' into the HindIII -> NotI sites of the cloned 5' -> 3' into the HindIII -> NotI sites of the cloned 5' -> 3' into the HindIII -> NotI sites of the cloned 5' -> 3' into the HindIII -> NotI sites of the cloned 5' -> 3' into the HindIII -> NotI sites of the cloned 5' -> 3' into the HindIII -> NotI sites of the cloned 5' -> 3' into the HindIII -> NotI sites of the cloned 5' -> 3' into the HindIII -> NotI sites of the cloned 5' -> 3' into the HindIII -> NotI sites of the cloned 5' -> 3' into the HindIII -> NotI sites of the cloned 5' -> 3' into the HindIII -> NotI sites of the cloned 5' -> 3' into the HindIII -> NotI sites of the cloned 5' -> 3' into the HindIII -> NotI sites of the cloned 5' -> 3' into the HindIII -> NotI sites of the cloned 5' -> 3' into the HindIII -> NotI sites of the cloned 5' -> 3' into the HindIII -> NotI sites of the cloned 5' -> 3' into the HindIII -> NotI sites of the cloned 5' -> 3' into the HindIII -> NotI sites of the cloned 5' -> 3' into the cloned 5' -> 3'
/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female; dev_stage=3 months old;
                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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/dev_stage="3 months old"
/note="organ: brain; Vector: lafmid BA; Site_1: HindIII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo_sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                    /sex="Female"
                                                                                                                                                                                                                                                                   /clone="c-1kd09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
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                                                                                                                                   'tissue_type="total brain"
                                                                                                                                                                                                                           clone.
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Pred. No. 1.8e+03;
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91002 EVRY
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AUTHORS
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Best Local S
Matches 10
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Best Local S
Matches 10
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                                                         CCCTATGGAG 248
                                                                                        CCCTATGGAG 10
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                                                                                                                        l Similarity
10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 349)

Adams, M.D., Dubnick, M., Kerlavage, A.R., Moreno, R., Kelley, J.M., Utterback, T.R., Nagle, J.W., Fields, C. and Venter, J.C., Sequence identification of 2,375 human brain genes
Nature 355, 632-634 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            The Institute for Genomic Research
9712 Medical Center Drive, Rockvil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M85318 349 bp
EST01434 Fetal brain,
clone HFBBA18 similar
M85318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Kerlavage,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M85318.1
                                                                                                                                                                                                                                                                                                                                                                                                               Email: arkerlav@tigr.org
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                                                                                                                                                                                                          /clone_lib="Fetal brain, Stratagene (cat#936206)"
/note="Vector: LambdaZAP-II; 17-18 wk gestation, female;
oligo-dT+ random primed cDNA synthesis; lambdaZAP-II
vector, 1.0kb average inser size."
1 96 c 73 g 101 t 7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isolate-muscular atrophy patient; tissue_type-total brain; total mrNA was oligo (dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA vector. Clone library from B.Soares, Psychiatry Dept. Columbia University, USA. Normalization_method: Bento Soares, P.N.A.S in press"

Bento Soares, P.N.A.S in press"

72 c 55 g 90 t 4 others
                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="ATCC (inhost):77543"
/db_xref="ROB:D0S11E"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                      clone="HFBBA18"
                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                    100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST Stratagene (cat#936206) to Alu repetitive ~ --
                                                                                                                                    Score 10;
Pred. No.
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Pred. No.
                                                                                                                     Mismatches
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Best Local
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                                                                                                                                           Hum. Mol
93372851
                                                                                                                                                                                                                                                                                                                                                      g315075
T03839.1
                               Contact: Hutchinson GB
Dept. of Medical Genetics, University of British Columbia
Canadian Genetic Diseases Network
Rm. 416, 2125 East Mall, Vancouver, B.C. V6T 124
Tel: (604)822-9240
                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 667)

Rommens, J.M., Lin, B., Hutchinson, G.B., Andrew, S.E., Goldberg, Y.P., Glaves, M.L., Graham, R., Lai, V., McArthur, J., Nasir, J. et al.

A transcription map of the region containing the Huntington disease
                                                                                                                                                                                                                                                                                                                                                                                      703839 EST 14-J
GT0024 GeneTrack, 4p16.3 JM Rommens Homo sapiens cDNA
similar to Some L1 sequence similarity, mRNA sequence.
T03839
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Email: hutch@ulam.generes.ca
                                                                                                                                                                                                                                                                                                   Homo sapiens
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Secerne, Rhabditina; Rhabditoidea; Rhabditidae, 1 (bases 1 to 335)

McCombie,W.R., Kelley,J.M., Aubin,L., FitzGerald,M.G., Wu,A., Adams,M.D., D. Venter,J.C. and Flelds,C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: arkerlav@tigr.org
Seg primer: M13 Foward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans
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T01239.1 GI:277720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
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/db_xref-"taxon:6239"
/clone-"CEES044"
/clone_11b-"Early embryo, Stratage
67 c 64 g 85 t 3
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Pred. No. 2e+03;
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t 3 others
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Matches 10; Conserv
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EUtheria; Primates; Catarrulu, ....
1 (bases 1 to 422)
1 (bases 1 to 422)
Rommens, J.M., Lin, B., Hutchinson, G.B., Andrew, S.E., Goldberg, Y.P., Rommens, J.M., Graham, R., Lai, Y., McArthur, J., Nasir, J. et al. Glaves, M.L., Graham, R., Lai, Y., McArthur, J., the Huntington disease
                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Hutchinson GB
Dept. of Medical Genetics, University of British Columbia
Canadian Genetic Diseases Network
Rm. 416, 2125 East Mall, Vancouver, B.C. V6T 124
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T03843.1 GI:315082
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14, 1993 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                             hutch@ulam.generes.ca
Location/Qualifiers
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       /clone_lib="geneTrack, 4p16.3 JM Rommens"
/clone_lib="GeneTrack, 4p16.3 JM Rommens"
/note="cDNA from frontal cortex RNA and from a pool
prepared from fetal brain, frontal cortex, bone marrow and
liver RNA. The cDNAs were hybridized to immobilized
isolated yeast artificial chromosomes from the 4p16.3
region. Following washing at high stringency, cDNA
segments that had specifically hybridized were eluced,
amplified by PCR and cloned. Clones were mapped back to
the YACS. Inserts were sequenced using both standard (T3
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/clone="gt24"
                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="gt131"
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/note="cDNA from frontal cortex RNA and from a pool
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T7) and custom primers.
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Pred. No. 2.3e+03;
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                                                                                                       162 CCCTATGGAG 153
                                                                                                                                       1 CCCTATGGAG 10
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TO4417 400 bp mRNA ES 464 Lambda-PRL2 Arabidopsis thaliana cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hum. Mol. Genet. 2, 93372851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 236)
Rommens, J.M., Lin, B., Hutchinson, G.B., Andrew, S.E., Goldberg, Y.P., Glaves, M.L., Graham, R., Lai, V., McArthur, J., Nasir, J. et al. A transcription map of the region containing the Huntington disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Hutchinson GB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                          Similarity
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ilarity 100.0%;
Conservative
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                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
                                                                                                                                                                                                                                                                      /clone_lib="GeneTrack, 4p16.3 JM Rommens"
/note="cDNA from frontal cortex RNA and from a pool
prepared from fetal brain, frontal cortex, bone marrow and
liver RNA. The cDNAs were hybridized to immobilized
isolated yeast artificial chromosomes from the 4p16.3
region. Following washing at high stringency, cDNA
segments that had specifically hybridized were eluted,
amplified by PCR and cloned. Clones were mapped back to
the YACs. Inserts were sequenced using both standard (T3
and T7) and custom primers. " 7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hutch@ulam.generes.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GeneTrack, 4p16.3 JM Rommens Homo sapiens cDNA clone gt159y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="gt159y"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
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                                                                                                                                                                        Score 10; DB 20;
Pred. No. 1.9e+03;
); Mismatches 0;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 20;
ST 06-NOV-1997
clone 40E11T7, mRNA
                                                                                                                                                                                                        Length 236;
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g315945
T04785.1
                                                                                                                                                                                                                                                                                                                                   10;
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Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                 Arabidopsis thaliana
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T04417.1 GI:315577
                                                               thale cress.
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Michigan State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Thomas Newman
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                                                                                                                                                   sequence.
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                                                                                                                                                                                                                                                                                                                                                  Similarity
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primer: T7 dye primer
                                                                                                                                                                                                                                                                                                                                100.0%; ilarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                       .7-353-0854
                                                                                                   GI:315945
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/clone="40E11T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="var columbia"
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                                                                                                                                                          13 bp mRNA EST 06-NOV-1199
Arabidopsis thaliana cDNA clone 3DIT7P, mRNA
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                                                                                                                                                                                                                                                                                                                                               Score 10;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                              Length 400;
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Contact: Adams, MD
The Institute for Genomic Research
932 Clopper Road, Gaithersburg, MD 20878
                                                                                                                                                                                                                                                                                                                                                                                                            T06534 357 bp mRNA EST 30-JUN-1993 EST04423 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFBDU78 similar to Lymphocyte function associated antigen-3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Retzel, E. and Somerville, C. genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA plant Physiol. 106, 1241-1255 (1994)
                                                                                                                                                                                                                                                                                                                              T06534.1
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                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence
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                                                                                                                                                                                                                                                           Homo sapiens
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MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E.
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McIntosh, L., Ohlrogge, J., Raikhel, N.,
                                                                                                             Nature Genet.
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                         Adams, M.D., Kerlavage, A.R., Fields, C. and Venter, J.C.
                                                                                                                                                                                             Eutheria; Primates; l (bases 1 to 357)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                 from human brain
                                                                                                                                                     ,400 expressed sequence tags identify diversity of transcripts
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ilarity 100.0%;
Conservative (
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/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/Lambda PRL2 is a cDNA 11brary derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated eticlated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques. The vector is BRL's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
oligo dT primed cDNA.

" 5 others
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/db_xref="taxon:3702"
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                                                                                                          4, 256-267 (1993)
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Pred. No. 2.1e+03;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 413;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence.
T13875
                                                                                                                                                                                                                                                                                                                                                                                        Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 453)
Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H.,
McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M.,
Retzel,E. and Somerville,C.
Retzel,E. and Somerville,C.
Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
plant Physiol. 106, 1241-1255 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2040 Lambda-PRL2 Arabidopsis thaliana cDNA clone 42G2T7, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mdadams@tigr.org
Seq primer: M13-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                     Seq primer:
                                                                                                                                                                                                                                                                                                     Pax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thale cress.
                                                                                                                                                                                                                                                                                                                                                    ansing,Mi
el: 517-353-0854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
/clone_lib-"Lambda-PRL2" Site_1: Sal; Site_2: Not; /note="Vector: lambda 21p-Lox; Site_1: Sal; Site_2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Fetal brain, Stratagene (cat#936206)"
/note="Vector: LambdaZAP-II; 17-18 wk gestation, fema:
oligo-dr + random primed cDNA synthesis; lambdaZAP-II
vector, 1.0kb average inser size."
a 67 c 68 g 106 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="ATCC (inhost):83193"
/db_xref="taxon:9606"
/clone="HFBDU78"
                                                                                                                                                       /organism="Arabidopsis thaliana"
/strain="var columbia"
/db_xref="taxon:3702"
/clone="42G2T7"
                                                                                                                                                                                                                                                                Location/Qualifiers
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1. .357
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Pred. No. 2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA
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same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The CDNA inserts were directionally cloned with Sal-Not arms using oligo dI primed cDNA. "

115 a 83 c 115 g 130 t 10 others
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DASE COUNT 115 a 83 c 115 g 130 t 10 others origin

Query Match
Best Local Similarity 100.0%; Score 10; DB 20; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 1 CCCTATGGAG 10

Lililii 1

Db 205 CCCTATGGAG 196

0

Search completed: September 17, 1999, 21:28:03 Job time: 14267 sec

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Perfect score:
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                          Score
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gb_p12:*
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               Description
   X64174 A.azollae
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JOURNAL
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                            Anabaena azollae
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena
1 (bases 1 to 1799)
Nierzwicki-Bauer, S.A.
Direct Submission
Submitted (15-JAN-1992) S.A. Nierzwicki-Bauer, Rensselaer
Polytechnic Institute, Plant Science Group, Biology Depart
Bth Street, Troy, New York, 12180, USA
2 (bases 1 to 1709)
Gebhardt, J.S. and Nierzwicki-Bauer, S.A.
Characterization of psbA gene family expression in symbiot
                                                                                                                                                      X64174.1 GI:38650
Dl protein; P680-apoprotein; photosystem II
photosystem II reaction centre; psbA gene.
Anabaena azollae.
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A.azollae psbA gene
X64174
           Unpublished
                     Anabaena azollae
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X68595 A.pleuropne
U14553 Anabaena sp
D10848 Alkalophili
D17312 Bacillus ce
D14037 Bacillus ce
D14037 Bacillus ce
D84432 Bacillus su
M77505 Bacillus su
M750832 B.lichenifo
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AB001781 Chlamydia
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AB001786 Chlamydia
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AB001818 Chlamydia
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AP000001 Pyrococcu
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                                                                                                                                     Anabaena
                                                                                                                                                                                protein;
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                                symbiotic
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16 Bacillus su
90 B.sphaericu
                                                                           Department,
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Result No.

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RESULT 2
AB001778/c
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Chlamydia psittaci
AB001778
                                                                                                                                                                                                                    Direct Submission
Submitted (10-MAR-1997) to the DDBJ/EMBL/GenBank databases.
Tatsufumi Takahashi, School of Veterinary Medicine, Rakuno Gakuen
Univ. Epizootiology; 582 Bunkyodai-Midorimachi, Ebetsu, Hokkaido
069, Japan (Tel:011-386-1112(ex.4233), Fax:011-387-5890)
2 (bases 1 to 1507)
                                                                                                                                                                                                                                                                                                                                                     Bacteria;
                                                                                                                                                                                                                                                                                                                                                                    Chlamydia psittaci (strain:6BC, Chlamydia psittaci
                                                                                                                                                                                                                                                                                                                                                                                                    AB001778.1 GI:1902841
16S ribosomal RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                       Takahashi,T
                                                                                                                                                                         Phylogenetic analyses of Chlamydia
                                                                                                                                                                                                       akahashi, T., Masuda, M., Tsuruno, T., Mori, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 100
LO; Conservative
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YPIGGGSESDGMPLGISGTENEMIVEQAEHNILMHPEHHLGVAAVFGGSLFSAMEGSL
VTSSLVRETTETESQNYGYKFGQEEETYNIVAAHGYFGRLIFQYASFNNSRSLHFFLA
AWPULGIWETALGVSTMAFELMGENEQSIIDSQGRVIGTWADVINRANLGMEVMHER
NAHNFPLDLAAGDVAPVALTAPPING"

376 c 324 g 538 t
                                                                                                           Location/Qualifiers
1. .1507
             /product="16S rRNA"
312 c 441 g
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|ACFVIAFIAAPPVDIDGIREPVAGSLLYGNNIISGAVVPSSNAIGLHFYPIWEAASL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="var. caroliniana"
/db_xref="taxon:1164"
                                                            /db_xref="taxon:812"
                                                                           /strain="6BC, ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="D1 protein"
/protein_id="CAA45515.1"
/db_xref="PID:g38651"
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/note="P680-apoprotein of
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Chlamydia psittaci gene
AB001779
                                                                                      AB001780.1 GI:1902843
16S ribosomal RNA.
Chlamydia psittaci (isolate:Bud-11F from a budgerigar) DNA.
Chlamydia psittaci
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
1 (bases 1 to 1507)
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Chlamydia psittaci
AB001780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (10-MAR-1997) to the DDBJ/EMBL/GenBank databases. Tatsufumi Takahashi, School of Veterinary Medicine, Rakuno Gakuen Univ., Epizootiology; 582 Bunkyodai-Midorimachi, Ebetsu, Hokkaido 069, Japan (Tel:011-386-1112(ex.4233), Fax:011-387-5890) 2 (bases 1 to 1507) Takahashi, T., Masuda, M., Tsuruno, T., Mori, Y., Takashima, I. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydia psittaci (strain:Bud-1) DNA.
Chlamydia psittaci
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
1 (bases 1 to 1907)
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10; Conser
Submitted (10-MAR-1997) to the DDBJ/EMBL/GenBank databases. Tatsufumi Takahashi, School of Veterinary Medicine, Rakuno Gakuen Univ., Epizootiology; 528 Bunkydai-Midorimachi, Ebetsu, Hokkaido 069, Japan (Tel:011-386-1112(ex.4233), Fax:011-387-5890)
                                                                                                                                                                                                                                                                                                                                                        l Similarity
10; Conserv
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16S ribosomal
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                                                            Direct Submission
                                                                        ľakahashi, T
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nilarity 100.0%;
Conservative 0
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312 c 442 g
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/strain="Bud-1"
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Pred. No. le+04;
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                                                                                                                                                                                                           rRNA,
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le+04;
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budgerigar)

no Gakuen Hokkaido

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RESULT 6
AB001782/c
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ORIGIN
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AB001781/c
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                                                                              TATGTTTTAG 184
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Chlamydia psittaci gene
AB001781
                                                                                                                                                                                                                                                                                                                                                                                                      submitted (10-MAR-1997) to the DDBJ/EMBL/GenBank databases. Tatsufumi Takahashi, School of Veterinary Medicine, Rakuno Gakuen Univ., Epizootiology; 582 Bunkyodai-Midorimachi, Ebetsu, Hokkaido 069, Japan (Tel.011-386-1112(ex.4233), Fax:011-387-5890)

2 (bases 1 to 1507)

7 (bases 1 to 1507)
       AB001782
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
1 (bases 1 to 1507)
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                                                                                                                                                                                                                                                                                                                                                Unpublished
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Takahashi,T., Masuda,M.,
                                                                                                                                                                                                                                                                                                                                                                           Phylogenetic analyses of
                                                                                                                                                                                                                                                                                                                                                                                              Kikuchi, N
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                                                                                                                                                                                                                                                                   /organism="Chlamydia psittaci"
/isolate="Bud-16F from a budgerigar"
/db_xref="taxon:812"
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312 c 441 g
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1. .1507
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312 c 441 g
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/isolate="Bud-11F from a budge
       1507
                                                                                                                                                   100.0%;
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                                                                                                                                     Score 10; DB 1; Length 1507; Pred. No. 1e+04; ; Mismatches 0; Indels
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Pred. No.
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le+04;
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AB001783/c
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                                                                                                   Submitted (10-MAR-1997) to the DDBJ/EMBL/GenBank databases. Tatsufumi Takahashi, School of Veterinary Medicine, Rakuno Gakuen Univ., Epizoottology; 582 Bunkyddai-Midorimachi, Ebetsu, Hokkaido 069, Japan (Tel:011-386-1112(ex.4233), Fax:011-387-5890)
                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydophila abortus
                                                                                                                                                                                                      Unpublished (1997)
                                                                                                                                                                                                                                                                                  Bacteria; Chlamydiales;
1 (bases 1 to 1507)
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Chlamydia psittaci
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
                                                                                                                                                                 Direct Submission
                                                                                                                                                                               Takahashi,T.
                                                                                                                                                                                                                                      Phylogenetic analyses
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Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   069, Japan (Tel:011-386-1112(ex.4233), Fax:011-387-5890)
2 (bases 1 to 1507)
Takahashi,T., Masuda,M., Tsuruno,T., Mori,Y., Takashima,I. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydia psittaci gene
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ilarity 100.0%;
Conservative (
             /organism-"Chlamydophila abortus"
/specific_host-"Ovis arites"
/strain-"B577, ArCC VR-656"
/db_xref-"taxon:83555"
                                                                        Location/Qualifiers
1. .1507
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312 c 441 g
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/isolate="Bud-5695 from a budgu
/db_xref="taxon:812"
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Pred. No. 1e+04;
Mismatches
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Chlamydia
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psittaci"
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14-MAY-1999 strain B577.

from birds based on the

Length 1507;

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AUTHORS
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                                                                                                                            RESULT 9
AB001787/c
LOCUS
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ORIGIN
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AB001786/c
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Best Local S
Matches 10
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Matches 10; Conserv
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         Chlamydia psittaci
Bacteria; Chlamydiales;
1 (bases 1 to 1507)
Takahashi,T.
                                                                                                    AB001787 1507 bp
Chlamydia psittaci gene
AB001787
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (10-MAR-1997) to the DDBJ/EMBL/GenBank databases. Tatsufumi Takahashi, School of Veterinary Medicine, Rakuno Gakuen Univ., Epizootiology; 582 Bunkyodai-Midorimachi, Ebetsu, Hokkaido 069, Japan (Tel:011-386-1112(ex.4233), Fax:011-387-5890) 2 (bases 1 to 1507) Takahashi, T., Masuda, M., Tsuruno, T., Mori, Y., Takashima, I. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia psittaci
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia:
1 (bases 1 to 1507)
                                                     Chlamydia psittaci (strain:Itoh) DNA
                                                                    16S ribosomal RNA.
                                                                              AB001787.1 GI:1902850
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Chlamydia psittaci
AB001786
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ilarity 100.0%;
Conservative
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/strain="GCP-1"
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Pred. No. 1e+04;
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Pred. No.
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TATGTTTTAG
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                                                     10;
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                       Submitted (10-MAR-1997) to the DDBJ/EMBL/GenBank databases. Tatsufumi Takahashi, School of Veterinary Medicine, Rakuno Univ. Epizootiology: 582 Bunkyodal-Midorimachi Ebetsu. Ho 069, Japan (Tel:011-386-1112(ex.4233), Fax:011-387-5890)
                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydia psittaci (isolate:Izawa-1 from a budgerigar)
Chlamydia psittaci
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
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AB001788
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                                                                                                                                                                                                                                                                                                                                                                                Takahashi,T.
Direct Submission
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10; Conserv
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2 (bases 1 to 1507)
Takahashi,T., Masuda,M., Tsuruno,T., Mori,Y., Takashima,I.
                                                                                                                                                                                                                                                                                              2 (bases 1 to 1507)
Takahashi,T., Masuda,M., Tsuruno,T., Mori,Y.,
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                                                                                                                               /product="168 rRNA"
312 c 441 g
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/isolate="Izawa-1 from
/db_xref="taxon:812"
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l. .1507
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psittaci gene
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/strain="Itoh"
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AB001789/c
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                                                                                                                         submitted (10-MAR-1997) to the DDBJ/EMBL/GenBank databases: Tatsufumi Takahashi, School of Veterinary Medicine, Rakuno Gakuen Univ., Epizootiology; 582 Bunkyodai-Midorimachi, Ebetsu, Hokkaido 069, Japan (Tel:011-386-1112(ex.4233), Fax:011-387-5890)

2 (bases 1 to 1507)

Takahashi, T., Masuda, M., Tsuruno, T., Mori, Y., Takashima, I. and
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Chlamydia psittaci ge
AB001790
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                                                                  16S rDNA sequence Unpublished (1997)
                                                                                                                                                                                                                                 Direct Submission
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16S ribosomal RNA
                                                                                                  Phylogenetic analyses of
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2 (bases 1 to 1507)

Takahashi, T., Masuda, M., Tsuruno, T., Mori, Y., Takashima, I. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydia psittaci (strain:Koala) DNA.
Chlamydia psittaci
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
1 (bases 1 to 1507)
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Chlamydia psittaci
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16S ribosomal RNA.
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                                      Location/Qualifiers
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/organism="Chlamydia psittaci"
/isolate="Mizuno-1F from a budgerigar"
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/strain="Koala"
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Pred. No. 1e+04;
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for 16S rRNA,
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for 16S rRNA,
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                                                             AB001802 1507 bp Chlamydia psittaci gene f
AB001802 g1902865
AB001802.1 GI:1902865
AB001802.1 GI:1902865
Chlamydia psittaci (strain:PgAu46) DNA. Chlamydia psittaci Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia. 1 (bases 1 to 1507) Takahashi,T.
                                                                                                                                                                                                                                                l Similarity
10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (10-MAR-1997) to the DDBJ/EMBL/GenBank databases. Tatsufumi Takahashi, School of Veterinary Medicine, Rakuno (Univ. Epizootiology; 582 Bunkyodai-Midorimachi, Ebetsu, Ho) 069, Japan (Tel:011-386-1112(ex.4233), Fax:011-387-5890) 2 (bases 1 to 1507) Takahashi, T., Masuda, M., Tsuruno, T., Mori, Y., Takashima, I.,
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teria; Chlamydiales; Chlamydiaceae; Chlamydia.
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Submitted (10-MAR-1997) to the DDBJ/EMBL/GenBank databases.
Tatsufumi Takahashi, School of Veterinary Medicine, Rakuno Gakuen Univ., Epizootiology; 582 Bunkyodai-Midorimachi, Ebetsu, Hokkaido 069, Japan (Tel:01-386-1112(ex.4233), Fax:011-387-5890)
2 (bases 1 to 1507)
Takahashi,T., Masuda,M., Tsuruno,T., Mori,Y., Takashima,I. and
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
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21-NOV-1989.
16-MAY-1988; 119024.
16-MAY-1988; JP-119024.
TOA Nenryo Kogyo KK, Fu
WPI; 90-005177/01.
P-PSDB; R04024-30.
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 Glycine
Key
              05-JUN-1990 (first entry)
Enod2a genomic clone.
Enod2; soybean; root nodule; regulatory region; nodulin 75;
Glycine max (L) Merr. cv. Williams.
                                                                                                                                                                                                                                                                                                                                      DNA indicating complement to RNA gene of Human Immunodefictency Virus type 2 used for new vaccine or diagnostic for AIDS virus.

Claim 2; Fig.4; 12pp; Japanese.

cDNA to novel HIV-2 (GH-1) has been integrated into plasmid pDC HIV-2(GH-1). Useful for diagnosis and vaccination against the virus. Carries 7 overlapping genes in varrious reading frames, includding Gag, Pol and Env.

Sequence 9360 BP; 3211 A; 1944 C; 2317 G; 1888 T;
                                                                                  Q03098 standard; cDNA; 3060
Q03098;
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cDNA to HIV-2 RNA.
HIV; AIDS; Vaccine; pUC-HIV-2(GH-1).
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540. .9304
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30-JUN-1989; 306666.
01-JUL-1988; US-214297.
(LUBR) Lubrizol Genetics.
Franssen H, Bisseling AH;
WPI; 90-009296/02
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P-PSDB; R04116, R04117.

Enod2 gene regulatory region - used for early expression of structural gene in developing root nodule of soybean plant.

Disclosure; page il-13; 18pp; English.

The sequences contains the Enod2a gene regulatory region (tag a) which is used to construct a recombinant DNA molecule for the early expression of structural gene in soybean root nodules. Two open reading frames are present, ORF1 and ORF2 (R04116 and R04117 resp.) but it is thought that ORF1 actually encodes the protein, N-75.

Sequence 3060 BP; 1013 A; 731 C; 406 G; 910 T;
                                                                                                                                                                                                                                                                                                                                       Q03097 standard; cDNA; 3856
                                                                                                                                                                                                                                                                             05-JUN-1990 (first entry)
Enod2b genomic clone.
Enod2; soybean; root nodule;
                                                                                                                                                                                                                                        Glycine max (L) Merr. cv. Williams. 
Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1177
      EP-349338-A.
03-JAN-1990.
                                                                                    cds
                                                                                                                                                                                                                        misc_rna
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Conservative
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/*tag= i
1404
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/*tag= 7
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1490. .1494
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/*tag= a
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.750. .2469
                                                                                                    'note-"actual
                                                                                                                         label-ORF1
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                                                                                                                                                                                                                                                                               regulatory region; nodulin 75; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 10; DB 1; Length 3060; Pred. No. 1.1e+03; Indels
                                                                                                  coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coding sequence of Enod2 encoding N-75"
                                                                                                  sequence of
                                                                                                    Enod2
                                                                                                  encoding N-75"
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Best Local S
Matches 10
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(LUBR) Lubrizol Genetics.

Franssen H, Bisseling AH;

WPI; 90-009296/02.

P-PSDB; R04119.

Franssen H, Bisseling AH;

P-PSDB; R04119.

Foldlie, R04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-OCT-1989 (first entry)
DNA of human retinoblastoma gene exons with flanking regions.
Human; retinoblastoma gene; flanking regions; cDNA;
screening; tumours; probes; exons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1981 TATGTTTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      screening; to
Homo sapiens
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01-JUL-1988; US-214297
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                                                                                                                                       exon 14
exon 15
exon 16
                                                                                                                                                                                                                   intron
exon 13
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exon 17
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  (2.8 kb)
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8680..8736
9140..9171
9252..9328
9629/9630
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5734/5735
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5248/5249
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6381/6382
                                                               30/9. .10075
10322/10323
10564
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3549/3550
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2550
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7061/7062
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                              10564. .10682
10911/10912
11335 11370
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996. .8112
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. 1.1e+03;
ches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PT - used for screening individuals for defective retino-blastoma
PT gene and treating these patients.

S Disclosure; fig 6; 71 pp; English.

C DNA encoding human retinoblastoma (RB) gene exons and flanking regions
C The CDNA (see P90599 and N90490) can be used to screen individuals
C for the presence of the mutated RB gene. The RB polypeptide
C can prevent retinoblastoma formation, and corresp. antibodies
C can be used in tumour immunodiagnosis. Refer to patent for more
S sequence analysis.details.
S sequence 18177 BP; 5765 A; 2997 C; 3177 C.
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Best Loc
Matches
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27-JUL-1989; U00293.
23-JAN-1988; US-16525.
(LDRYJ) Dryja T P.
Dryja T P; Friend S; Yandell D
WPI; 89-233856/32.
P-PSDB; P90599.
                                                                                                                                     EP-310136-A.
05-APR-1989.
03-OCT-1988; 116329.
02-SEP-1988; US-238937, t
(UYRO-) Rockefeller Univ-
Cerami A, Beutler B, Wolf
WPI; 89-101477/14.
                  New cytokine which induces inflammation obtd. by purificn of mediator substance stimulated macrophage cells Figure 15; 46pp; English.

Cytokine MIP-1 is composed of two components.
                                                                                                                                                                                                                                                                                                                                                               Mouse
Key
                                                                                                                        P-PSDB; P93591.
                                                                                                                                                                                                                                                                                                     mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                  inflammatory cytokine Inflammatory cytokine; MIP-1 beta component; mouse macrophage cell line RAW 264.7.
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Total cDNA from clone for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N90728
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    MIP-1 alpha
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132. .341
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composed of as initially
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Pred. No. 9.8
); Mismatches
  two components, MIP-lalpha and MIP-lbeta recovered from murine cells (mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIP-1 beta component
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14641/14642
14834...14977
15488...15538
15952/15953
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13411. .13574
13883/13884
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13204
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12278/12279
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. 9.8e+02;
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                                                                            supernatant
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Best Local S
Matches 10
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R 04-APR-1988; US-17562.

R (RESE) Research Corporation Technologies Inc.

R Shaw GM, Hahn BH, Kong LI, Lee SW;

R WPI; 89-324223/44.

T Novel virus of the HIV-2 family + used in the prodn. of diag reagents, vaccines and therapies for AIDS and AIDS-related d Claim 37; page 47-53; 66pp; English.

C This is used as a source of recombinant viral components in development of diagnostic assays for HIV-2 viruses.

Q Sequence 9822 BP; 3359 A; 2023 C; 2441 G; 1999 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
(MICR-) Microprobe Corp.

Schwartz DE, Adams TH;

WPI; 89-11406/15.

Hybridisation test for human papilloma virus in cell smears -
by reaction with long labelled probe specific for particular
virus types, esp. for examining cervical smears
Disclosure; ; 39pp; English.

The patent is for a rapid in situ hybridisation assay for detecting and
typing human papilloma virus (HPV) in non-frozen cellular smears fixed t
a support in absence of aldehyde-based crosslinking reagents. The assay
                                                                                                                                                                                                                                   06-APR-1989.
30-SEP-1988; U03367.
02-OCT-1987; US-103979.
                                                                                                                                                                                                                                                                                                           Human papilloma
WO8902934-A.
                                                                                                                                                                                                                                                                                                                                                                                                      Partial nucleotide type 33 (HPV-33)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      macrophage cell line RAW 264.7). Inflammatory cytokine may identify idiopathic or invasive stimuli or determining the stimulated, spontaneous or idiopathic pathological states i induces fever in rabbits and superoxide formation in vitro neutrophils.

Sequence 653 BP; 139 A; 174 C; 141 G; 199 T;
                                                                                                                                                                                                                                                                                                                                                         Human papilloma cellular smear;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N91602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-MAR-1990 (first
Entire HIV-2/ST prov
                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-OCT-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibodies
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10; Conserv
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10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                              virus; type 33; in cervical carcinoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                          human
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AIDS-related
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ced diseases
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Matches 10
               N82025;
22-OCT-1990 (first entry)
Fragment containing rat lipocortin
recombinant rat lipocortin; rat abo
                                                                                                                                                                                                                                                      Tuber-specific expression cassette - for prodn. of transgenic potato plants.

Disclosure; p; German.

1.527 kb Drai/Drai fragment of the patatin B33 promoter (+14 to -151 was inserted into plasmid pBI 101, next to the coding region of beta-glucuronidase and a poly-A containing nopaline-synthase termina The resultant expression cassette pBI 101 B33 was transferred to an agrobacterium (LBA 4404) which was used to infect potato leaves. sequence 1975 BP; 690 A; 265 C; 310 G; 710 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprises: (1) combining nucleic acid in the sample with at least one detectable probe able to hybridise with 1 or more HPV types; and (2) detecting presence or absence of hybrid complexes. Opt. several probes are used, eg one for HPV types 6 and 11, associated with benign warts, and one for types 16, 18, 31, 33 and 35, associated with cervical cancer. The assay can differentiate between HPV types. It is esp. used as a secondary test. The probes can be synthesised or cloned. Sequence 774 BP; 270 A; 132 C; 163 G; 209 T;
                                                                                                                                                                                                                                                                                                                                                                         18-DEC-1989; 250117.
21-DEC-1988; DE-843527.
(GENB-) INST GENBIOL FORSCH.
ROCHA-SOSA M, SONNEWALD U, Frommer WB, Willmitzer
WPI; 90-195269/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-Nov-1990 (first entry)
DraI/DraI fragment of the patatin gene B33 promoter.
Expression cassette; transgenic potato plant; patatituber; specific regulatory region; plasmid pBI 101; b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nopaline; termina
Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q05057 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            603 TATGITTIAG 612
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                                                                                                                                                                     TATGTTTTAG 10
                                                                               standard;
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      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label=DraI/DraI_promoter_fragment
/note="from patatin gene B33"
1738 .1740
                                                                               DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
177. .1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function-translation start
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                                                                               1355
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Pred. No. 1.1
); Mismatches
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Pred. No.
                             abominal
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1.1e+03;
0;
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                             dropsy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ant; patatin gene B33;
pBI 101; beta-glucuronidase;
                                                                                                                                                                                                                     Length 1975;
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Matches 10
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See also
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                           Human
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence of LAV-II ROD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               claimed. mRNA was isolated from rat abdominal dropsy cells and synthesised from it. Probes were synthesised according to the partial amino acid sequence of rat lipocortin (see N82038 and N82039). These were used to isolate plasmids conty the desired sequence of lipocortin DNA.

See also P82063
                                                                                                                                                                                                                                                                                                                                                                                                                                                               N80859;
15-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N80859 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1203 TATGTTTTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant rat lipocortin obtd using gene derived fro Disclosure; ; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 88-365616/51.
P-PSDB; P82062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-NOV-1988.
08-MAY-1987; JP-112145.
08-MAY-1987; J6-JP-11214
(YAMA) Yamanouchi Pharm
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10; Conservative
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J6-JP-112145.
                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
entire HIV-2 ROD
/note-"p81781'
8529. .9299
/*tag- k
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                                               note-"p81780"
3242. .8508
                                                                                     /note="p81779"
3220. 8372
                                                                                                                                      /*tag= g
/note="p81778"
                                                                                                                                                                                                                                       note="p81775"
654. .5968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA; 9643
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                                                                                                                                                                                                                                                                                                                   note="p81773"
841. .5485
                                                                                                                                                                                                                                                                                                                                                       ote="p80801"
128. .4908
                                                                                                                                                                                                  ote="p81776"
.7. .6113
                                                                                                                                                                             te="p81777"
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6. .5654
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Pred. No.
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Length 1355;

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CDNA

dropsy

Key

N82025

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RESULT 11

N80435/c

ID N80435;

AC N80435;

DT 16-DEC-1990 (first entromath)

DE Entire sequence of LAV El

KW HIV; HTLV II; AIDS; diax

OS Lymphadenopathy associaty

FH Key 1.08

FT misc_feature 1.08

FT misc_feature 99.182

FT misc_feature 99.182

FT misc_feature 99.182

FT misc_feature 1.182
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Best Local S
Matches 10
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15-APR-1987; FR-005398,
(INSP) Inst Pasteur(ALIZ/).
Alizon M, Montagnier L, Guett
Tiollais P, Chakrabarti L, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; P80801, p81773, p81774, p81775, p81776, p81777, p81778, p81779, p81780, p81781, p81782.

New peptide(s) with immunological properties of HIV-2 envelope protein having the structure of similar immune deficiency virus proteins, useful in diagnosis and of vaccine components

Disclosure; Fig 1A; 86pp; French.

The SQ in n80859 was deposited on 21/2/86 at the CNCM under number I-522, reference name LAV-II ROD. It is the cDNA to HIV-2 ROD genomic RNA. SQ was compared with the SQ of the genome of SIV (Mac) (n80860) to identify
                      cds
                                                       cds
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                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                            Entire sequence of LAV EL I HIV; HTLV III; AIDS; diagnosis; vaccine; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TATGTTTTAG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATGTTTTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9643 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
llarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                 /*tag- b
/label-U5
8683. .9138
/*tag- c
                                                                                                                                                                                                                                                                                                                            /label-R
99. .182
                                                                                                                                                                                                                                                                                                                                                                                     associated
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                                                                                                                                                                                                                                     9139. .9236
/*tag= d
/label=R
                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                  label=ENV, P81858
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                                                                                                                                                                                                                                                                                                                                                    /*tag= a
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label=F, P81859
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label-POL,
5222
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                                                                                                   abel≖R, P81856
                                                                                                                                                                                                                          .1835
                                                      . 8388
                                                                                                                        .5452
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                                                                                                                           g
-0, P81855
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                                                                  P81857
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                                                                                                                                                                                                      P80884
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2399 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>;</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                              hybridisation;
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CC LAV ELI (n80436) and LAV MA L (n80437) were isolated from the peripheral blood lymphocytes of patients. The different AIDS virus isolates of the DNA sequences can be used for detection of the new LAV viruses or CC related viruses or DNA proviruses in eg biological samples. The proteins of repetides can be used for detection of antibodies induced in vivo and CC present in biological fluids. The DNA can also be used for the expression of LAV virus antigens for the produ. of antibodies for the CC detection of proteins related to the LAV viruses, partic. for diagnosis of AIDS or pre-AIDS.

Sequence 9236 BP; 3360 A; 1642 C; 2190 G; 2044 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                       New HIV-2 retrovirus causing AIDS and antibodies and complementary nucleic ac Claim 5; Page 29-30; 67pp; French. HIV-2 has RNA, esp. the gag and env reg 70% homologous or even 90%, correspondi regions of HIV-2 ROD.
GAGRODN includes coding regions for pl6 p26:nucleotides 406-1155;
pl2:nucleotides 406-1156;
pl1:nucleotides 406-1566.
HIV-2 retrovirus is infectious for huma
    See also N82199 for t
R and U3 regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-JUN-1986; EP-40138
(INSP) Inst Pasteur.
Alizon M, Sonigo P, W
WPI; 88-014396/02.
                                      morphological and immunological properties of the strains CNCM I-50 -532, -642 and -643. HIV-2 causes AIDS and is distinct from HIV-1. The sequence can be used diagnostically (in hybridisation tests).
                                                                                                                                                                                                                                                          Sonigo P, Brun-Vezinet WPI; 88-149264/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO8707906-A.
30-DEC-1987.
22-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                     05-DEC-1990 (first entry)
GAGRODN sequence from HIV-2 ROD corresp. to the HIV-2 gag gene.
Human immunodeficiency virus-2; HIV-2; AIDS; HIV-2 ROD; gag gen
env gene; GAGRODN; p16; p26; p12; ss.
                                                                                                                                                                                                                                               P-PSDB; P82676
                                                                                                                                                                                                                                                                                                          (INSP) Inst Pasteur.
                                                                                                                                                                                                                                                                                                                        21-NOV-1986;
22-JAN-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N82198 standard;
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                                                                      retrovirus is infectious for human T4 lymphocytes and has the ological and immunological properties of the strains CNCM I-502.
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10; Conser
regions.
1566 BP;
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ilarity 100.
Conservative
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EP-400151.
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                              the ENVRN
536
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Rey M, R
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Pred. No. 1e+03;
; Mismatches (
                            sequence
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338
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                            and N82200
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420
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o the gag a
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RESULT
IN 10887,
ID N.
AC N.
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1 TATGTTTTAG 10 ||||||||| | TATGTTTTAG 91

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standard; DNA;

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Best Local Similarity 100. Matches 10; Conservative
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The sequence encodes the gag protein of a new HIV-2 virus genome is infectious for human T4-lymphocytes. Abs and probes may be raised, useful in HIV-2 vaccination and diagnosis respectively. See also N70886, N70886, N70888-89, P70550-53.

Sequence 1566 BP; 536 A; 336 C; 420 G; 272 T;
                                                                                                                                                                                                                                        Q10947 standard; DNA; 4355
Q10947;
24-MAY-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Montagnier L, Chamaret S, Sonigop, Burnvezine F; WPI; 87-221261/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIV virus gag sequence.
Immunodeficiency virus; HIV-2;
                                                                                                                                                                               -1991 (first entry)
Coronavirus E2 gene.
Coronavirus; BCV; E2; E3; vaccine;
coronavirus - Quebec isolate.
                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
ilarity 100.0%;
Conservative
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                                                                            /product= E2
7. .13
/**-
                                    /*tag= b
/note= "conserved intergenic region"
14. .64
                                                                                                                                                              location/Qualifiers
 .4027
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Pred. No. 1.1e+03;
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ches 0;
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Fig. 1.MAY-1990; US-359293.

R (GENE-) GENE-TRAK SYST.

A (GENE-) GENE-TRAK SYST.

A (GENE-) GENE-TRAK SYST.

BAB J, Buharin A, Williams C, Mahan D, Lane DJ, King W; WPI; 91-007228/01.

R WPI; 91-007228/01.

R WPI; 91-007228/01.

R Nucleic acid probes - specific for r-RNA or r-DNA of Chlamydia PT trachomatis, useful in hybridisation assay for detection of e.g. PT trachomatis, useful in hybridisation assay for detection of e.g. PT sexual transmitted diseases.

PS Claim 3; Page 32; 35pp; English.

CC The probe is one of nine 16S rRNA-targeted probes which are specific to Chlamydia trachomatis bacteria. It may be used in a variety of cassay systems to detect e.g. respiratory, ocular or sexually creamitted diseases. See also Q10092 and Q10094-Q10110.

SQ Sequence 35 BP; 12 A; 7 C; 3 G; 13 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T E3 - useful as vaccine component

S 1 - useful as vaccine component

S 2 - useful as vaccine component

S 2 - useful as vaccine component

C 2 - useful as vaccine component

C 3 - useful as vaccine component

C 4 - useful as vaccine component

C 4 - useful as vaccine component

C 6 - useful as vaccine component

C 6 - useful as vaccine component

C 6 - useful as vaccine component

C 7 - useful as vaccine component

C 8 - useful as vaccine component

C 6 - useful as vaccine component

C 6 - useful as vaccine component

C 7 - useful as vaccine component

C 8 - useful as vaccine component

C 9 - useful as vaccine component

C 9 - useful as vaccine component

C 9 - useful as vaccine

C 1 - useful as vaccine

C 2 - useful as vaccine

C 3 - useful as vaccine

C 4355 BP; 1219 A; 702 C; 852 G; 1582 T;
                                                                                                                                                                                 Query Match
Best Local
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Best Local
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07-MAR-1991.
10-AUG-1999; CA0252.
22-AUG-1989; US-397689.
(VETE-) VETERINARY INFECTIO.
Parker MD, COX GJ, Babiuk LA;
WEI; 91-087247/12.
P-PSDB; R11061,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q10093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAR-1991 (first entry)
Probe 782 to Chlamydia trachomatis 16S rRNA.
16S rRNA; sexually transmitted diseases; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 TATGTTTTAG 173
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                                                                                       1 TATGTTTTAG 10
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7 TATGTTTTAG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
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/label= transmembrane_domain
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Pred. No.
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Pred. No.
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ches 0;
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                                                                                                                                                                                                    DB 1;
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P-PSDB; P70554

(INSP ) INST PASTEUR. (MONT/) MONTAGNIER L.

22-JAN-1987; 21-NOV-1986; 24-MAR-1986;

03-MAR-1986; 18-MAR-1986;

FR-001985. US-835228. FR-003881. FR-004215. US-916080. US-933184. EP-400151.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

VERSION	Ž	LOCUS	D20858/c	RESULT 1
D20858.1 GI:504678	HUMGSU839 Human promyelocyte Homo sapiens cDNA cione mp0405 3' mRNA sequence.	D20858 208 bp mRNA EST 30-JUL-1996		

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Okubo, K., Fukushima, A., Yoshii, J., Nilyama, T., Kojima, Y.,
Voshinari, H., Arimoto, J. and Matsubara, K.
Gene expression of human promyelocytic cell line HL60 before and after induction of differentiation. A new application of 3'directed cDNA sequencing unpublished (1993)
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1 (bases 1 to 208)

Murakawa,K., Matsubara,K., Fukushima,A., Yoshii,J. and Okubo,K. Chromosomal assignments of 3'-directed partial cDNA sequences representing novel genes expressed in granulocytoid cells Genomics 23, 379-389 (1994)
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 191) Sudo, K., Chinen, K. and Nakamura, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Okubo,K., Fukushima,A., Yoshii,J., Niiyama,T., Yoshinai,H., Arimoto,J. and Matsubara,K. Institute for Molecular and Cellular Biology Osaka University
                               Contact: Yusuke Nakamura
Institute of Medical Science
University of Tokyo
4-6-1, Shirokanedai, Minato-ku,
Tel: 81-3-5449-5372
Fax: 81-3-5449-5433
                                                                                                                                                   Genomics 24, 276-279 (1995) 95213017
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2058 expressed sequence tags (ESTs) from a human fetal lung cDNA
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yusuke@ims.u-tokyo.ac.jp
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/note="Female, adult, cell_line
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/db_xref="taxon:9606"
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National Institute of Genetics
Yata 1111, Mishima, Shizuoka 4:
Tel: 0559-75-0771
Fax: 0559-75-6240
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                        /clone_lib="Yuji Kohara unpublished cDNA"
note="dev_stage="Varied, sex=Hermaphrodite
tissue_type=whole animal"
68 c 71 g 84 t. 3 others
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/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
/clone="yk23c8"
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/db_xref="taxon:9606"
/clone_lib="Human fetal lung"
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                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutherla: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 339)
Adams, M.D., Dubnick, M., Kerlavage, A.R., Moreno, R., Kelley, J.M., Utterback, T.R., Nagle, J.W., Fields, C. and Venter, J.C.
Sequence identification of 2,375 human brain genes
Nature 355, 632-634 (1992)
                                                                                                                         The Institute for Genomic Research 9712 Medical Center Drive, Rockville, Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                   9273397
M79084.1
                                                                                                                                                                     Bioinformatics
                                                                                                                                                                                 Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                         EST
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EST01232 Subtracted Hippocampus,
Sapiens cDNA clone HHCPK27, mRNA
M79084
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10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411,
Tel: 0559-75-0771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Yuji Kohara
Gene Library Lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nema
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Toward an expression map of the C.elegans genome Unpublished (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kohara, Y., Mitsuki, H., Nishigaki, A., Motohashi, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhabditina; Rhabditoidea; Secernentea; Rhabditia; Rhabditoidea; Rhabditidae; Peloderinae; 1 (bases 1 to 259)
                                                       il: arkerlavetigr.org
primer: M13 Forward.
Location/Qualifiers
                                                                                                              3018699423
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Location/Qualifiers
/organism="Homo sapiens"
/db_xref="ATCC (inhost):78612"
/db_xref="GDB:D0S2053E"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Yuj1 Kohara unpublished cDNA"
/note="dev_stage="varied, sex=Hermaphrodite male,
tissue_type="whole animal"
48 c 26 g 73 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                   GI:273397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
/clone="yk37a3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
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oderinae; Caenorhabditis.
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#936205) Homo
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families and potential disease gene
Nature Genet. 1, 124-131 (1992)
93250983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
1 (bases 1 to 403)

"allav.T.M., FitzGerald,M.G.,
                                                                                                                                                                                                                                                                                                                                                                               The Institute for Genomic | 9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Kerlavage, Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McCombie,W.R., Adams,M.D., Kelley,J.M., FitzGerald,M.G.,
Utterback,T.R., Khan,M., Dubnick,M., Kerlavage,A.R., Venter,J. and
                                                                                                                                                                                                                                                                                                                                                    Fax: 3018699423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M79559 403 bp
WEST00096 M1xed stage,
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100.0%;
ilarity 100.0%;
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                                                                                                                                                                                                                                                                                                                         arkerlav@tigr.org
                                                                                                        /Clone_lib="Mixed stage, Stratagene (cat. #937006)"
/note="Vector: Uni-ZAP XR; C. elegans mixed stage cDNA
library. Strategene catalog #937006. The library is oligo
dT primed and directionally cloned in the Uni-ZAP XR
vector."

4 3 c 81 g 164 t 4 others
                                                                                                                                                                                                                 /organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/clone="CEMSB03"
                                                                                                                                                                                                                                                                                         ocation/Qualifiers
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66 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Subtracted Hippocampus, Stratagene (cat.
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Mismatches 0;
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Score 10; DB 20; Pred. No. 1.6e+04; Mismatches 0;

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| TATGTTTTAG
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Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota, Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Eukaryota, Metazoa; Nematoda; Secernentea; Peloderinae; Caenorhabditis
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
1 (bases 1 to 509)
Waterston, R., Martin, C., Craxton, M., Huynh, C., Coulson, A.,
Hillier, L., Durbin, R.K., Green, P., Shownkeen, R., Halloran, N.,
Hillier, L., Wilson, R., Berks, M., Du, Z., Thomas, K., Thierry-Mieg, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M89400 509 bp mRNA EST CELO8B11 Chris Martin sorted cDNA library Caer cDNA clone cm08b11 5' similar to cytochrome b
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                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecular Biology
Box 8232,4566 Scott Ave.,St. Louis,MI 63110,USA,or,Hills
Road,Cambridge CB2 20H,UK
Tel: (USA) (314)3627072 or (UK) (0223)248011
Fax: (USA) (314)3624137 or (UK) (0223)402008
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A survey of expressed genes in Caenorhabditis elegans
Nature Genet. 1, 114-123 (1992)
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                                                 T02576 239 bp mRNA 0213C3 cbsPfHB3.1, Debopam Cl clone PF0213C, mRNA sequence
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(USA) Dept. of Genetics or (UK)
(USA) Washington Univ. School of Medicine or (UK) MRC Laboratory
                                   T02576
                                                                                                                                                                                                                                                                                                                                                                               151
                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rw@nematode.wustl.edu or
                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: lambdaphage SHLX2; Mixed stage hermaphrodite cDNA library. Partially normalized by successively picking groups of clones that didn't hybridize to previously picked clones. Vector: lambdaphage SHLX2 (Lipshitz, D.H. et al., Gene 88:25-36 (1990)) Host: MC1061
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/strain="Bristol N2"
/db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Chris Martin sorted cDNA library"
/lab_host="MC1061"
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Pred. No.
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jes@mrc-lmba.cambridge.ac.uk
                                                                                                                                                                                                                                                                                  DB 20;
1.5e+04;
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                                                                       Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 02-DEC-1992
Y Caenorhabditis eleg
                                                                                                                                                                                                                                                                                                  Length 509;
                                                                                                                                                                                                                                                                                                                                                                                 9 others
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                                                                   26-MAY-1992
falciparum cDNA
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JOURNAL
MEDLINE
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MEDLINE
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Best Local
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Chakrabarti,D., Reddy,G.R., Dame,J.B., Almira,E.C., Laipis,P.J., Ferl,R.J., Yang,T.P., Rowe,T.C. and Schuster.S.M. Analysis of expressed sequence tags from Plasmodium falciparum Mol. Biochem. Parasitol. 66, 97-104 (1994)
                                                                                                                              Eutherla; Primates; Catarrill, ....
Eutherla; Primates; Catarrill, ....
1 (bases 1 to 344)
1 (bases 1 to 344)
Khan, A.S., Wilcox, A.S., Polymeropoulos, M.H., Hopkins, J.A., Khan, A.S., Wilcox, A.S., Polymeropoulos, M.H., Hopkins, J.A., Stevens, T.J., Robinson, M., Orpana, A.K. and Sikela, J.M. Stevens, T.J., Robinson, M., Orpana, A.K. and genetic mapping of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Pathobiology
University of Florida
2015 SW 16th Ave., Bldg. 1017,
Tel: 352 392 4700
Fax: 352 392 9704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               malaria parasite P. falciparum
Department of Pharmacology University of Colorado Hea
                                          Contact: Sikela JM
                                                                                   ဝ္
                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                     Nature Genet. 2, 180-185 (1992)
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                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dame@icbr.ifas.ufl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Glone_lib="cbs9fHB3.1, Debopam Chakrabarti"
//lab_host="E, coli XLI-Blue"
//note="Vector: pBlueScript SK(+); PolyA+ RNA, from
asynchronous blood stage parasites of the cloned Honduran
asynchronous blood stage parasites of the cloned Honduran
HB3 isolate cultured in vitro, was reverse transcribed
using an oligo dT-Xho I primer. Second strand was prepared
using RNase H and DNA polymerase I. Gadapters were
ligated to the cDNA, and it was cleaved with Xho I.
Prepared fragments were ligated into EcoR I + Xho I
double-digested pBlueScript SK(+), and transformed E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Plasmodium falciparum"
/db_xref="taxon:5833"
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Pred. No.
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    Health Sciences Center
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ORIGIN
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Matches 10
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Box C236, 4200 E.
Tel: 3032708637
Fax: 3032707097
                                                                                                                                                                                                                                                 Contact: Adams, MD
The Institute for Genomic Research
932 Clopper Road, Gaithersburg, MD
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 336)
Adams,M.D., Kerlavage,A.R., Fields,C. and Venter,J.C.
3,400 expressed sequence tags identify diversity of transcripts
from human brain
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T05062
                                                                                                                                                                                           Seq primer: M13-21
                                                                                                                                                                                                                                                                                                                                         93364420
                                                                                                                                                                                                                                                                                                                                                          Nature Genet.
                                                                                                                                                                                                            Email: mdadams@tigr.org
                                                                                                                                                                                                                                Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  il: nikki@tally.uchsc.edu
primer: -21Ml3 Universal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
   99
 Ø
/clone_lib="Fetal brain, Stratagene (cat#936206)"
/note="Vector: LambdaZAP-II; 17-18 wk gestation, fema
oligo-dT + random primed cDNA synthesis; lambdaZAP-II
vector, 1.0kb average inser size."
a 53 c 85 g 89 t 10 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #937201, Stratagene) was constructed by directional cloning and oligo d(T)-priming in Lambda ZAP II phage utilizing mRNA from a 17 week human fetus (total brain)."
75 c 76 g 95 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="ATCC (Inhost):86749"
/db_xref="GDB:D0S2872E"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="FB2484"
/clone=llb="Fetal brain, Stratagene"
/note="Vector: Lambda ZAP II; The FB library (catalog
                                                                                    /db_xref="ATCC (inhost):81799"
/db_xref="taxon:9606"
/clone="HFBCQ55"
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Pred. No. 1.7e+04;
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Query Match

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T05247/c
LOCUS
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Best Local S
Matches 10
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EST03029 Fetal brain,
clone HFBCS21 similar
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 385)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mdadams@tigr.org
Seq primer: M13-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Adams, MD
The Institute for Genomic Research
932 Clopper Road, Gaithersburg, MD 20878
Tel: 301869056
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T05141.1 GI:316293
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Adams, M.D., Kerlavage, A.R., Fields, C. and Venter, J.C.
3,400 expressed sequence tags identify diversity of transcripts
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                                                             human.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                            100.0%;
ilarity 100.0%;
Conservative 0
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/clone=llb="Fetal brain, Stratagene (cat#936206)"
/clone=llb="Fetal brain, Stratagene (cat#936206)"
/note="Yector: LambdaZAP-II; 17-18 wk gestation, 1
cligo-dT + random primed cDNA synthesis; lambdaZAF
vector, 1.0kb average inser size."
104 g 88 t 4 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism-"Homo sapiens"
/db_xref-"ATCC (inhost):81871"
/db_xref-"taxon:9606"
                                                                                            GI:316399
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Stratagene (cat#936206) Homo sapiens cD
to EST containing O family repeat, mRNA
                                                                                                                                                                                                                                                                                                              Score 10; DB 20;
Pred. No. 1.7e+04;
; Mismatches 0;
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; Mismatches
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hes 0;
                                                                                                                                                                                                                                                                                                                                           Length 358;
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                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                           station, female;
lambdaZAP-II
                                                                                                                                                       sapiens cDNA
                                Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                     Contact: Dame JB
Department of Pathobiology
University of Florida
2015 SW 16th Ave., Bldg. 1017, G
Tel: 352 392 4700
Fax: 352 392 9704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene sequence tags from Plasmodium falciparum genomic DNA fragments prepared by the genease activity of mung bean nuclease Proc. Natl. Acad. Sci. U.S.A. 90, 9867-9871 (1993)
                                                                                                                                                                                                                                                                                                                                 Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 364)
Reddy,G.R., Chakrabarti,D., Schuster,S.M., Ferl,R.J., Almira,E.C.
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Plasmodium falciparum
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T09635.1 GI:319467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Other_ESTs: 0211m7
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10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Dame, J.B.
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Seq primer: M13-21.
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                                                                                                                                                                                                                                                                                                                             primer: T3
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                                                                                                                                                                                                                                                                                                                                                      dame@icbr.ifas.ufl.edu
/clone_lib="gmbPfHB3.1, G. Roman Reddy"
/lab_host="E. coli XL1-Blue"
/note="Vector: pBlueScript SK(+); Genomic DNA, fr
/note="Vector: pBlueScript SK(+); Genomic DNA, fr
                                                                                                                                                             /clone="0211m"
                                                                                                                                                                                  organism="Plasmodium/db_xref="taxon:5833"
                                                                                                                                                                                                                                                                                          Location/Qualifiers
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/note="Vector: LambdaZAP-II; 17-18 wk gestation, fema:
/note="Vector: L
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/db_xref="ATCC (inhost):81973"
/db_xref="taxon:9606"
/clone="HFBCT86"
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1 (bases 1 to 318)

Takeda, J., Yano, H., Eng, S., Zeng, Y. and Bell, G.T.
A molecular inventory of human pancreatic islets: se of 1000 cDNA clones
Hum. Mol. Genet. 2, 1793-1798 (1993)
                                                                                                                                                                                                                                                                                                                                    Univ. of Chicago
5841 s. Maryland Ave.,MC1028,Chicago
Tel: 3127029116
Fax: 3127020271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9390727
T10573.1
                           Similarity
                                                                                                                                                                                                                                                                                                    Seq primer: SK primer
                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Bell GI or Takeda J
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                                                                                                          114
        Conservative
                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="hbc156"
/clone_lib="Human pancreatic islet"
/note="Vector: Lambda ZAPII; Site_1: Eco RI; Site_1; mRNA was prepared from normal adult human isluwas directionally synthesized from the Xho I in to the EcoRI site. cDNA was size fractionated to sequences <1000 bp in size."

14 a 66 c 58 g 80 t
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                                                                                                                                                                                                                                                                                                                 g-bell@uchicago.edu
                                                                                                                                                                                                                                                                                     Location/Qualifiers
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a 61 c 51 g 151 t 7 others
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1.8e+04;
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1.7e+04;
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                                     Length 318;
     Indels
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                                                                                                                                             islets. cDNA in the vector
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T10574/c
Search completed: September 17, 1999, 21:28:05 Job time: 14269 sec
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Best Local Similarity 100.0%;
Matches 10; Conservative 0
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158 TATGTTTTAG 149
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5841 S. Maryland Ave.,MC1028,Chicago IL 60637
Tel: 3127029116
Fax: 3127020271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: g-bell@uchicago.edu
Seq primer: SK primer.
Location/Qualifiers
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HHMI
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 324)
1 (Dases 1, Yano,H., Eng,S., Zeng,Y. and Bell,G.I.
Takeda,J., Yano,H., Eng,S., Zeng,Y. and Bell,G.I.
A molecular inventory of human pancreatic islets; sequence analysis of 1000 cDNA clones
https://doi.org/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10.1006/10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               r10574.1 GI:390728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /Clone_lib="Human pancreatic islet"
/note="Vector: Lambda ZAPII; Site_1: Eco RI; Site_2: Xho
/note="Vector: Lambda ZAPII; Site_1: Eco RI; Site_2: Xho
/note="Vector: Lambda ZAPII; Site_1: Eco RI; Site_2: CDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. cDNA was size fractionated to remove
sequences <1000 bp in size."
a 67 c 63 g 79 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="hbc160"
                                                                                                                                                                                                                                                                                                                                                                                                                           0,
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pred. No. 1.8e+04;
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Upstream sequence
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Plasmid pBG381 inc
Part 1 of cDNA der
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M13 VHPCR1 with Ig
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Nucleotide sequenc
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Light chain antibo
Anti-Leu 3a heavy
Human 32K alveolar
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Q03006;
29-MAY-1990 (fir:
Full length T4 cDI
                                                                                                               PISDE: AN. 1007302/01.
WPI; 90-007302/01.
P-PSDB; R04032.
Combinations of soluble T4 protein and anti-retroviral agent -
Combinations of soluble T4 protein and prevention of AIDS,
                       having synergistic activity in treatment and prevention of AIDS, ARC and HIV infection.

ARC and HIV infection.

Disclosure; fig 2; 100pp; English.

Soluble T4 constructs may be produced by truncating this sequence, remove the transmembrane and intracytoplasmic domains whilst retain the extracellular region responsible for HIV binding. The sol. T4 in combined with an anti-viral agent such as AZT.

See also 003005.

Sequence 6151 BP; 1493 A; 1589 C; 1586 G; 1483 T;
                                                                                                                                                                                        08-JUN-1989; U02453.
10-JUN-1988; US-204645.
20-ARR-1989; US-341080.
(GEHO-) General Hospital Corp
Fisher RA, Schooley RT, Hirsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Combinations of soluble T4 protein and anti-retroviral agent - having synergistic activity in treatment and prevention of AIDS, ARC and HIV infection.

Disclosure; h.

Disclosure; h.

Soluble T4 constructs may be produced by truncating this sequence, to remove the transmembrane and intracytoplasmic domains whilst retaining the extracellular region responsible for HIV binding. The sol. T4 is combined with an anti-viral agent such as AZT.

See also Q03006.

Sequence 7377 BP; 1760 A; 1954 C; 1902 G; 1761 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44
                                                                                                                                                                                                                                                                               W08911860-
                                                                                                                                                                                                                                                                                              Full length Soluble T4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEHO-) General Hospital Corp.
(BIOJ) Biogen Inc.
Fisher RA, Schooley RT, Hirsch
WPI: 90-007302/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JUN-1988;
20-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-MAY-1990 (first entry)
Full length T4 cDNA of plasmid pl70-2.
Soluble T4; pl70-2; anti-retroviral agent; AIDS; ARC; HIV; AZT.
W08911860-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q03005 standard; cDNA; 7377
Q03005;
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962 CTCTCCACAG 971
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nes 10; Conservative
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                                                                                                                                                                                                                                                                                        (first entry)
T4 cDNA of plasmid pBG381.
pBG381; anti-retroviral agent;
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US-341080.
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X26905
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Pred. No. 1.
                                                                                                                                                                                          (BIOJ) Biogen
MS, Johnson VA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MS, Johnson VA, Walker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; 1
1.1e+03;
                                                                                                                                                                                                                                                                                         AIDS; ARC;
                                                                                                                                                                                          Inc.
Walker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
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6.6 kb transcript
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Regult No.

Length

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Full length T4
Full length T4 Description

a

1000.00 1000.0

Human angiotensin Modified human lyr Plasmid p170.2 end

enc

Sequence of new pl Bovine Bone Morpho Sequence encoding Sequence encoding Sequence encoding

Upstream sequence

Scoring table: Perfect score: Sequence:

IDENTITY\_NUC

311585 seqs, 125096042 residues

tabase :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Title:

US-08-956-518A-92

CTCTCCACAG 10

Run 욙

95:

nucleic

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nucleic search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd

September 18, 1999, 00:33:37; Search time 425.19 Seconds (without alignments) 5.884 Million cell updates/sec

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A DNA sequence of a VH region gene.
VH region gene: imunoglobulin; HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP-327000-A.
09-AUG-1989.
30-JAN-1989; 101583.
30-JAN-1988; JP-20255.
08-UIL-1988; JP-171385.
(KAGA ) The Chemo-Sero-Therapeutic Research Institute.
(KAGA ) The Chemo-Sero-Therapeutic Research Institute.
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N90493;
                                                                                                                                                                                                                                                                                                                                                                                                                                      C-terminus of the superoxide dismutase C-100 fusion Hepatitis C virus; cDNA; fusion polypeptide C100-3; Non-A, non-B hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prevention of AIDS
Disclosure; Fig 5; 33pp
The DNA is a VH region
Sequence 660 BP; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric anti-human immune virus antibodies - contg. mouse vregions and human constant regions for diagnosis, treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Takatsuki K;
WPI; 89-229050/32.
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26-JUL-1989.
18-NOV-1988;
18-NOV-1987;
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N90334;
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                                                                                GB2212511-A.
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  G27024.
US-122714
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278. .646
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28. .42
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gion gene. See P90542, N90491-2, and N90495
184 A; 155 C; 144 G; 177 T;
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Pred. No. 1.1
0; Mismatches
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Pred. No. 1.1
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superoxide dismutase;
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Query Match
Best Local
EP-328404-A.
16-CCT-1989:
10-FEB-1989: 301291.
12-FEB-1988: GB-8803228.
(MEDI) Meddical Research Council.
Clark MR, Riechmann L, Waldmann H,
WPI: 89-235722/33.
P-PSDB; P90917.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence shows the sequence of the C-terminus of the superoxide dismutase (SOD)-C100 fusion polypeptide. The sequence encodes antigens which react with antibodies in patients with non-A non-B hepatitis (NANBH). The CDNA can be used to design probes, or to synthesise polypeptides, which are used to disgnose HCV-induced NANBH, to raise antibodies for immunoassay or treatment, or to produce vaccines raise attree b shows the SOD C-terminal; c shows an adaptor; d shows the NANBH polypeptide; and e shows an extra sequence. See also P90182,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus gene - used polypeptide(s) and antibodies of infection.
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Heavy chain variable domain; complementary determining antibody; Campath-1; lymphoma; immunosuppression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NANNEH polypeptide; and e shows an extra sequence. N90303-33, and N90335-6. Sequence 1310 BP; 262 A; 388 C; 378 G;
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WPI; 89-215054/30.
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N90502;
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Houghton M, Choo QL, Kuo G;
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ilarity 100.0%;
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339. .353
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237. .:
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110. .:
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Pred. No. 1.1
0; Mismatches
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PT Transient expression system for recombinant proteins -
PT comprising eukaryotic host cell transfected with vector
PT encoding trans-activating protein and expression vector
PS bisclosure; '44 pp; English.

CC Expression vector pF8CIS contains the cytomegalovirus enhancer and prom-
Expression vector pF8CIS contains the cytomegalovirus enhancer and prom-
CC enter, the cytomegalovirus splice donor site and a portion of an intron,
CC enter of the Ig variable region intron and splice acceptor site, the cDNA encoding
CC prodn. of a desired heterologous protein in a eukaryotic host cell with a vector
CC The method comprises: transfecting a eucaryotic host cell with a vector
CC an expression vector having a sequence of a ds DNA comprising, a
CC encoding trans-activating protien; transfecting the host cell with
CC stabilising sequence downstream of a promoter and upstream of a DNA
CC encoding the amino acid sequence of the desired protein, and a poly-
CC The pref. host cells are human embryonic kidney cells (293) or JW2.
CC The method provides useful quantitites of a desired protein in a
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Best Local
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                                                                                                                                                                                                                                                                         Gorman
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22-SEP-1988; 308784.
25-SEP-1987; US-101712
                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNA sequence of portion of plasmid pr8CIS containing cytcenhancer, promoter and splice donor site and Ig variable plasmid pr8CIS; cytomegalovirus; enhancer; promoter; stabilising sequence; splice donor intron sequence; Ig va splice acceptor sequence; human embryonic kidney cells (2 Cytomegalovirus +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N90695 standard; DNA; 919
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determining region of
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|228 CTCTCCACAG 237
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10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 /note="IGE synthetic 897. .916
                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Begin RNA"
800. .900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Cytomegalovirus 733. .900
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codes rat immunoglobulin heavy chain (see p90917).

and b show where RNA begins, h and i encode signal
                                                                                                                                                                                                                                                                                                                                                 'note="PstI-ClaI converter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acceptor sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"stabilising sequence, ie.
sequence, the Ig variable region
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rat origin and foreign variable
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Pred. No. 1.1
); Mismatches
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thes 0;
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ble domain framework
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PT Transient expression system for recombinant proteins -
PT comprising eukaryotic host cell transfected with vector
PT encoding trans-activating protein and expression vector
PS Disclosure; ;44 pp; English.

CC Expression vector pF8SCIS contains the SV40 enhancer and promoter, the
CC Expression vector pF8SCIS contains the cDNA encoding factor VIII and the
CC intron and splice acceptor site, the cDNA encoding factor VIII and the
CC intion and splice acceptor site, the cDNA encoding factor VIII and the
CC SV40 polyadenylation and transcription termination sites.

CC desired heterologous protein in a eukaryotic host cell with a vector
an expression vector having a sequence of a ds DNA comprising, a
CC encoding trans-activating protein; transfecting the host cell with
CC stabilising sequence downstream of a promoter and upstream of a DNA
CC encoding the amino acid sequence of the desired protein, and a poly-
CC The pref. host cells are human embryonic kidney cells (293) or JW2.
CC The method provides useful quantitites of a desired protein in a
CC relatively short period of time without having to establish continuous
CC specific vector components and certain trans-activating proteins.

SC Specific vector components and certain trans-activating proteins.
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N90696
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Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                        Gorman CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-UUL-1990 (first entry)

DNA sequence of portion of plasmid pF8SCIS containing SV40 enhapromoter, cytomegalovirus splice donor site and Ig intron plasmid pF8SCIS; cytomegalovirus; SV40; enhancer; promoter; stabilising sequence; splice donor intron sequence; Ig region; splice acceptor sequence; human embryonic kidney cells (293);
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573. .590
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/note="Stabilising sequence which includes
/note="Stabilising sequence which includes
/note="Stabilising sequence,"
- and splice acceptor
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361. .580
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RESULT
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Reshaped light chain variable domain HuVLLYS
Eukaryotte host.
Ep-338745-A.
25-00:m-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-APR-1989; 303767.
16-APR-1988; GB-009050.
(CELL) Celltech Ltd.
Owens RJ, Winter GP, Riechmann
WPI; 89-311183/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CTCTCCACAG 10
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543 CTCTCCACAG 552
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Method of prodn. of recombinant FV fragments
by transformed host cells contg. expression
pisclosure; fig. 2; 12pp; English.
pisclosure; Fig. 2; 12pp; English.
Sequence 527 BP; 136 A; 156 C; 130 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                             wpI; 89-30934/42.

New luminescent chimeric proteins - useful in highly sensitive immunoassays, eg for HIV immunoassays, eg for HIV English.

Disclosure; page 35; 79pp; English.

Osed to express the chimeric variable 4-hydroxy-3-nitrophenyl (NP) used to express the chimeric variable antigen/aequorin protein, in J558L myeloma or other cells expressing antigen/aequorin protein, in J558L myeloma or other cells expressing antigen/aequorin protein, in J558L myeloma or other cells expressing antigen/aequorin protein is used as a diagnostic.

lambda 1 light chain. This protein is used as a diagnostic.

Sequence 150 BP; 35 A; 38 C; 38 G; 39 T;
                                                                                                                                                                                                                                                                                                                                                                                                               05-OCT-1989.

05-OCT-1989.

00-MAR-1988; US-173231.

24-MAR-1988; US-173231.

(IGEN) Igen Inc.

(IGEN) Igen Inc.

(IGEN) Igen Inc.

(IGEN) Well MJ:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W08909393-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Start of coding region acquorin/NP fusion protein Human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N91481;
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                                                                                                   l Similarity
10; Conserv
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nilarity 100.0%;
Conservative 0;
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Pred. No. 1.1
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(BEHW) Behringwerke.
Domdey H. Marget M. V
WPI; 89-310861/43.
P-PSDB; P93079.
                                              Query Match
Best Local S
Matches 10
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25-OCT-1989.
12-APR-1989;
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Heavy chain of monoclonal antibody 646
Monoclonal antibody 6A4, heavy chair
Key
64. 540
cds /*tag- a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monoclonal antibody to Pseudomonas aeruginosa - and DNA coding for variable antibody regions.

Variable antibody regions.

Claim 1; page 6; 7pp; german.

The sequence has a variable and constant region. Monoclonal antibody 6A4 reacts with the OMP-1 protein of all 19 known serotypes of P.aeruginosa. reacts with the OMP-1 protein of all 19 known serotypes of acarrier for It is used for therapy and diagnosis of infection, and as a carrier for drugs. The antibody is 1962a subclass.

Sequence 540 BP; 145 A; 144 C; 130 G; 121 T;
                                                                                                                                                                                                                                                                                                                                                                                          N91820 standard; I
N91820;
22-MAR-1990 (firs
                                                                                                                                                                                                                                      W08909622-A.
19-0CT-1989, U01578
13-APR-1988, US-181862.
15-APR-1988, US-181862.
(PROT-) Protein Design L
                                                                                                                                                                                                                                                                                                                                                    22-MAR-1990 (first entry)
DNA sequence of the V and J regions of the anti-Tac heavy chain.
Anti-Tac monoclonal antibody; heavy chain; V region; J region;
interleukin-2 receptor; human T-cells; chimeric antibody.
                                                                                                         New interleukin-2 receptor-specific chimeric antibodies -
treating T-cell mediated disorders.

treating T-cell mediated disorders.

Disclosure; Fig. 2; 46pp; English.
The anti-Tac heavy chain is produced by ATCC CRL 9688. It
mouse/human chimeric antibody, which is specifically react
interleukin-2 receptors on human T-cells.

sequence 443 BP; 117 A; 114 C; 110 G; 102 T;
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32 CTCTCCACAG '
                                                                                                                                                                                                                                                                                                                                          Mus muscularis.
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P-PSDB; P93151.
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1 CTCTCCACAG
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milarity 100.0%;
Conservative 0;
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illarity 100.(
Conservative
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heavy chain; I
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Pred. No. 1.1
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                                                       Score 10; DI
Pred. No. 1.1
); Mismatches
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hes 0;
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1.1e+03;
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Recombinant protein mfr. - using balanced inductive control system, esp. for mfg.tissue plasminogen activator. Disclosure; fig. 3; 48pp; English.

The EIK variant of t-PA is described in EP-199574 and is characterised by substitutional mutations that eliminate a proteolysis site. Plasmid pCT-eik.2 cotains CMV enhancer/promoter region, the Ig splice acceptor, the Sp6 promoter and RNA start, the T7 promoter, the TrpE leader RBS, the altered preprot-PA gene and the SV40 polyA site.

altered preprot-PA gene and the SV40 polyA site.

altered preprot-PA gene and the SV40 polyA site.
                                                                                                                                                                                                                                                                                                                                                                                                       misc features apeptides, and and a resp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence of humanised light chain variable domain. Heavy chain variable domain; complementary determi Campath-1; lymphoma; immunosuppression.
                                                                                                                       Miller HI;
                                                                                                                                          23-JUN-1988; U02127.
24-JUN-1987; US-065794.
                                                                                                                                                                       WO8810307-A.
                                                                                                                                                                                                                     Tissue
                                                                                                                                                                                                                               Fragment
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                                                                                                                                                                                                                                                           N93069
                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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Antibody which binds to antigen C
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Clark MR, Riechmann L, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP-328404-A.
16-OCT-1989.
10-FEB-1989; 301291.
12-FEB-1988; GB-8803228.
                                                                                                    P-PSDB; P94866
                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                         regions.
                                                                                                                                (GETH) Genetech.
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                                                                                                                                                                                                                    plasminogen activator;
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444. .600
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237. .571
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                                                                                                                                                                                                                                                                                                                                                                                                                encode complementary
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w where RNA begins, h and i encode sign
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Matches 10
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07-JAN-1988; US-141649, U
(BIOJ) Biogen Inc.
Fisher RA, Gilbert W, Sat
WPI; 89-085519/11.
    DNA sequences coding for soluble T4-like used in immuno:therapeutic and immunosupp preventing, treating or detecting AIDS Disclosure; ; 207pp; English.

It is the nucleotide sequence of region e mature T4 sequence of plasmid pBG393. It
                                                                                                                                                                                                                                                                                                                01-AUG-1990 (first entry)

Nucleotide sequence of gene encoding mature T4 sequence of plasmid pBG393

including soluble T4-like (sT4) polypeptide number 8 (sT4#8)

HIV; soluble T4-like polypeptide 8; immunotherapeutic; prophylactic;

plasmid pBG393; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                          N90648;
01-AUG-1990 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA sequences coding for soluble T4-like polypeptide(s) - used in immuno:theraputic and immunosuppressive compsns. and for preventing, treating or detecting AIDS Disclosure; 207pp; English.

It is the nuclectide sequence of the plasmid pBG396. The sequence was isolated from 2 libraries: a landa gt coDNA library derived from T cell tumour line REX and a landa gt10 cDNA library derived from peripheral blood lymphocyes (PBL). For screening, a series of chemically synthesised antisense oligonuclectide DNA probes based on the known T4 protein screening as series.
                                                                                                                                                                                                                                                      09-MAR-1989
                                                                                                                                                                                                                                                                              WO8901940-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        N90648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunotherapeutic, prophylactic and diagnostic compsns. It can to purify HIV from a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BIOJ) Biogen Inc.
Fisher RA, Gilbert W,
WPI; 89-085519/11.
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07-JAN-1988;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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difference analysis (RDA) experiment;
encoding MHC class III HLA-RP1"
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/tissue_type="inner and middle ear"
/dev_stage="fetus"
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                                                                                                                                        Spermatophyta;
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hyta; Magnollophyta; Lillopsida; Poales;
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D21568.1
                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 270)

Nishiguchi, S., Joh, T., Horie, K., Zou, Z., Yasunaga, T. and Shimada, K. A survey of genes expressed in undifferentiated mouse embryonal carcinoma F9 cells: characterization of low-abundance mRNAs J. Biochem. 116, 128-139 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact:
                                                                                                                                                        Contact: Kazunori Shimada
Department of Medical Genetics, Division of Molecular Biomedicine
Research Institute for Microbial Diseases, Osaka University
3-1, Yamadaoka, Suita, Osaka, 565, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUS69C02 mouse embryonal
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2-1-2 Kannondai, Tsukuba
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06-879-8326.
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/note="Vector: pBluescript II SK+; Site_1: SalI;
NotI; cDNA prepared from rice callus mRNAs by usi
oligo(dT) as a primer and ligating to the SalI-No
of pBluescript II SK+ phagemid.
a 114 c 127 g 69 t 4 others
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                                             /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="69C02"
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/db_xref="taxon:4530"
               /clone_lib="mouse embryonal carcinoma cell line F9" 63 c 81 g 26 t 4 others
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Mus musculus

Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 253)

Nishiguchi,S., Joh,T., Horie,K., Zou,Z., Yasunaga,T. and Shimada,K.

A survey of genes expressed in undifferentiated mouse embryonal

carcinoma F9 cells: characterization of low-abundance mRNAs
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D28603.1
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                                                                                                                                   EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411,
Tel: 0559-75-0771
Fax: 0559-75-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Toward an expression map of the C.elegans genome Unpublished (1994)
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi
                                                                                                                   house mouse
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Kohara,Y., Mitsuki,H., Nishigaki,A., Motohashi,T.,
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Location/Qualifiers
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/note="dev_stage=varied, sex=Hermaphrodite male,
tissue_type=whole animal"
89 c 82 g 125 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref=-traxon:6239"
/map="18 q21.1-q21.3"
/clone="yk6b9"
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                   126 CTCTCCACAG
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D31189.1
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HUML12839 Human fetal
D31189
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                                                                                                                                                                                                                                              Email: yusuke@ims.u-tokyo.ac.jp
Insert Length: 825 Std Error:
High quality sequence stop: 1.
Location/Qualifiers
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Tel: 81-3-5449-5372
Fax: 81-3-5449-5433
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1 (bases 1 to 290)

Sudo, K., Chinen, K. and Nakamura, Y.
2058 expressed sequence tags (ESTs) from a human fetal lung c
                                                                                                                                                                                                                                                                                                                                                             University of Tokyo
                                                                                                                                                                                                                                                                                                                                                                         Contact: Yusuke Nakamura
Institute of Medical Science
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Department of Medical Genetics, Division of Molecular Biomedicine
Research Institute for Microbial Diseases, Osaka University
3-1, Yamadaoka, Suita, Osaka, 565, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biochem. 95096008
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                                                                                                                                                                      /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/clone_lib-"Human fetal lung"
78 c 78 g 61 t
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82 c 58 g 50 t 7 others
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/db_xref="taxon:10090"
/clone="04G11"
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                                                                              Score 10; DB 20;
Pred. No. 8.5e+03;
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ches 0;
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08-FEB-1995 mRNA sequence

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D31359.1
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 300)
Sudo,K., Chinen,K. and Nakamura,Y.
                         Contact: Yusuke Nakamura
Institute of Medical Science
University of Tokyo
                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                          HUML13517 Human fetal lung Homo sapiens cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: yusuke@ims.u-tokyo.ac.jp
Insert Length: 2137 Std Error: 0.00
High quality sequence stop: 377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4-6-1, Shīrokanedāi, Minato-ku, Tokyo 108, Tel: 81-3-5449-5372
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HUML13208 Human fetal lung
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1 (bases 1 to 233)
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95213017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Yusuke Nakamura
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., Shirokanedai, Minato-ku, Tokyo 108,
81-3-5449-5372
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/db_xref="taxon:9606"
/map="710B10; 15"
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83 c 82 g 63 t
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Genethon Centre de recherche sur le Ge
1, rue de 1'Internationale, BP60 91002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
95277534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B. Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Poulic Sebastiani-Kabaktchis, C. and Tessier, A. Sebastiani-Kabaktchis, C. and Tessier, A.
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1 (bases 1 to 274)
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Insert Length: 586 Std Error:
High quality sequence stop: 400.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 33169472800
Fax: 33160778698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Genethon
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Single read. removed at sequ
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/tissue_type="total brain"
/dev_stage="3 months old"
/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: Not1; sex=Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total
brain; total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"
a 70 c 53 g 86 t
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/db_xref="taxon:9606"
/clone_lib="Human fetal lung"
72 c 59 g 55 t
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                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                 /clone_lib="normalized infant brain cDNA'
/sex="Female"
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/clone="c-lpal2"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 387)
Adams, M.D., Dubnick, M., Kerlavage, A.R., Moreno, R., Kelley, J.M., Utterback, T.R., Nagle, J.W., Fields, C. and Venter, J.C.
Sequence identification of 2,375 human brain genes
Nature 355, 632-634 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L26703 239 bp mRNA
MUSF139A lambda unizap male testis
                                                                                                                                                                                    M77875
EST01459 Fetal
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Kerr,S.M., Vambrie,S., McKay,S.J. and Cooke,H.J. Analysis of cDNA sequences from mouse testis Mamm. Genome 5, 557-565 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST.
                                                                                             Homo sapiens
                                                                                                                                                                           clone
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459 Fetal brain,
HFBCA49 similar
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/note="Vector: lambda unizap; lambda unizap library from
mail mouse testis " 32 t 1 others
a 62 c 78 g 32 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism-"Mus musculus"
/strain-"Swiss"
/db_xref-"taxon:10090"
/clone-"F139"
                                                                                                                                   GI:273613
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NA clone F139,
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoldea; Rhabditidae; Peloderinae; Caenorhabditi
1 (bases 1 to 335)
                                                                                                                                                                                                                                                                                                                               The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                   Bioinformatics
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Tel: 3018699056
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Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                    Fax: 3018699423
                                                                                                                                                                                                                                                                                                            Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Kerlavage, AR
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primer: M13 Reverse.
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/clone="HFBCA49"
/clone=lib="Fetal brain, Stratagene (cat#936206)"
/clone="Vector: LambdaZAP-II; 17-18 wk gestation, female;
/note="Vector: LambdaZAP-II; 17-18 wk gestation, female;
oligo-dT + random primed cDNA synthesis; lambdaZAP-II
vector, 1.0kb average inser size."
a 100 c 104 g 94 t 2 others
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/clone_lib="Mixed stage, Stratagene (cat. #937006)"
/note="Vector: Uni-ZAP XX; C. elegans mixed stage cDNA
/note="Vector: Uni-ZAP XX; C. elegans mixed stage cDNA
library . Strategene catalog #937006. The library is ol:
dT primed and directionally cloned in the Uni-ZAP XR
                                                                                                      /clone="CEMSA52"
                                                                                                                           /organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
                                                                                                                                                                                                   Socation/Qualifiers
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/db_xref="GDB:D0S885E"
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/db_xref="ATCC (inhost):
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RESULT 14
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi;
1 (bases 1 to 472)
MCComble,W.R., Adams,M.D., Kelley,J.M., FitzGerald,M.G.,
Utterback,T.R., Khan,M., Dubnick,M., Kerlavage,A.R., Venter,J. an
HUMRTPGEAO Subtracted human sapiens cDNA, mRNA sequence. M91496
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The Institute for Genomic Research
The Medical Center Drive, Rockville, MD 20850 USA
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wEST00347 Mixed stage, Stratagene (cat. #9
elegans cDNA clone CEMSE18, mRNA sequence.
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Seq primer: M13 Foward.
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/note="Vector: Uni-2AP XR; C. elegans mixed stage cDNA
/ilbrary . Strategene catalog #937006. The library is oligo
dT primed and directionally cloned in the Uni-2AP XR
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/clone="CEMSE18"
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                                                                                                                                                                                                                                                                                             Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditi;
1 (bases 1 to 353)
1 (Combie, W.R., Kelley, J.M., Aubin, L., Goscoechea, M., M., FitzGerald, M.G., Mu, A., Adams, M.D., Dubnick, M., Kerlavage, A.R., Venter, J.C. and Fields, C.A.
Caenorhabditis elegans cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T01961 353 bp mRNA EST wEST02682 Early embryo, Stratagene (cat. #937007) elegans cDNA clone CEESX81, mRNA sequence.
                                                                                                                               Email: arkerlav@tigr.org
Seg primer: Ml3 Foward.
                                                                                                                                                                                  9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056
                                                                                                                                                                                                                                    Bioinformatics
                                                                                                                                                                                                                                                    Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                       Unpublished (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g278442
T01961.1 GI:278442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Metheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 209)

Gleser, L. and Swaroop, A.

Expressed sequence tags and chromosomal localization from a subtracted retinal pigment epithelium library genomics 13, 873-876 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g275912
M91496.1
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                                                                                                                                                                                                                The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kellogg Eye Center, University of Michigan
1000 Wall Street, Ann Arbor, MI 48105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Swaroop, A.
Department of Ophthalmology
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ilarity 100.0%;
Conservative (
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            /organism-"Caenorhabditis elegans"
/db_xref-"taxon:6239"
/clone-"CEESX81"
/clone-11b-"Early embryo, Stratage:
/clone_11b-"Early embryo, Stratage:
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Pred. No. 7.9e+03;
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t 5 others
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OM nucleic - nucleic search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

September 18, 1999, 00:33:38; Search time 425.19 Seconds (without alignments)
5.884 Million cell updates/sec

Run on:

44

10

100.0 1593 100.0 116277

Q53404 X20249

Eleusine Borrelia

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RESULT 1
Q03618/c
1D Q03618 standard; DNA; 4885 BI
AC Q03618;
DT 01-AUG-1990 (first entry)
DE Phosphoenolpyruvate carboxyla
KW Phosphoenolpyruvate carboxyla
Corynebacterium glutamicum.
FH Key Location/Qual
FT cds /*tag= a
PN EP-358940-A.
FH EP-358940-A.
PN EP-358940-A.
PN 21-MAR-1990.
8-AUG-1989; 114632.
PR 12-SEP-1988; GB-021319.
PR (DEGS) Degussa AG.
PI Bachmann B, Thierbach GD, Kal
PI Wiret JF, Lepage P, Lemoine )
PR WPI; 90-084832/12.
PT Deoxyribonucleic acid fragmer
PT obtd. from corynebacterium gl
PT phosphoenolpyruvate carboxyla
PS Disclosure; p; English.
CC PPC 1s important as a key enz
CC levels of L-AAs.
SQ Sequence 4885 BP; 1071 A.
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                                                                             11-SEP-1989.
09-FEB-1988; US-876819.
05-FEB-1985; US-876819.
(CETU) Cetus Corp.
Kaswasaki ES, Ladner MB, Van Arsdell JN, Wang AM, Ralph P, Coyen MY;
WPI; 89-255732/35.
                                                                                                                                                                                                                                                                                                                   05-JAN-1990 (first entry)
HindIII fragment of human CSF-1.
Colony stimulating factor; immunosuppression; lymphokine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4295 GTCTCCCCAG 4286
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Disclosure; p; English.

PPC is in the anaplerotic function of the cell,

PPC in the cell indirectly increases biosynthetic

by increasing oxaloacetate levels, it indirectly increases biosynthetic

levels of L-AAs.

Sequence 4885 BP; 1071 A; 1356 C; 1318 G; 1139 T; 1 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bachmann B, Thierbach GD, Kalinowski Viret JF, Lepage P, Lemoine Y; WPI; 90-084832/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphoenolpyruvate carboxylase (ppc)
Phosphoenolpyruvate carboxylase; ppc;
Corynebacterium glutamicum.
Key
Location/Qualifiers
cds
921. 3677
                                 Human and murine colony stimulating immunosuppression caused by eg chem
                                                                   P-PSDB; P91458
                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deoxyribonucleic acid fragment, for L-amino acid obtd. from corynebacterium glutamicum strain coding
                                                                                                                                                                                 US4847201-A.
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                                1mmunosuppression
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821. .822

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4a-4c; 30pp; English
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                              nulating factors, CSF-1 - u eg chemotherapy, and obtd.
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Pred. No. le+03;
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Result No.

B

Description

Q03618

Human colony Gastrin recombinan Phosphoenolpyruvat HindIII fragment o

Stimu

100.0

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ACV synthetase gen Human dopamine Di DNA encoding Facto Endoglucanase ENDO Sequence of endogl Sequence of tuf3 g DNA of hgEco-1, en DNA encoding maski

P40 genomic DNA. N Retinal cGMP phosp Human HSF cDNA seq ACVS gene pcbAB, M

Immunoglobulin D-r First half of part

encoding hepat

Sequence of gamma-

LVDJ regions of Nucleotide sequenc

Sequence encoding Recombinant

receptor

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Myotonic dystrophy
Human endothelial
Human brain Expres
Human brain Expres
Human vitamin D re

n brain Expres n vitamin D re n cyclin D1 pr ocan DNA. Euka

5-Substd. hydantio Cyclin D1 promoter Human cardiac cGI Murine TC-CSF. New Gamma subunit of h

Sequence of a part Sequence of human Fetal calf TP-like Sequence encoding

centromeric

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Scoring table:

IDENTITY\_NUC

GTCTCCCCAG 10

311585 segs, 125096042 residues

Perfect score:

0;

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RESULT
N90234
ID N
AC N
DT 1
                                                    PT Recombinant DNA encoding gastrin - also comprising promoter and signal peptide coding regions, inserted into shuttle vector to produce PT gastrin in yeast or E.coli.

PS Claim; page 524 and fig 2: 10pp; Japanese.

CC The recombinant DNA effectively produces gastrin in high quantities.

CC The recombinant DNA effectively produces gastrin into a shuttle CC vector which can grow in yeast or E.coli, eg pAM62, CV37, pAT77, YEP51, CC YEP52 or pjDB218. The DNA encoding signal peptide is, eg from human CC gastrin, MFalphal (yeast secretion hormone), yeast invertase, killer CC toxin, yeast alkaline or acid phosphatase, human alpha-cc amylase or human trypsin inhibitor. DNA encoding gastrin is from, eg H653. See also P90331. Misc. feature d is Sau3A site, e is Sau3A site, g is PvuII site, h is HindIII site, i is Sau3A site.

CC fis HindIII site, g is PvuII site, h is HindIII site, i is Sau3A site, and j is Sau3A site. The CDS is minus the intron.

CC Bases 262-318 encode signal peptide, and bases 319-429 encode gastrin.
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Matches' 10
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24-JUN-1987; 156745.
24-JUN-1987; JP-156745.
(AJIN) Ajinomoto KK.
WPI; 89-1/6418/24.
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for enhancing prodn. of white blood cells or treating viral or bacterial infectious diseases or tumours Figure 2a·2c; pp. 3/7-5/7; 62pp; English.

It is the sequenced portion of a 3.9kb HindIII fragment encoding human CSF-1 sequences. It is used in the mfr. of a compsn. useful for enhancing prodn. of white blood cells, including neutrophils, from stem cells. It is also used in mfr. of a compsn. useful for treatment/ prophylaxis of bacterial or viral infectious diseases (esp. cytomegalovirus or Gram-negative sepsis), for the treatment of sarcoma or melanoma, for stimulating antibody-dependent cellular cytotoxicity (ADCC), and for wound healing.

Sequence 2045 BP; 410 A; 455 C; 514 G; 466 T; 200 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N90749;
                                                                                                                                      28-JUN-1990 (first entry) Fragment of clone lambda HK65a Kallikrein gene; vasodilator; n
                                                                                                                                                                                              N93197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human colony stimulating factor-1 (CSF-1) Cytomegalovirus; CMV; Human colony stimulating factor-1; CSF-1; cytomegalovirus; CMV; Gram-negative sepsis; sarcoma therapy; melanoma therapy; ADCC; antibody-dependent cellular cytotoxicity; wound healing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-SEP-1988; U03234.
14-SEP-1988; US-243253,
(CETU) Cetus Corp.
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16-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              intron
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                                                                                                                   sapiens
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                                                                                                                                                                                                                  standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                       ch 100.0%; l Similarity 100.0%; 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              recombinant colony
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2538: .2697
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3967: .4256
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218. .340
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341. .1581
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2538:
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                                                                                                   Location/Qualifiers
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1582. .1650
/*tag= d
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                                                                                                                                      vasodilator; male,
                                                                                 . 848
                                                                                                                                                                                                                  5406
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Pred. No. 1.1e+03;
Mismatches 0;
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                                                                                                                                  g. kallikrein gene.
infertility; lambda
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21-JUN-1988; US-209530.
19-JUN-1989; US-366377.
(CHIR-) Chiron Corp.
                                                                              P-PSDB; R04724.

Recombinant polynucleotide(s) encoding glucose oxidase and vectors conty. them, secreting glucose oxidase or hyper-glycosylated analogues into medium Disclosure; B-6; 108pp; English.

Disclosure; B-6; 108pp; English.
        The cDNA can also be used to isolate GO-encoding sequences from other sources. Its encoded GO is used in desugaring eggs, removing oxygen from moist food prods, beverages, flavours and hermetically-sealed food packages, and in detection and estimation of glucose in industrial solr and body fluids, eg blood and urine. This sequence is the same as that given in Fig 5B of the patent, but with the addition of one Guanine at the start of the sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful as vasodilators and for treating male in Table V; page 13; 43pp; English.

Lamda HK64a is a subclone produced from clones bourne human fetal liver genomic library using clone DNA as a probe.

See also N93193-8.

Sequence 5406 BP; 974 A; 1864 C; 1309 G
                                                                                                                                              Rosenberg S;
WPI; 90-022535/03.
                                                                                                                                                                                                                  WO8912675-A.
28-DEC-1989.
                                                                                                                                                                                                                                                                                 mat_peptide
                                                                                                                                                                                                                                                                                                                   misc_difference
                                                                                                                                                                                                                                                                                                                                                   Glucose oxidase; As glucose estimation.
                                                                                                                                                                                                                                                                                                                                                                                     Nucleotide
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09-SEP-1990
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Q03143 standard;
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New recombinant kallikrein
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Lin FK, Lu HS;
WPI; 89-009139/02.
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30-JUN-1988;
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00-JUN-1987; US-068594.
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10; Conserv
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sequence of
 2024 BP;
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32. 97
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Pred
615 C;
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male infertility.
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 515 G;
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 445 T;
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                                                                                                                                                                                                                                                                                            Fig 5B-1-5B-6'
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Best Local
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Polypeptide fragments encoded by the DNA sequence are ar
Polypeptide fragments encoded by the DNA sequence are ar
HBV and may be used as a vaccine or in detection. Peptic
cultured in a suitable bacterial host such as E.coli.
Sequence 2743 BP; 638 A; 728 C; 579 G; 797 T;
                                                                                                                                                                                                                                                                                                      LVDJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant sequence encoding hepatitis B antigens. Hepatitis B virus; vaccine; HBV; ds. Synthetic.
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                                                                                                                                                                                                                  Homo
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27-DEC-1978; GB-050039
01-NOV-1979; GB-037910
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                                                                                                        misc_feature
                                                                                                                                                                                                                                      vaccine; contraceptive;
                                                                                                                                                                                                                                                           variable region;
                                                                                                                                                                                                                                                                                 Anti-human sperm-
                                                                                                                                                                                                                                                                                                                             09-NOV-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant DNA encoding Hepatitis used in detection of infection and
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                                                                                                                                                                                                                                                         regions of human sperm-immobilising monoclonal antibody human sperm-immobilising monoclonal antibody; leader regable region; joining region; constant region; sterility;
                                                                                                                                                                                                                sapiens.
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                                                                                                                                                                                                                                                                                                                                                                        standard;
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87. .634
                                                                                                     /product-variable region 528. .610
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1521. .
                                                                                                                                                                       622. .91:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 10;
Pred. No.
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1e+03;
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30-MAY-1988; 272412.
15-NOV-1986; JP-272412.
15-NOV-1986; JP-272412.
(TOFU) TOA NEMRYO KOGYO KK.
WPJ; 88-187839/27.
P-PSDB; P81259.
                                                                                                              Human laminin Bl chain polypeptide fragment, and expression vector: for inhibition of tumour metastasis, wound remedy diagnostic agent etc Claim 1; Fig 1; 20pp; Japanese.

Polypeptide may be produced from a transformed expression system under the control of a tac promoter/operator, an SD sequenc of metapyrocatechase and laq gene.

The gene product has cell binding affinity, and may be used in inhibition of metastasis and infection, wound healing, cell growt as a reagent for laminin assay.

Sequence 1399 BP; 291 A; 376 C; 412 G; 320 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell strain producing human sperm-immobilising monoclonal antibody has at least V-gene in H chain coding genetic family and V gene in chain of DNA originating from antibody of sterile woman.

Disclosure; ; 14pp; Japanese
A 1.85 kb LVDJ segment is inserted into psV2gpt together with a constant gamma 1 region. A cell strain, pref. a myeloma cell, can produce the Ab with immobilising value (SISO) of at least 5000, sperm agglutination value at least 1:1600 dilution, specifically reacting against human ejaculated sperm. The product can be used
1155 GTCTCCCCAG 1146
                                                                                                                                                                                                                                                                                                                               17-SEP-1990.
07-MAR-1989; 052835
                                                                                                                                                                                                                                                                                                                                                                                    03-FEB-1991 (first entry)
Sequence encoding human laminin
Metastasis; cancer; cell growth
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See also N81654-N81656.
1071 BP; 250 A;
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                                                                                                                                                                                                                                                                                                                     07-MAR-1989;
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
J02234679-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reacting against human ejaculated sperm.
as a vaccine and contraceptive.
                                                                                                                                                                                                                                                                                        07-MAR-1989; JP-052835.
(SAGA ) SAGAMI CHEM RES CENTRE
NPI; 90-325616/43.
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944. .995
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/label-joining_region
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Pred. No. 1.1e+03
); Mismatches 0
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Pred. No.
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factor; tac promoter; ds.
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RESULT 10

Q11415 standas
Q11415;
D1 Q11415 standas
AC Q11415;
DE Ryanodine rec
KW Q11415;
ET Ryanodine rec
KW Malignant hypo
KW alignant hypo
KW anaesthetics;
FY retloulum; ss
OS Homo sapiens.
FY rolya_signal
FY polya_signal
FY polya_site
FY misc_rna
FY mis
                                                                                                                                                   04-APR-1991.
21-SEP-1990; CA0312.
25-SEP-1989; US-612726.
(HSCR-) HSC R & D Partnership.
(UTOR) Univ. Toronto Innova.
(TORO-) Toronto Hospital.
Worton RG, Maclennan DH, Britt E
          p-PSDB; RIISIO.

Purified DNA specific for human ryanodine receptor - useful for diagnosis of mailgnant melanoma.

Claim 1; Fig 2; 49pp; English.

The sequence was obtd. from several overlapping clones isolated from a human skeletal muscle cDNA library in lambda gt10. The ge (located on chromosome 19) encodes the human ryanodine receptor
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/note= "3.8 kb; (6349 .8717
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/note- "2.0 kb;
13826. .15467
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15439. .15
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'note= "1.6 k
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'note= "2.4 kb;
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note= "1.0 kb; cl
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ote- "1.2 kb; cla
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20-APR 1989; J01044.
14-OCT-1988; JP-170041.
09-JUL-1988; JP-170041.
(EDUC-) Education Found Fujita (MITK MITH).
(EDUC-) Education Found Fujita (MITK MITH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HRR), a calcium release channel which spans the gap between the transverse tubule and the sarcoplasmic reticulum (SR) in muscle. The sustained muscle contraction in malignant hyperthermia (MH) may be caused by the release of calcium into the muscle cell cytoplasm from the SR. This is due to a defect in the gene encoding HRR. Sequences from the gene can be used for diagnosis of MH using FRPL analysis (see tags e-m).
                                                                                        Q11707 standard; DNA; Q11707;
                                                                                                                                                                                                                                                                                                              encoding human 1gX (X = 1gG3, 1gG4, 1gG4, 1gG4, 1gG4, 1gG4). The DNA sequences are obtd. from suitable human celline, e.g. marrow cells, and pref. ARA-10 or Daudi, using a probe for the 1gJH region, and cloned using a vector such as a plasmid (pref.) lambda-phage.

Sequence 1196 BP; 276 A; 312 C; 345 G; 263 T;
                                                                                                                                                                                                                                                                                                                                                                                              specific control of prodn. of specific classes of antibody.

Disclosure: Fig 9B; 79pp; Japanese.

Sigma-gamma-3 and -4 are switch sequences for Cx genes upstream,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kurowawa Y, Away A, jShizuka
WPI; 89-130043/17.
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Sequence of gamma-3 intron switch sequences for immunoglobulin
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                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant DNA switch sequences for immunoglobuline genes . specific control of prodn. of specific classes of antibody.
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                                         Immunoglobulin D-region heavy chain major cluster lymphoid tumour diagnosis; human; Ig; diversity re
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                                                                         25-JUL-1991
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llarity 100.0%;
Conservative (
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Location/Qualifiers 776. .862
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225. .1196
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Pred. No. 1.1e+03;
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Pred. No. 9.
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s 0;
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11-APR-1991.
19-DEC-1989;
19-DEC-1988;
19-JUN-1989;
19-DEC-1989;
                                           6743
                                                                                                                                                                    Human immunoglobulin gene - for diagnosis and monitoring of lymphoid tumour esp. in leukaemia Claim 2; Fig 2; 35pp; Japanese .

The sequence is a 15kb fragment of the D(H) region of the human gene (between D(LR4) and D(LR2)). See also Q11708.

Sequence 14928 BP; 3308 A; 4995 C; 4066 G; 2559 T;
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JP-154623.
JP-329005.
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Matches 10
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(BIOG-) BIOGEN INC.
Murray K, Schaller HE;
WPI; 86-138858/22.
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03-FEB-1986; U0238.
05-FEB-1985; US-688359.
30-APR-1985; US-728834.
14-JUN-1985; US-744924.
18-JUL-1985; US-756814.
21-JAN-1986; US-821068.
20-JUN-1986; US-876819.
P-PSDB; P61103

New recombinant DNA molecules - useful in cloning and expressing DNA sequence coding for hepatitis B virus antigenic poly:peptide for use in vaccines

Claim 4; page 37-8; 42pp; English.

The DNA sequence encodes a polypeptide with hepatitis B virus (HBV) antigenicity. The polypeptide is an HBV surface or core antigen. HBV antigens and genes can be obtd. In substantial amts. and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                        N60295 standard; DNA; 549 BP.
N60295.
01-AUG-1991 (first entry)
DNA encoding hepatitis B virus polypeptide.
DNA encoding hepatitis B virus; ss DNA; vaccine; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis
EP-182442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant colony stimulating factor-1 protein - is obtd. by recombinant DNA procedures for use in enhancing immune system and for treating monocytes to increase interferon prodn.

Disclosure; Fig 4a-b; 82pp; English.

The CSF-1 protein claimed is esp. human CSF-1, or it may have an equiv. AA sequence, with deletion or conservative substitution of one or more AA, esp. between positions 158 and 224; 51 and 52 and/or 191,192 and193; 15-20 and/or 75-84. The protein is esp. mCSF-1, or 158 deleted CSF-1 or asp (59)-CSF1.

Sequence 861 BP; 167 A; 204 C; 251 G; 199 T;
                                                                                                                                                                                                                                                                                    01-NOV-1979;
01-JAN-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kawasaki ES, Ladner MB,
Coyne MY, Warren MK;
WPI; 86-225459/34.
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Immune system;
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5 GTCTCCCCAG 534
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GB-050039.
GB-037910.
EP-201908.
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Pred. No. 1.1
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abel= C-rich_motif
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uncontaminated form, and may be used to produce vaccines. The polypeptide may be used to diagnose HBV infection. The polypeptide may be expressed using a vector. HBV has a narrow host range and cannot be grown in tissue culture systems, so it has not previously been available in quantity.

Sequence 549 BP; 132 A; 134 C; 122 G; 161 T;
  h 100.0%;
Similarity 100.0%;
10; Conservative (
       0
  Score 10; DB 1;
Pred. No. 1.1e+03;
; Mismatches 0;
     0:
                                               Length
     Indels
     0;
Gaps
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Q12759 standard; DNA; 4382 Q12759; (first entry) factor; AIDS; cytokine; 1022. .1057 /\*tag= b Location/Qualifiers number-. 909 ₽P н helper

4099. .4218 /\*tag= e /number= 5 /number= 3
2464. .2595
/\*tag= d
/number= 4 346. .350 796. .849 1143. .1175 /\*tag= c /\*tag= g /label= C-rich 370. .376 \*tag= ımber-\_motif

/note- "interferon /note= abel - C-rich\_motif .750 .633 "AP-1 binding regulatory factor-1 site' binding

.398

labellabel - Alu\_sequence polydG-dT\_stretch
"Z\_DNA; enhancer-like activity." m transcription\_start\_site

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Search completed: September 18, 1999, 00:33:39 Job time: 18979 sec
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Best Local Similarity 100
Matches 10; Conservative
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25-JUL-1991.
08-JAN-1991; U00145.
08-JAN-1990; US-462158.
(RESE ) RES CORP TECHN INC.
Vansnick J, Uyttenhove C, Simpson RJ;
WPI; 91-238026/32.
                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; R13217.

Nucleic acid encoding for P40 T-cell growth factor - for patients with AIDS or compromised immune systems, also allows increased prodn. of other cytokine(s).

Claim 2; Fig 14; 122pp; English.

The sequence was obtd. from a clone, lambda H40.3a1, isolated from a genomic library using a murine P40 cDNA clone as a probe. The sequence, or the cDNA sequence obtd. using the sequence, can be inserted into a vector for expression of P40 in a host organism. The protein is useful for stimulating the proliferation of certain subsets of T helper cells e.g. in AIDS patients or immune
                                                                                                                                                                                                                                                                                                                        compromised patients.
See also Q12760, and Q13660-Q13663.
Sequence 4382 BP; 1210 A; 922 C;
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/note- "reduces mRNA stability"
4357. .4362
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/note= "reduces mRNA stability"
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note "reduces mRNA stability"
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Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

VERSION	ACCESSION		DEFINITION	LOCUS	D20867/c	RESULT 1
D20867.1 GI:504687	D20867	mRNA sequence.	1848 Human promyelocyte Homo sapiens cDNA cl	D20867 200 bp mRNA EST 30-JUL-1996		

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1 (bases 1 to 200)

Murakawa,K., Matsubara,K., Fukushima,A., Yoshii,J. and Okubo,K.

Chromosomal assignments of 3'-directed partial cDNA sequences representing novel genes expressed in granulocytoid cells Genomics 23, 379-389 (1994)

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Okubo, K., Fukushima, A., Yoshii, J., Niiyama, T., Kojima, Y.,
Okubo, K., Fukushima, A., Yoshii, J., Niiyama, T., Kojima, Y.,
Yoshinari, H., Arimoto, J. and Matsubara, K.
Gene expression of human promyelocytic cell line HL60 before and after induction of differentiation. A new application of 3'directed
                                                                                                                          Osaka University
3-1 Yamada-oka,Suita,Osaka 565,Japan.
                                                                                                                                                                                           Contact: Okubo,K., Itoh,K., Yoshii,J., Yokouchi,H. Institute for Molecular and Cellular Biology
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3-1 Yamada-oka,Suita,Osaka 565,Japan.
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/note-"Female, adult, cell_line - HL60, cell_type -
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58 c 40 g 42 t 5 others
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/db_xref="taxon:9606"
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           Caenorhabditis elegans.
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                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contect: Kazunori Shimada
Department of Medical Genetics, Division of Molecular Biomedicine
Research Institute for Microbial Diseases, Osaka University
3-1, Yamadaoka, Suita, Osaka, 565, Japan
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/clone_lib="mouse embryonal carcinoma cell line
/clone_lib="mouse embryonal carcinoma cell line
/clone_10="mouse embryonal carcinoma cell line
/clone="86G01"
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/db_xref="taxon:10090"
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/clone_lib="Human colon mucosa"
/note="Adult male, tissue_type -
31 c 37 g 46 t
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National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411,
Tel: 0559-75-0771
Fax: 0559-75-6240
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Toward an expression map of the C.elegans genome Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D8-AUG-1994 EST 08-AUG-1994 CELK024B7F Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA clone yk24b7 5', mkNA sequence.
                                                                                                                                                                                                                                                                                                                                 Tabara, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
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                                                                                                                                                                                               Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411,
Tel: 0559-75-0771
Fax: 0559-75-6240
                                                                                                                                                                                                                                                                                                              Toward an expression map Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Rhabditina; Rhabditoidea; Rhab
1 (bases 1 to 360)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                  Contact: Yuji Kohara
                                                                                                                                                                                                                                                                                                                                                               Kohara, Y., Mitsuki, H., Nishigaki, A., Motohashi, T.,
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Location/Qualifiers
                                                                                                                                                                ykohara@ddbj.nig.ac.j.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cione_lib="Yuji Kohara unpublished cDNA"
/note="dev_stage="varied", sex=Hermaphrodite male,
tissue_type=whole animal"
78 c 83 g 112 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
/clone="yk11b4"
             /clone_lib="Yuji Kohara unpublished cDNA"
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tissue_type=whole animal"
49 c 88 g 78 t 1 others
                                                                            /organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
/clone="yk24b7"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                 of the C.elegans genome
                                                                                                                                                                                                                                                                                                                                                                                                    oda; Secernentea; Rhabditia; Rhabditida; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                   Sugimoto, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis
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D36081/c
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REFERENCE
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Best Local Similarity
Matches 10; Conserv
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Best Local
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Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota, Metazoa, Nematoda, Secernentea, Rhabditia, Rhabditida;
Rhabditina, Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
1 (bases 1 to 360)
Vohana V Mitcuki U Nichicaki a Mothbachi T Sugimoto A and
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D36081.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411,
Tel: 0559-75-0771
Fax: 0559-75-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D36081
                                                                                                                                            D37701 418 bp mRNA EST 08-AUG-1994 CELKOO8D8F Yuj1 Kohara unpublished cDNA Caenorhabditis elegans cDNA clone yk8d8 5', mRNA sequence.
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             Caenorhabditis elegans.
Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota, Metazoa, Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Yuji Kohara
                                                                                                                                                                                                                                                                                                                                             Similarity
 (bases 1 to 418)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ykohara@ddbj.nig.ac.j.
Location/Qualifiers
                                                                                                                                                                                                                                                                239
                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Yuj1 Kohara unpublished cDNA"
/note="dev_stage=varied, sex=Hermaphrodite male,
tissue_type=whole animal"
86 c 124 g 51 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:528019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="yk28h3"
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/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
                                                                                                GI:526082
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Pred. No. 9.7e+03;
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9.7e+03;
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BASE COUNT
ORIGIN
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D41072
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AUTHORS
TITLE
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Best Local s
Matches 10
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JOURNAL
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                                                                                                                                                                                                                                                                                                                               Oryza sativa.
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Enbryophyta; Poales;
                                                                                                                                                                                                                           Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
2-1-2 Kannondai, Tsukuba
                                                                                                                                                                                                                                                                                                                                                                                                                                        D41072
9571561
D41072.1
                                                                                                                                                                                                                                                                                                    l (bases 1 to 391)
Sasaki, T., Miyao, A. and Yamamoto, K.
Rice cDNA from callus 1995
Unpublished (1995)
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Fax: 0559-75-6240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Toward an expression 
Unpublished (1994)
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                                                                                                                                                                                0298-38-7441
                                                               72
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                                                                                                                                              tsasaki@abr.affrc.go.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ykohara@ddbj.nig.ac.j.
Location/Qualifiers
                                                     /clone_lib="Rice shoot"
/note="Etiolated shoot |
140 c 119 g
                                                                                            /strain="Nipponbare, sub_species Japonica"
/db_xref="taxon:4530"
                                                                                                                     /organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:571561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Clone_lib="Yuji Kohara unpublished cDNA"
/note="dev_stage=varied, sex=Hermaphrodite male,
tissue_type=whole animal"
94 c '99 g 121 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
/clone="yk8d8"
       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    391 bp mRNA EST 15-1
s shoot Oryza sativa cDNA, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
    Score
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Pred. No.
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    10;
                                                      (8 days old)"
54 t 6 o
  DB
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  20;
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Length 391;
                                                   6 others
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AUTHORS
                                                                           Matches
                                                                                              Query Match
Best Local
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KEYWORDS
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F02878/c
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                                  1 GICTCCCCAG 10
     228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                            Local
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GTCTCCCCAG 219
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                                                                                        Similarity
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Genexpress_library_idt: C; Genexpress_sequence_idt:
Seq primer: (-21)Mi3_universal.
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1 (bases 1 to 324)

Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C.,

Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B.,

Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Pouliot, Y.,

Sebastiani-Kabaktchis, C. and Tessier, A.

IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 33169472800
Fax: 33160778698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genethon Centre de recherche sur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
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Single read. removed at seque
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#SC1ED092 normalized infant brain cDNA Homo sapiens cDNA clone c-led09 3', mRNA sequence.
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                                                                    Conservative
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                                                                                                                                                                                              isolate=muscular atrophy patient; tissue_type=total brain; total mRNA was oligo-(dT) primed and directions cloned 5′ -> 3′ into the HindIII -> NotI sites of the lafmid BA vector. Clone library from B. Soares, Psychia Dept. Columbia University, USA. Normalization_method:
                                                                                                                                                                      Bento Soares, P.N.A.S in press"
84 c 119 g 53 t
                                                                                                                                                                                                                                                                                       /note="Organ: brain; Vector: lafmid BA; Site_1: HindIII; Site_2: NotI; sex=Female; dev_stage=3 months old;
                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="c-led09"
                                                                                                                                                                                                                                                                                                                                          /tissue_type="total brain"
/dev_stage="3 months old"
                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="normalized infant brain
/sex="Female"
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                                                                                     100.0%;
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                                                            Score 10; DB 20;
Pred. No. 9.4e+03;
; Mismatches 0;
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RESULT 10 F03210/c

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g437469
L26678.1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1, rue de l'Internationale, BP60 91002 EVRY
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                             mRNA sequence.
                                                                                                                                                 L26678 52
MUSF080A lambda
                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                     ouse mouse.
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R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="total brain"
/dev_stage="3 months old"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
/site_2: NotI; sex=Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total
brain; total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
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/db_xref="taxon:9606"
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                                                                         GI:437469
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53 c 71 g 67 t
                                                                                                                                                 unizap male testis Mus musculus cDNA clone F080,
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                                                                                                                                                                                                                                                                                                                                           score 10; DB 20;
Pred. No. 9e+03;
; Mismatches 0;
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GTCTCCCCAG 265
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Location/Qualifiers
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MUS167A lambda
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                                                                                                                                                                                                                                                                 Contact:
                                                                                                                                                                                                                                                                                           95093181
                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; I (bases 1 to 401)

Kerr,S.M., Vambrie,S., McKay,S.J. and Cooke,H.J. Analysis of cDNA sequences from mouse testis Mamm. Genome 5, 557-565 (1994)
                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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/note="Vector: lambda unizap;
mail mouse testis" 127 c 129 g 132 t
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                                                                                                                               /clone_lib="lambda unizap male testis"
/note="Vector: lambda unizap; lambda unian testis"
nail mouse testis " 71 t 6 oth
                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="F167"
                                                                                                                                                                                                            /organism="Mus musculus"
/strain="Swiss"
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Pred. No. 1.1e+04;
                                                                 Score 10; DB 20;
Pred. No. 9.9e+03;
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EST00839 Hippocampus, Stratus
Clone HHCMC15, mRNA sequence.
                                                                                 The Institute for Genomic Research 9712 Medical Center Drive, Rockvil: Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                          Adams, M.D., Dubnick, M., Kerlavage, A.R., Moreno, R., Ke Utterback, T.R., Nagle, J.W., Fields, C. and Venter, J.C. Sequence identification of 2,375 human brain genes Nature 355, 632-634 (1992)
                               Email: arkerlav@tigr.org
Seq primer: M13 Reverse.
Location/Qualifiers
                                                                                                                                            Bioinformatics
                                                                                                                                                       Contact: Kerlavage, AR
                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 397)
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M78691.1 GI:273006
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1 (bases 1 to 309)

Jouy: -S., Goold, R.D. and Myers, R.M.

Localization of the alpha 2-macroglobulin receptor-associated chromosome (LRPAP1) and other gene fragments to human Genomics 24, 410-413 (1994)
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∕organism≖"Homo sapiens"
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/note="tissue_type = brain striatum"
84 c 87 g 94 t 6 o
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/db_xref="taxon:9606"
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an brain striatum Homo sapiens cDNA clone Y20, mRNA
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Pred. No. 9.3e+03;
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         Similarity 100.
10; Conservative
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Seq primer: M13 Forward.
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1 (bases 1 to 338)

Adams,M.D., Dubnick,M., Kerlavage,A.R., Moreno,R., Kelley,J.M.
Utterback,T.R., Nagle,J.W., Fields,C. and Venter,J.C.
Sequence identification of 2,375 human brain genes
92168112
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EST02297 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA
clone HFBCN54, mRNA sequence.
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/clone-lib="Fetal brain, Stratagene (cat#936206)"
/clone-lib="Fetal brain, Stratagene (cat#936206)"
/note="Yector: LambdaZAP-II; 17-18 wk gestation, femal
/note="Yector: LambdaZAP-II; 17-18 wk gestation, femal
/note="Yeta" catherists of the cathering for the cathering female ca
                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="ATCC (inhost):81353"
/db_xref="cDB:D85881E"
/db_xref="taxon:9606"
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/note="Vector: lambdazAP-II; Female, 2 years; oligo-
random primed cDNA synthesis; lambdazAP-II vector, 1
average insert size."
a 106 c 96 g 88 t 3 others
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/db_xref="GD8:D0S1679E"
/db_xref="taxon:9606"
/clone="HHCMC15"
100.0%; Score 10; DB 20; 100.0%; Pred. No. 9.5e+03; tive 0; Mismatches 0;
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Copyright (c) 1993 - 1998 Compugen Ltd.
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1 (bases 1 to 392)

Gault, J., Robinson, M., Berger, R., Drebing, C., Logel, J., Hopkins, Moore, T., Jacobs, S., Meriwether, J., Choi, M.J., Kim, E.J., Walton, i Buiting, K., Davis, A., Breese, C., Freedman, R. and Leonard, S. Genomic organization and partial duplication of the human alpha7 neuronal nicotinic acetylcholine receptor gene Genomics 52 (2), 173-185 (1998)
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2 (bases 1 to 392)
Leonard,S., Gault,J., Logel,J., Drebing,C., Robinson,M., Berger,R.,
Breese,C., Davis,A., Hopkins,J. and Freedman,R.
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G40486
AB011396
AB016897
HS431P23
AC003066
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AC007224
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HS2IEA
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HSARA7A
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286099 Herpes spi
277661 H. sapiens m
27066443 Homo sapi
2712168 C. familiari
271219 X. laevis 28
271219 Homo sapi
271219 Homo sapi
271219 M. musculus
271219 M. jaevis 28
2712227 Homo sapi
271224 Homo sapi
271212 Herpes simp
2714112 Herpes simp
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2714112 Herpes simp
2714113 HSV1 (strail
271216 C. Strail
271218 C. Strail

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X70297 H.sapiens m

AC007686 Homo sapi

295399 Caenorhabid

M29385 Herpes simp

M29384 Herpes simp

M29384 Herpes simp

M29384 Horpes simp
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J00184 Human alpha
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Hopkins, J., Walton, K.,

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U62436.1
                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1876)

Elliott, K.J., Ellis, S.B., Berckhan, K.J., Urrutia, A.,
Chavez-Noriega, L.E., Johnson, E.C., Velicelebi, G. and Harpold, M.M.
Comparative structure of human neuronal alpha 2-alpha 7 and beta 2-beta 4 nicotinic acetylcholine receptor subunits and functional expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and beta 4 subunits
                                                                                                                                                                                                                                                                                           Human nicotinic acetylcholine receptor alpha7 subunit precursor, mRNA, complete cds.
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Submitted (15-OCT 1997) Psychiatry, University of Colorado Health Sciences Center, 4200 E. 9th Ave., Denver, CO 80262, USA Location/Qualifiers
          2 (bases 1 to 1876)
Elliott, K.J.
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Direct Submission
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                                                       Neurosci. 7 (3),
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/clone="CHRNA7-P"
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/db_xref="taxon:9606"
/chromosome="15"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (28-JUN-1996) Kathryn J. Elliott, SIBIA Neurosciences, Inc., 505 Coast Blvd. So., La Jolla, CA 92037, USA Location/Qualifiers
                Peng, X., Katz, M., Gerzanich, V., Anand, R. and Lindstrom, J. Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from the SH-SYSY cell line and determination of pharmacological properties of native receptors and functional alpha 7 homomers expressed in Xenopus occytes
7 homomers expressed in Xenopus occytes
801. Pharmacol. 45 (3), 546-554 (1994)
                                                                                                                                                                                                                                                9496606
x70297.1 GI:496606
                                                                                                                                                                                                                                                                                                                              H.sapiens mRNA for neuronal nicotinic acetylcholine receptor
                                                                                                                             Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ bases 1 to 2087)
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ilarity 100.0%;
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LLNWCAWFLRWKRPGEDKVRPACQHKQRRCSLASVENSAVAPPPASNGNLLYIGFRGL
DGVHCVPTPDSGYVCGRNACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANNFRCQ
DESEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFVEAVSKDFA"
139. . 1578
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PDGQIMKPDILLYNSADERFDATFHTWLVNSSGHCQYLPPGIFKSSCYIDVRWFPFD
VQHCKLKFGSWSYGGWSLDLOWQEADISGYIPGEWDLVGIPGKRSERFYEGCKEBYD
DVTFTVTMRRRTLYYGLNLLIPCVLISALALLVFLLPADSGEKISLGITVLLSLTVFM
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/clone_lib="SIBIA lambda
/cell_line="IMR32"
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/db_xref="gII:1458120"
/translation="MRCSPGGVWLALAASLLHVSLQGEFQRKLYKELVKNYNPLERPV
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/product="nicotinic acetylcholine receptor alpha7
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REFERENCE AUTHORS TITLE

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Ratcliffe, A.,

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                              CTGGCTGGCGCTGGCGCGCTCCTGCACG 447
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 168919)

Rowen,L., Madan,A., Qin,S., Abbasi,N., Dors,M., Dickhoff,R., James,R., Loretz,C., Lasky,S., Madan,A., Prescott,S., Ratcliffe,A.,
                                                                                                                                                                                  AC007686 168919 bp
Homo sapiens chromosome
SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (04-FEB-1993) M. Katz, Univ of Pennsylvania School Medicine, Dept of Neuroscience, 36th & Hamilton Walk, Rm 235 Stemmler Hall, Philadelphia, PA 19104, USA Location/Qualifiers
                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 Katz,M.
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DESEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFVEAVSKDFA"
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LLVAEIMPATSDSVPLIAQYFASTMIIVGLSVVVTVIVLQYHHHDPDGGKMPKWTRVI
LLNWCAWFLKMKRPGEDKVRPACQHKQRRCSLASVEMSAVGPPPASNGNLLYIGFRGL
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andsopltyyfslslloimdydeknoylttniwlomswtdhylownysbypgyktyrf
pdgoiwkpdillyngaderfdatfhinylynssghcoylppgifksscyidyrwfpfd
yohcklkfgswsyggwsldlomoeadisgyipngewilygipgkrserfyecckepyp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="neuronal nicotinic acetylocholine receptor
alpha-7_subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="PID:g496607"
/db_xref="GI:496607"
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protein_id="CAA49778.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="brain"
/cell_type="neuroblastoma"
/cell_line="SHSY-5Y"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 3.2e-09;
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14 clone BAC 2289B16 map 14q24.3, LOW-PASS
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*NOTE: his record contains 192 individual
*sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
*and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
*However, it should not be assumed that this clone
*will be sequenced to completion. In the event that
the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rowen, L., Madan, A., Qin, S., James, R., Loretz, C., Lasky, Shaffer, T. and Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shaffer, T. and Hood, L. Sequencing of human chunghlished
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S., Madan,A., Prescott,S., Ratcli
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mat\_peptide BASE COUNT ORIGIN

RESULT AC007686

DEFINITION

SOURCE ORGANISM

CEYWORDS

ERSION CCESSION

REFERENCE

AUTHORS

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416

67

127

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296

9

Matches

146;

24794

25663:

28254:

27381:

contig gap of contig gap of contig gap of contig gap of contig

ig of 849 bp in length of unknown length ig of 870 bp in length of unknown length of unknown length of 1871 bp in length lig of 877 bp in length lig of 878 bp in length of unknown length of so bp in length ig of 872 bp in length ig of 872 bp in length

23945

24793:

32539

33390:

gap of contig gap of contig gap of contig

ig of 837 bp in length
of unknown length
of unknown length
of 858 bp in length
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34255:

31681 30823 29964 29127 28255 27382 26505 25664

32538: 31680:

30822: 29963:

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35106 34256 33391

36869: 36030: 35105:

of unknown

925 bp in length known length 839 bp in length

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Oy 293 CGCGAGCCGAGCGGAGGTGCCTCTGTGGCCGCAGGCCGAGGCCGAGCAGCCGAG 352	173 42654 233 42714	031; 194; 19GGTGAG 	gap of unknown lengt 71467 72361: contig of 895 bp in gap of unknown lengt 72362 73206: contig of 845 bp in 16.1%: Score 73.6; DB 35;	gap of unknown lengt 69757: contig of 834 bp in gap of unknown lengt 70628: contig of 871 bp in gap of unknown lengt 71466: contig of 838 bp in	gap of unknown lengt 66289: contig of 838 bp in gap of unknown lengt 67174: contig of 885 bp in gap of unknown lengt 68020: contig of 846 bp in gap of unknown lengt 68903: contig of 883 bp in	* 61150 62022; contig of 873 bp in length  * 62023 gap of unknown length  * 62023 62858; contig of 836 bp in length  * 62859 63733; contig of 875 bp in length  * 62859 63733; contig of 875 bp in length  * 63734 64579; contig of 846 bp in length  * 64580 65451; contig of 872 bp in length	of 866 bp in unknown lengt of 840 bp in unknown lengt of 865 bp in unknown lengt of 857 bp in unknown lengt	gap of unknown lengt 56874: contig of 888 bp in gap of unknown lengt 57721: contig of 847 bp in gap of unknown lengt

9

41170

42014:

gap c gap c

40284

41169:

39449

40283:

gap o gap c

38585 37735 36870 36031

39448: 38584:

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if unknown length
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42015

42927:

gap c

gap c

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g of 845 bp in length
f unknown length
g of 913 bp in length
f unknown length
g of 861 bp in length
f unknown length
f unknown length
g of 862 bp in length
g of 862 bp in length

gap c

42928

43789

46383:

45491: 44650:

gap c conti gap c conti

47232:

gap of contig

48952 48097 47233 46384 45492 44651

> 48951: 48096:

gap of contig gap of contig

49832

gap of contig gap of contig gap of contig gap of contig gap of contig

of unknown length
of of 841 bp in length
of unknown length
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                             GACAGCCGAGACGTGGAGCGCGCCGG 368
                                                           166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (09-JUN-1999) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RQ, UK and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu
On Jun 11, 1999 this sequence version replaced gi:4725958. Order of segments is not known; 800 n's separate segments. IMPORTANY: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG; PHASE1.
Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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59268 c 58805 g 109715 t
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/db_xref="taxon:6239"
/chromosome="V"
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0.0076;
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MEDLINE
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Best Local
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666 CCGGGGGGACGGGGGGGGGG
                                                                                                                          277 CGGCTCCTTAAAGGCGCGCGAGCCGAGCGGGGGGGGGCGCTCTGTGGCCGCAGGCGCAGGC 336
                                                                                                                                                                                                                                    97
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The junctions between the repetitive and the short unique sequences of the herpes simplex virus genome are determined by the polypeptide-coding regions of two spliced immediate-early mRNAs J. Gen. Virol. 65, 451-466 (1984)
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Alphaherpesvirinae; Simplexvirus.
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                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAA45849.1"
/db_xref="pID:g330284"
/db_xref="GI:330284"
/db_xref="GI:30284"
/translation="MSWALKTTDMPSDSSRCTHRTYGDVCAEIHKREREDREAARTAV
TDPELPLLCPPDVRP"
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/db_xref="taxon:10310"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="immediate early protein
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Pred: No.
689
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RESULT HS2IE

DEFINITION

HS2IE Herpes

1560 bp simplex virus

type

DNA Pe 2

VRL immediate-early

(IE4) protein mRNA,

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                                                                                                                         GGGACGGGGGACGGGGGACGGGGGGGGACGGGGGAC
                                                                                                                                                        GCAGGCGCAGGCCGACAGCCGAGACGTGGAGCGCGCCGGC
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M29384.1
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M29384
HSGG1 43058 bp DNA PRI 19-MAR-1997 Human DNA sequence from cosmid GG1 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16pl3.3 Contains
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/db_xref-"taxon:10310"
95...>1560
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/db_xref="PID:9555152"
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CB10 1RQ, UK. E-mail enquires: humpub@sanger.ac.uk
IMPORTANT: This sequence is the entire insert of clone GG1. This
clone was sequenced at the Institute of Molecular Medicine. The
true left end of clone GG1 is at 1 in this sequence. The true righ
end of clone GG1 is at 43058.
GG1 is from a 280kb clone contig extending from the telomere of
16p. Higgs D.R., Filnt J. unpublished. MRC Molecular Haematology
Unit, Institute of Molecular Medicine, Oxford.
GG1 came from the Los Alamos, flow sorted human Chromosome 16
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Z84721.1 GI:1817575
16p13.3; alpha-globin;
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1 (bases 1 to 43058)
Flint, J. and Higgs, D.R.
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                                                                                                                                  /note="Alusg 1 6864. 7000
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/note="L1ME3A repeat: matches 2. .146 of consensus"
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/chromosome="16"
/map="16p13.3"
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1. .43058
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/note="AluJb repeat: matches 7.
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/note="Alux repeat:
incomplete_repeat"
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/note="L1MB8 repeat: matches 134.
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                                                                                     7045 .7351
/note="Aluy repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                     note-"Alux repeat: matches 297. .1 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note-"FRAM repeat: matches 98.
                                                                                                                                                                                            3320. .6503
note="L1MB7 repeat:
                                                                                                                                                                                                                            714. .6184
note="LIMB5 repeat:
                                                                                                                                                                                                                                                             ncomplete repeat"
                                                                                                                                                                                                                                                                                 'note-"AluSg repeat:
                                                                                                                                                                                                                                                                                                                  note-"Alusg repeat: matches 1.
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                                                                                                                                                                                                                                                                                                                                                                                     repeat: matches 182.
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                                                        matches 294. .394 of consensus"
                                                                                      matches 1.
                                                                                                                           matches 1. .136 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            matches 297. .133 of consensus;
                       matches
                                                                                                                                                             matches 295.
                                                                                                                                                                                              matches 2. :208 of consensus"
                                                                                                                                                                                                                              matches 922.
                                                                                                                                                                                                                                                                                   matches 130.
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                     229.
                                                                                        .301 of consensus
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                       .569 of consensus
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                                                             'note-"AluJo repeat:
8715. .18833
                                                                                                                                                         'note-"AluJo repeat:
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8296 .8597
/note="Alux repeat: matches 1. .301 of consensus"
                                                                                                         note-"AluJo repeat:
                                                                                                                                                                                                                                                       note="AluJo repeat:
                                                                                                                                                                                                                                                                                            note="Alux"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'db_xref="PID:e300370"
'db_xref="PID:g1817576"
'db_xref="GI:1817576"
                                                                                                                                                                                                                                                                                                                                      note="3 copies of 36 mer 83 % conserved" 5747. .15875
                                                                                                                                                                                                                                                                                                                                                                                                                                                              db_xref="SWISS-PROT:P02008"
translation="MSLTKTERTIIVSMWAKISTQADTIGTETLERLFLSHPQTKTYF
HFDLHPGSAQLRAHGSKYVAAVGDAVKSIDDIGGALSKLSELHAYILRVDPVNFKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product="zeta-globin 1"
protein_id="CAB06552.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note-"AluSg repeat: matches 1. .297 of consensus" oin(13773. .13867,14755. .14959,15135. .15263)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10382. 10428
'note="AluX' repeat: matches 13. .294 of consensus'
'note="AluSx/g repeat: matches 245. .291 of consens ncomplete repeat"
Office 10652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="AluSx repeat:
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0. .12317
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mplete repeat"
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"AluSx repeat: matches 1. .19449
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                     .19130
                                                                                                                                                                                                                                                                                                           .16541
                                                                                                                                                                                           HIUY repeat: matches 1,
.17506
                                                                                                                                                                                                                                                                                       repeat: matches 301.
                                                                                                                                                                                                                                                                                                                       repeat: matches 145.
                                         matches 744. .865 of consensus"
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                                                                                                                          153.
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                                                                                                                                                                                                     .297 of consensus"
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             . 296
                                                                         .301 of consensus"
                                                                                                                                                                                                                                                     .136 of consensus;
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           Of.
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Best Local Similarity

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                                                                                                                84 GACTGGGGGTGGAGGTGCCCGGAGCGTACCCAGCGCGGGAGTACCTCCCGCTCACACCT 143
                                                                                                                                                       24 CTGGCCTTGGGCAGCCCCTGGCCTGGCCAGAGGCCGAGAGGCCGAGAGCCCGCTCGGTGGA 83
                                                                  CGGGCTGCAGTTCCCTGGGTGGCCGGCCGAGACGCTGGCCCGGGCTGGAAGGGATGGCCGGG
                                             Conservative
                                                                                                                                                                                                                                   /note="match: multiple ESTs; similar to HEMOGLOBIN ALPHA-D; match: 5' EST H57023 clone 204625; match: 8' EST H67154 clone 21
                                                                                                                                                                                                                                                                                                         24135. .24680
/note="39 copies of 14 mer 90
                                                                                                                                                                                                                                                                                     note="Putative CpG island"
                                                                                                                                                                                                                                                                                                                                                                              note-"Alux repeat: matches 1 ..302 of consensus"
oin(23985. .24079,25345. .25549,25891. .26019)
                                                                                                                                                                                                                                                                                                                                 product="zeta-globin 2"
db_xref="PID:e300371"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1471. .21542
note="2 copies of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="AluSg repeat: matches 154.
ncomplete repeat"
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.9431. .19593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="4 copies of 37 mer
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note="2 copies of
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                                                                                                                                                                                                   13.8%; 52.7%;
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96. .21067
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50. .21433
ce="2 copies of 37 n
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e="2 copies of 36
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                                                                                                                                                                                         0,
                                                                                                                                                                                       Score 63.2; DB 10;
Pred. No. 0.13;
0; Mismatches 123;
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                                                                                                                                                                                                                                                                                                          mutation
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                                                    repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5'- zeta - pseudozeta - pseudoalpha-1 - alpha-2 - alpha-1 -3'. The gene sequence shown below is considered a pseudogene because of the terminating codon at base 429. There are only two additional single-base differences between the coding sequences of the zeta and pseudozeta genes, although there are conspicuous differences in the 5' and 3' flanking regions. Moreover the first intron of this locus demonstrates length variation, apparently stemming from the repeat sequence 'acagigggaggg', which is also found in the zeta gene and, in a similar form, in the 5' flank of the human insulin gene. The repeat sequence 'cgggg' is characteristic of the second introns of the zeta genes [1].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The human alpha globin gene cluster, chromosome 16, spans about 30 kb and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human alpha globin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pseudogene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     roudfoot, N.J., Gil, A. and Maniatis, T.
he structure of the human zeta-globin
early identical pseudogene
eall 31 (3 Pt 2), 553-563 (1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 2685)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       duplication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens DNA
1977. .1981
/note="repeat:
2313. .2541
/gene="phbz"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:183792
                                                                                                                                                                                                                                                                 /gene="phbz"
/note="t in phbz;
                                                                                                                                                                                                                                                                                                            'gene="phbz"
29
                                                                                                                                                                                                                                                                                                                                                                                 gene="phbz"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /map="16p13.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
                                                                                       .972. .2312
'gene="phbz"
                                                                                                                                            gene-"phbz"
                                                                                                                                                                          note"
                                                                                                                                                                                                                                  'gene="phbz"
                                                                                                                                                                                                                   number-
                                                                                                                                                                                                                                                                                                                                            codon_start=]
oin(411. .505
                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="phbz"
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                                                                        umber-
                                                                                                                                                                                                                                                                                                                                                                                                                              umber-1
                                                                                                                                                              .1971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene cluster on chromosome 16: psizeta
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                                                                                                                                                                               sequence
                                 sequence, copy 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                 .1971,2313. .2441)
                                                                                                                                                                                                                                                                                                                                            .1971,2313.
                                                                                                                                                                             сору
                                                                                                                                                                                                                                                                       द्रव
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                                                                                                                                                                                                                                                                   (see <humhbal>)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 located on the short arm of includes the following five
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           closely linked
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSV2HG52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local
                                                                                                                                                                                                                                                                                                                                                           ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 CGGGCTGCAGTTCCCTGGGTGGCCGCCGAGACGCTGGCCCGGGCTGGAGGGATGGCGGGG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 CTGGCCTTGGCCTGGCCTGGCCAGAGCCGGAGAGCCCGCTCGGTGGA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
                                                                                                                                                                                                                                                                                                                                                                                                                   capsid protein; neurovirulence factor; protease; protein kinase; ribonucleotide reductase large subunit; ribonucleotide reductase small subunit; RL1 gene; RL2 gene; RS1 gene; tegument protein; thymidine kinase; UL1 gene; UL10 gene; UL11 gene; UL12 gene; UL12 gene; UL13 gene; UL13 gene; UL13 gene; UL13 gene; UL14 gene; UL15 gene; UL15 gene; UL15 gene; UL15 gene; UL16 gene; UL17 gene; UL13 gene; UL19 gene; UL10 gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGGTCGCGGGGCCGGGCCC 2270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGGGGACGGGGGGGGGGGGCTCGTCACGTGGAGAGGCGCGCGGGGGGCGGGGCGGGGC 263
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                                                                                             1 (bases 1 to 154746)
McGeoch, D.J., Moss, H.W., McNab, D. and Frame, M.C.
DNA sequence and genetic content of the HindIII 1 region in the short unique component of the herpes simplex virus type 2 genome:
identification of the gene encoding glycoprotein G, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human herpesvirus 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              capsid associated tegument protein; capsid protein;
genome; deoxyribonuclease; deoxyuridine triphosphat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSV2HG52 154746 bp DN
Herpes simplex virus type
                                 evolutionary comparisons
J. Gen. Virol. 68 (Pt 1)
                                                                                                                                                                                                                                                                             Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         olymerase; envelope protein; glycoprotein B; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lycoprotein D; glycoprotein E; glycoprotein G; glycoprotein H; lycoprotein I; glycoprotein I; glycoprotein K; glycoprotein K; glycoprotein L; glycoprotein E; glycoprotein E; glycoprotein E; glycoprotein E; glycoprotein E; glycoprotein; minor capsid protein; membrane-associated phosphoprotein; minor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (strain HG52), complete genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10;
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JOURNAL MEDLINE REFERENCE AUTHORS
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Barnett, B.C., Dolan, A., Telford, E.A., Davison, A.J. and McGeoch, D.J. A novel herpes simplex virus gene (UL49A) encodes a putative membrane protein with counterparts in other herpesviruses J. Gen. Virol. 73 (pt 8), 2167-2171 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McGeoch, D.J., Cunningham, C., McIntyre, G. and Dolan, A. Comparative sequence analysis of the long repeat regions and adjoining parts of the long unique regions in the genomes of herpes simplex viruses types 1 and 2 J. Gen. Virol. 72 (Pt 12), 3057-3075 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 154746)
Everett,R.D. and Fenwick,M.L.
Comparative DNA sequence analysis of the host shutoff genes of different strains of herpes simplex virus: type 2 strain HG52 encodes a truncated UL41 product
J. Gen. Virol. 71 (Pt 6), 1387-1390 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (25-FEB-1997) A. Dolan, MRC Virology Unit, Church Street,, Glasgow,, G11 5JR, UK
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dolan, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90278430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 154746)
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vpaydsgtavesapaassllrrwllvpqaddsddadyagnddaewansppsegggkap
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                                             oin(2303. .2377,2785. .3462,3644. gene="RL2"
                                                                                                                                                                                                         /product="neurovirulence
1738. .1743
                                                                                                                                                                                                                                                                                                                                                                     rpt_family="7"
161. .547
                                                                                                                                                                                                                                                                                                                                                                                                                             PEARARARARAHEDGGPAEEEEAAAAARGSSAAAGPGRRAV'
                                                                                                                                                                                                                                                                                                                                                                                                                                           aprgkvcfsprvqvrhlvawetaarlarrgswareradrdrfrrrvaaaeavigpcle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140. .126810
/gene="RL1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="human herpesvirus 2"
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                                                                                                                                               gene="RL2"
                                                                                                                                                                                                                                                    number-
                                                                                                                                                                                                                                                                                                                                               rpt_family="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="a sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oin(440. .934,1089. .1379)
gene="RL1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'db_xref="taxon:10310"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="SWISS-PROT:P28283"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="start of TRL (terminal copy of Long Repeat region)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ımber≖
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .154746
                                                                                                                                                                                                                                                                                                            family="5"
                                                                                                                                                                      .124947
                                                                                                                                                                                                                           factor"
                                                                 . 5368)
                                                                                                                     gene
                                                                                Sgo
                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="4"
3644. soc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="proposed LAT
5618. .5623
/gene="RL2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(4811)
/gene="RL2"
                                                                                                                                               /db_xref="PID:g1869823"
/db_xref="GI:1869823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(7732)
'gene="RL2"
                                                                                                                                  'db_xref="SWISS-PROT:P28278"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           function="modulator of cell state and gene expression"
4655. .4771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="start of |
427. .10101
gene="UL1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="proposed LAT splice donor site (5'AT species)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="RL2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="RL2"
                                                                                                                                                                                                                                                  427. .10101
gene="UL1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    jene="RL2"
                                                                                                                                                                                                                                                                                                                                                                            rpt_family="2"
276. .9297
                                                                                                                                                                                                                                                                                                                                                                                                                       note="primary transcription initiation site for latency speciated transcripts (LAT's)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          omplement(7025)
gene="RL2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      number-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGPGGGGLPOSSGRAARPRAAVAFRVRSPPRAAAAPVVSASADAAGPAPPAVPVDAH
APRSRMTQAQTDTQAQSLGRAGATDARGSGGPGAEGGPGVPRGTNTPGAAPHAAEGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'db_xref-"PID:e304156"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRSRHPWSREQGAPAPAGDAPAGHGE'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db_xref="SWISS-PROT:P28284"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         umber=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _family="3"
                                                                                                                                                                                                                                                                                                                                                           _family-"1"
                                                                                                                                                                                                                                                                                                            UL (Long Unique region)"
                                                                                                                                                                                                 glycoprotein L"
)6761.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          splice acceptor site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           end
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133510 GACGGGGGACGGGGGACGGGGGGACGGGGGCCGGGGGGACGGGGACGGGACGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37
polymerase; envelope protein E; glycoprotein B; glycoprotein C; glycoprotein D; glycoprotein T; glycoprotein B; glycoprotein B; glycoprotein H; glycoprotein H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCGGGGGACGGCCCGGGGGACGGGCCGGGGGGACGGGGGACGGGCCGGGGG 133329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCCCTGGCCTGGCCAGAGGCGCGAGGCCCGAGAGCCCGCTCGGTGGAGACTGGGGGTGGA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACGGGCCGGGGGACGGGCCGGGGGACGGGCCGGGGGCCGGGGCCGGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCGGGCGACAGCCGAGACGTGGAGCGCGCCGGCTCGCTGCAGCTCCGGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGGCTCCTTAAAGGCGCGCGAGCCGAGCGGCGAGGTGCCTCTGTGGCCGCAGGCGCAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                capsid associated tegument protein; capsid protein; complete genome; deoxyribonuclease; deoxyuridine triphosphatase; DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSV2HG52
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simplex virus
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11033. .1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11033. .11734
/gene="UL3"
11033. .11734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="swiss-prot:p28275"
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Pred. No. 0.092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VRL 04-DEC-1998 (strain HG52), complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 17; Length 154746;
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AUTHORS
TITLE
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AUTHORS
TITLE
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MEDLINE
REFERENCE
AUTHORS
TITLE
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MEDLINE
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AUTHORS
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MEDLINE
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JOURNAL
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3 (bases 1 to 154746)
McGeoch, D. J., Cunningham, C., McIntyre, G. and Dolan, A.
McGeoch, D. J., Cunningham, C., McIntyre, G. and Dolan, A.
McGeoch, D. J., Cunningham, C., McIntyre, G. and Dolan, A.
McGeoch, D. J., Conningham, C., McIntyre, G. and Dolan, A.
McGeoch, D. J., Conningham, C., McIntyre, G. and Dolan, A.
McGeoch, D. J., Conningham, C., McIntyre, G. and Dolan, A.
McGeoch, D. J., Conningham, C., McIntyre, G. and Dolan, A.
McGeoch, D. J., Cunningham, C., McIntyre, G. and Dolan, A.
McGeoch, D. J., Cunningham, C., McIntyre, G. and Dolan, A.
McGeoch, D. J., Cunningham, C., McIntyre, G. and Dolan, A.
McGeoch, D. J., Cunningham, C., McIntyre, G. and Dolan, A.
McGeoch, D. J., Cunningham, C., McIntyre, G. and Dolan, A.
McGeoch, D. J., Cunningham, C., McIntyre, G. and Dolan, A.
McGeoch, D. J., Cunningham, C., McIntyre, G. and Dolan, A.
McGeoch, D. J., Cunningham, C., McIntyre, G. and Dolan, A.
McGeoch, D. J., Cunningham, C., McIntyre, G. and Dolan, A.
McGeoch, D. J., Cunningham, C., McIntyre, G. and Dolan, A.
McGeoch, D. J., Cunningham, C., McGeoch, C., McGeo
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2 (bases 1 to 154746)
Everett, R.D. and Fenwick, M.L.
Comparative DNA sequence analysis of the host shutoff genes of different strains of herpes simplex virus: type 2 strain HG52 encodes a truncated UL41 product
J. Gen. Virol. 71 (Pt 6), 1387-1390 (1990)
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1 (bases 1 to 154746)

McGeoch,D.J., Moss,H.W., McNab,D. and Frame,M.C.

Short unique component of the herpes simplex virus type 2 genome:

1 dentification of the gene encoding glycoprotein G, and

evolutionary comparisons

1 Gen. Virol. 68 (Pt 1), 19-38 (1987)
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Barnett, B.C., Dolan, A., Telford, E.A., Davison, A.J. and McGeoch, D.J. A novel herpes simplex virus gene (UL49A) encodes a putative membrane protein with counterparts in other herpesviruses J. Gen. Virol. 73 (Pt 8), 2167-2171 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human herpesvirus
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 154746)
                                                                                                                                       /rpt_family="6"
943. .1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                      440. .126810
/gene="RL1"
                                                                                                                                                                                                                                                                                                                                                                                     EAPHAAPAAACPPPPPRKERGPQRPLPPHLALRLRTTTEYLARLSLRRRRPPASPPÄD
APRGKVCFSPRVQVRHLVAWETAARLARRGSWARERADRDRFRRRVAAAEAVIGPCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="start of TRL (terminal copy of Long Repeat region)"
                                                                                                                                                                                                                                                                                                                                            Peararararahedggpaeeeeaaaaargssaaagpgrrav'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="CAB06759.1"
/db_xref="PID:e308397"
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                                                             /rpt_family="5"
1089. :1379
                                                                                                                                                                                                                                                 rpt_family="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="RL1"
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                    /codon_start=1
/product="virion glycoprotein L
/protein_id="cab06761.1"
/db_xref="pID:e304262"
/db_xref="pID:g1869823"
/db_xref="GI:1869823"
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2303.
                                                                                                                                                                               /gene-"UL1"
                                                                                                                                                                                                                                                                                                                                                              /rpt_family="1"
9298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(7732)
/gene="RL2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(7025)
/gene="RL2"
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2303. .124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="primary transcription initiation associated transcripts (LAT's)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLRSRHPWSREQGAPAPAGDAPAGHGE"
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                                                                                                                                                                                                                                                                                                 'note="start of UL (Long Unique region)"
                                                                                                                                                                                                                                                                                                                                    'gene="RL2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AT species)"
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618. .5623
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/product="neurovirulence factor"
1738. 1743
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'db_xref="PID:e304156"

'db_xref="PID:g1869822"

'db_xref="GI:1869822"
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'gene="RL2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          _family="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        splice donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              splice acceptor site"
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           REFERENCE
AUTHORS
TITLE
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SOURCE
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HSU40583
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Matches 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        337 CCGGGCGACAGCCGAGACGTGGAGCGCGCCGGCTCGCTGCAGCTCCGGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGCTCCTTAAAGGCGCGAGCCGAGCGGCGAGGTGCCTCTGTGGCCGCAGGCGCAGGC 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCCCTGGCCTGGCCAGAGGCGCGAGGGCCGAGAGCCCGCTGGAGACTGGGGGGTGGA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCTGGGTGGCCGCCGAGACGCTGGCCCGGGCTGGAGGGATGGCGGGGCCGGGGACGGGGGC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTGCCCGGAGCGTACCCAGCGCCGGGAGTACCTCCCGCTCACACCTCGGGCTGCAGTTC 156
                                                                                                                                                                                                                                   g1125076
U40583.1
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1977)

Logel, J., Drebing, C., Barnhart, M., Antle, C. and Leonard, S.

Nucleotide Sequence and Transcript Size of the Alpha-7 Neuron.
                                                                                                                                                                                                                                                                                                                                          HSU40583 1977 bp mRNA PRI 19-DEC-1995 Human alpha 7 neuronal nicotinic acetylcholine receptor mRNA,
                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                        complete
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11033. 177-
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11033. .1172
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                                                                                                                                                                                                                                      GI:1125076
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LTVKRGAAASHSKLGWDRFVGGVVQRLAARRPGLVFMLWGAHAQNAIRPDPRQHYVLK
FSHFSPLSKVPFGTCQHFLAANRYLETRDIMFIDWSV"
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/translation="MGFVCLEGLVVMCAMGAWGGSQATEYVLRSVIAKEVGDILRVPC/Translation="MGFVCLEGLVVMCAMGAWGAWGMTFLMDRHAQRAYLVNPELFAAGFXFTADDVSRAYEAFAFYFTAALYKEIRDALGSRKQAVSHAPVRAGCVNFDYSRTRRCFLEDLSHSVFFPADTQETTTRRALYKEIRDALGSRKQAVSHAPVRAGCVNFDYSRTRRCFLEDLSHSVFFPADTQETTTRRALYKEIRDALGSRKQAVSHAPVRAGCVNFDYSRTRRCFLEDLSHSVFFPADTQETTTRRALYKEIRDALGSRKQAVSHAPVRAGCVNFDYSRTRRCFLEDLSHSVFFPADTQETTTRRALYKEIRDALGSRKQAVSHAPVRAGCVNFDYSRTRRCFLEDLSHSVFFPADTQETTTRRALYKEIRDALGSRKQAVSHAPVRAGCVNFDYSRTRRCFLEDLSHSVFFPADTQETTTRRALYKEIRDALGSRKQAVSHAPVRAGCVNFDYSRTRRCFLEDLSHSVFFPADTQETTTRRALYKEIRDALGSRKQAVSHAPVRAGCVNFDYSRTRRCFLEDLSHSVFFPADTQETTTRRALYKEIRDALGSRKQAVSHAPVRAGCVNFDYSRTRRCFLEDLSHSVFFPADTQETTTRRALYKEIRDALGSRKQAVSHAPVRAGCVNFDYSRTRALYKEIRDALGSRKQAVSHAPVRAGCVNFDYSRTRRCFLEDLSHSVFFPADTQETTTRRALYKEIRDALGSRKQAVSHAPVRAGCVNFDYSRTRRCFLEDLSHSVFFPADTQETTTRRALYKEIRDALGSRKQAVSHAPVRAGCVNFDYSRTRRCFLEDLSHSVFFPADTQETTTRRALYKEIRDALGSRKQAVSHAPVRAGCVNFDYSRTRALYKEIRDALGSRKQAVSHAPVRAGCVNFDYSRTRACFLEDLSHSVFFPADTGETTTRRALYKEIRDALGSRKQAVSHAPVRAGCVNFDYSRTRACFLEDLSHSVFFPADTGETTTRRALYKEIRDALGSRKQAVSHAPVRAGCVNFDYSRTRACFLEDLSHSVFFPADTGETTTRRALYKEIRDALGSRKQAVSHAPVRAGCVNFDYSRTRACFLEDLSHSVFFPADTGETTTRRALYKEIRDALGSRKQAVSHAPVRAGCVNFDYSRTRACFLEDLSHSVFFPADTGETTTRRALYKEIRDALGSRTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHSTRACFLEDLSHST
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/translation="MFSASTTPEQPLGLSGDATPPLPTSVPLDWAAFRRAFLIDDAWR
PLLEPELANPLTABLLAEYDRRCQTEEVLPPREDVFSWTRYCTPDDVRVVIIGQDPYH
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/protein_id="CAB06762.1"
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'db_xref="GI:1869824"
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/db_xref="PID:e304157"
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Best Local Similarity 100.
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Streptomyces coelicolor c
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94585581
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Streptomyces coelicolor
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales, Streptomycineae, Streptomycetaceae; Streptomyces.
1 (bases 1 to 38532)
                                                                                                                                     acetyltransferase; ATP-binding; Clp-family ATP-binding protease; cseB; cseC; DNA repair; DNA-binding; ECF signa factor; exporter; L-aspartate oxidase; lrpA; Lsr2; mutr; nadigna factor; cotinate-nucleotide pyrophophorylase; pantoate-amino acid ligase; putative adenine glycosylase; response regulator; sensory histidine
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Health Sciences Center,
Denver, CO 80262, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MRCSPGGVWLALAASLLHVSLQGEFQRKLYKELYKNYNPLERPV
/translation="MRCSPGGVWLALAASLLHVSLQGEFQRKLYKELYKNYNPLERPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eceptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/product="alpha 7 neuronal nicotinic acetylcholine
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'dev_stage="20 yr old adul
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clone_11b="Clontech lambda gt10 cDNA library: human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        );HCKLKFGSWSYGGWSLDLQMQEADISGYIPNGEWDLVGIPGKRSERFYECCKEPYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ex="male"
                                                                                                                                                                                                                                                                 GI:4585581
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Pred. No.
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C-268-71 Pharma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for small overlap between neighbouring submissions.

Cosmid E94 lies between E7 and E126 on the AseI-E genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon (atg, gtg, ttg or (att)) which is preceded by an upstream initiation codon. Where possible we choose an initiation ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the instream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each QDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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Rinashi, H. and Hopwood, D.A.

A set of ordered cosmids and a detailed genetic and physical map for the 8 mb Streptomyces coelicolor A3(2) chromosome mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (12-APR-1999) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof.
David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 38532)
Oliver, K. and Harris, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bentley, S.D., Parkhill, J.,
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                                                                                                                                                                                                                                                            /note="Nominal overlap
complement(<1..1512)</pre>
                                                                                                                                                                                                                                                                                                                                                                                        complement(1.
                                          /protein_id="CAB40850.1
/db_xref="PID:e1424928"
                                                                                          /product="alanine-rich
                                                                                                                                                                                                               note="SCE94.01c,
                                                                                                                                                                                                                                     /gene="SCE94.01c"
                                                                                                                                                                                                                                                                                                               /gene="SCE94.01c"
                                                                                                                                                                                                                                                                                                                                                    /gene="SCE94.01c"
                                                                                                                                                                                                                                                                                                                                                                                                         /clone="cosmid E94"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Streptomyces
                                                                                                                    'label=SCE94.01c
                                                                                                                                                                                                                                                                                                                                                                                                                                     'db_xref="taxon:1902"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
                                                                                                                                          transl_table=11
                                                                                                                                                                                   בבא4.01c, partial
len: >503aa"
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                                                                      h hypothetical protein
.1"
                                                                                                                                                                                                                                                                                     with Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coelicolor"
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8 Š 용

RESULT

E7."

Sdo gene

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/Traisiation="MAANDRAAAPGKSGGSAGADGLMRASLSAVAPGTSLRDGLERVL
/Traisiation="MAANDRAAAPGKSGGSAGADGLMRASLSAVAPGTSLRDGLERVL
RGNTGGLIVLGSDKTYESMCTGGFYLDVEFTATRLRELCKLDGGIVLSSDLSKILRAG
VQLLPDPTIFTETGTRHRTADRVSKOVGFPYVSVSOSMRLIALYVDGORRVLEDSAA
ILSRANQALATIERYKLRLDEVAGTLSALEIEDLVTVRDVSAVAQRLEMVRRIATEIA
EYVVELGTDGRLLALOGLELIAGVEFBRELLVFDYVPEPTAKRSTYTDEALAELDKLS
EYVVELGTDGRLLALOGUELIAGVEFBRELLVFDYVPEPTAKRSTYTDEALAELDKLS
HAELLELSTVARALGYTGSPETLDSAVSPRGFRLLAKVPRLPGAIIDRLVEHFGGLQK
LLAASVDDLQTVDGVGEARARSVREGLSRLAESSILERYV"
                                                                 complement (4778.
                                                                                 Helix-hairpin-helix motif., complement(4778. .5158)/gene="SCE94.04c"
                                                                                                                           /note="Pfam match to entry PF00633 HHH, Helix-hairpin-helix motif., score 26.50,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similar to hypothetical proteins eg. TR:053571 (EMBL:AL022075) from Mycobacterium tuberculosis (358 aa)
                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="putative DNA-binding protein"
/protein_id="CAB40852.1"
/db_xref="pID:e1424930"
/db_xref="PID:94585584"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00633 HHH, Helix-hairpin-helix motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TKDGATAGPRLLEHLYDVYLHFEGDRHARLRLYRGYKNRYGTTDEVGCFELHDEGITG
LADFSGLFLTRRAEFYPGTCLTYTLEGRRPLYAEVQALTYDSQIFSPRRTTSGLETSR
VSMMLAYLEQRGRISALGKRDIYSATYGGYKLSEPAADLAVALALASAASDTFLPKNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="Maartksakerpsyrctecgwqtakwlgrcpecqawgtveeyga
Pavrttpgrvttsavpigqvdgrqatarstgvpeldrvlggglvpgavvlvagepgv
GKSTLLLDVAAKSASDEHRILYVTGEESASQVRLRADRIHAIDDHLYLAAETDLAAVL
GHLDAVKPSLLILDSVQTVASPEIDGAPGGMAQVREVAGALIRASKERGMSTLLVGHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"SCE94.02, possible DNA repair protein, len: 469a similar to many eg. SW:RADA_ECOLI RadA, DNA repair prot (mechanism unknown) from Escherichia coli (460 aa) fast scores; opt: 1218, z-score: 1309.3, E(): 0, (41.4% identity in 452 aa overlap). Contains Prosite match to PS000017 ATP/GTP-binding site motif A (P-loop)."
                                                                                                                                                                                                                                                                                                                                                                                                                  'db_xref="GI:4585584"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fasta scores; opt: 1338, z-score: 1480.9, E():
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note-"SCE94.03, possible DNA-binding protein, len: 374aa; similar to hypothetical proteins eg. TR:053571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVLPRSRRREATREEEDRR"
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abel=SCE94.03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VAIGEVGLAGEVRRVTGVQRRLSEAHRLGFTHALVPADPGRVPDGMKVLEVADMGDAL
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YDAYLDGLFTYCLSVLCDHDAATAALGDVLAIAERRGHRGPAPAADRRSWLYALARWA
CLRKLAEAKOKRPSTHAAGRPAPVTROTAOTTPTAPTTPTNDETHORHRSELALLAWP
EAAGTTPEOREALELAVRHHLAPHEVAAVLGTDLAATRELLASAACEVERTRAALAVV
ETGTCAGVARLTGDNRYVLSTALRRELVRHVDDCPRCRRTAERAIPGRWPGTSVTPAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="SCE94.02"
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/protein_id="CAB40851.1"
/db_xref="PID:e1424929"
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TVVAAPVLALWAAYRGTPVVEGEEGRSASASEAQDPDATDGESAGGAYGYENAGNAST
TPGTGFGEKGGADVSYEVVGVBGASGKAAGHLEVTAGHDGDTTLVTLTATGDAPVHWS
ASYGASWLYLSQSSGTLRPGEAVTVRVYVDHLREPSGRWSARVAVSPAGAVVAI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="SCE94.03"
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          unknown,
          len: 126aa"
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Best Local Similarity
                                                    33660 GCCGTCTCGGGGGCCAGCGGCCAGGAGGGCGGCTGCGGCGGG 33703
                                                                                                                                                                        33600
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                                                                                                                                                                                                                                                                                                                         266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 GGCTGCAGTTCCCTGGGTGGCCGCGAGACGCTGGCCCGGGCTGGAGGGATGGCGGGGG 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86 CTGGGGGTGGAGGTGCCCGGAGCGTACCCAGCGCGGGAGTACCTCCCGCTCACACCTCG 145
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                                                                                                      ACTCAACATGCGCTGCTCGCCGGGAGGCGTCTGGCTGGCGCTGG
                                                                                                                                                      TGGAGGCGGGTGCGGGGGGGCGGGGAGGGGGACGGTGGAGGCGGTGGGCGCGGTG
                                                                                                                                                                                                     GGTTTCGCGGCGGCTTCTGCGGGGCTCCTTGCCGGACTGCCGGGCCGCCGGGACGGCG
                                                                                                                                                                                                                                                                                                      GGGCGCGCCCCGGCTCCTTAAAGGCGCGCGAGCCGAGCGGAGGTGCCTCTGTGGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="PID:e1424932"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="SCE94.06"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="hypothetical
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/gene="SCE94.05"
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TPasgddaynasddcvegagslryrvtagsgitytvkwdrkpsapecgtppagsaka
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label=SCE94.04c
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47.0%;
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Pred. No. 0.23;
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CDS gene

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misc\_feature

repeat_region 7131. 7434  repeat_region 7131. 7434  repeat_region 717: 75354 match = HSALO023; putative*  repeat_region 717: 75354 match = HSALO023; putative*  repeat_region 717: 75354 match = HSALO023; putative*  pone 715(7711. 0813). 10597. 1570/.1570. 15834  gene 916(7711. 0813). 10597. 1570/.1570. 15848  cos 15802. 15933.16073. 1570/.1570. 15848  putative*  protein_do*Naman homolog of Mus muscallus BcBA Lisch7  putative*  protein_do*Naman homolog of Mus muscallus BcBA Lisch7  protein_do*Naman homolog of Muscallus*  repeat_region	repeat_region complement(6051. 6102)  /note="repeat match = HSAL04290; putative"  /rpt_family="Alu"	<pre>/rpt_tamily="Alu" repeat_region complement(88046091) repeat_region complement(88046091) /note="repeat match = HSALO4878; putative" /note="repeat match = HSALO4878; putative"</pre>	repeat_region 49265218 /note="repeat match = HSAL06523; putative"	repeat_region 44494565 /note="repeat match = HSALO1715; putative" /rot family="Alu"	/rpt_family="Alu"			repeat_region 40304168 /note="repeat match = HSAL03448; putative"	men "re	/note="repeat match = HSALO2043; putative" /rpt_family="Alu"	/note="repeat mattr notes."/ /rpt_family="Alu" 1367 2305	repeat_region 1350	repeat_region comp.tement(oii:	rpt_family="Alu"	repeat_region complement(134)  repeat_region complement (134)	/clone_lib="LL19NC03 R chromosome 19-specific cosmid	ast"	/chromosome="19" /cell line="5HL2-B"		FEATURES Location/Qualifiers source 1.41936	from hybrid 5HL2-B, which carries chromosome 19 as its only human chromosome.	omes	Biology and Biotechnology Research Program Lawrence Livermore National Laboratory		JOURNAL Submitted (10-DEC-1996) J.E. Lamerdin, Human Genome Center, Lawrence Livermore National Laboratory, 7000 East Ave, Livermore, Camero 4451 tanegardt lini gov owetornak.lini.gov	Lamerdin, J.E. Direct Submission	Eutheria; 1 (bases	NISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Ver	VERSION ADDUCTS: 1 51:190391; KEYWORDS chromosome 19; transcription factor. SOURCE human.	g1905917	N Homo sapiens DNA IIOm Chidmosome 19 Cosmito Acono genomic sequence, anonogo	CH19R30879 41936 bp	
	_feature	nt_region complement(12645/note="repeat match /rpt_family="Alu"	nt_region complement(12391 /note="repeat match /rpt_family="Alu"	/note="repeat match = /rpt_family="Alu" 120	/note="repeat matth" - /rpt_family="Alu" - t region complement(12334126	/rpt_family="Alu" /rpt_family="Alu" 12168 12279	t_region 1198112253 /note="repeat match = ALU;	t_region 1195/120/2 /note="repeat match /rpt familv="Alu"	/note="similarity: sapiens cDNA clone	/rpt_ramiry= Ard _feature	t_region 1035910498 /note="repeat match	/note="repeat macon - /rpt_family="Alu"	/rpt_family="Alu" t_region 9639. 9813	t_region 9099 9709 /note="repeat match	/note= repeat march /rpt_family="Alu"	t_region complement(95139555	<pre>t_region comprement(22): /note="repeat match /rst family="%li"</pre>	/rpt_family-"Alu"	epeat_region 83258609  'note="repeat match = ALU;	(Ted to:	t region	EDDWRSRDSRGPALTFIRDERWGGBSPRS LDDLFPSARESGSRSPTSNGGRSRAYMP PGEFFERENTERSTREET FROM THE PROPERTY OF THE PROPERY	CCPEARYAGKAATSUUTUT TOOLU TUUTUT TOOLU TUUTUT TOOLU TUUTUT TOOLU TUUTUT TOOLU TUUTUT TOOLU TUUTUT TUUTUT TOOLU TUUTUT TUUTU	/translation="ADITEDQTAWGDSGV" /translation="ADITEDQTAWGDSGV"	/protein_id="AAB51178.1" /db_xref="PII::91905918" /db_xref="FII::91905918"	/codon_start=2 /product="liver-specific bHLH:	mRNA" /note="putative"	"LISCH7" ion="human home	/gene="LISCH/" join(<79118030,108 1580215933,16075.		_region 71377589 /note="repeat match	/note="repeat match = /rpt_family="Alu"	region 71317434

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Matches
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Best Local
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   GTGGAGAGGCGCGGGGGGGGGGGGGGGGGGGGCGCCCCGGCTCCTTAAAGGCGCG
                                 GGCGCGAGGCCGAGAGCCCCGCTCGGTGGAGACTGGGGGTGGAGGTGCCCGGAGCGTACCC 114
                                                              GGCGGCGGCAGCAGCGGTGGCCGAGGCAGCGGGATCCAGACCC---GGGTCCAGCATGTC 18070
                                                                                                                     AGGGCGGGAGTACCTCCCGGTCACACCTCGGGCTGCAGTTCCCTGGGTGGCCGCCGAGA 174
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                                                                                                                                                                                                                                    155;
                                                                                                                                                                                                                                                                                      /translation="MMMLDPGLDPAASATAAAAASHDKGPEAEEGVELQEGGDGPGAE
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note-"similarity: gb|R36881|R36881; yf52a08.s1 Homo sapies cona clone 25687 3'. . . .; putative"
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sapiens cDNA clone 25701 3' similar t
16896. .16929
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16852. .16877
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                                                                                                                                                                                                                                                                                                                                                                                                                                           /function="ubiquitous transcription note="putative"
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16646. .16699
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16594. .16650
                                                                                                                                                                                                                                                                                                                                                                db_xref="GI:19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oin(18067. .18128,18411. .18457,18546. .18664,18768. .1
9412. .19562,19683. .19770,20048. .20106,27663. .27757,
7911. .28039,28132. .28221)
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Pred. No. 0.22;
0; Mismatches 134;
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44249 3'. . . ; putative"
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FEATURES
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ORGANISM
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AUTHORS
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Submitted (27-AUG-1996) P. Groenen,
Laboratory for Molecular Oncology,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14440 bp
H.sapiens USF2 gene
Y07661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
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CGAGCCGAGCGGCGAGGTGCCTCTGTGGCCGCAGGCGCAGGCCCGGGCGACA
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1 (bases 1 to 14440)
Groenen, P.M., Garcia, E., Debeer, P., Devriendt, K., Fryns, J.P. and Van de Ven, W.J.
Van de Ven, W.J.
Structure, sequence, and chromosome 19 localization of human USF2 and its rearrangement in a patient with multicystic renal dysplasi Genomics 38 (2), 141-148 (1996)
                                                         /translation="mdmldpgldpaasataaaaashdkgpeaeegvelqeggdgpgae
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5032. .5182,5303. .5390,5668. .5726,13284. .13378,
13532. .13660,13753. .13842)
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.032. .5182,5303. .5390,5668. .5726,13284. .13:
.3532. .13660,13753. .14380)
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                                   115 AGCGCCGGGAGTACCTCCCGCTCACACCTCGGGCTGCAGTTCCCTGGGTGGCCGAGA 174
                                             2766 a
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Search completed: September 17, 1999, 22:02:31 Job time: 16334 sec

## GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

19752

OM nucleic nucleic search, using sw model

Run on: September 18, 1999, 00:33:39; Search time 425.19 Seconds (without alignments)
268.910 Million cell updates/sec

Sequence: Perfect score: 1 AGAACGCAAGGGAGAGGTAG.....CTCCTGCACGGTAAAGCCAC 457 457 US-08-956-518A-94

Scoring table: IDENTITY\_NUC

311585 seqs, 125096042 residues

stabase : N\_Geneseq\_36:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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T91361 V62176 Q462176 Q462181 T35233 V62133 V62160 Q57657 T27547 V32641 V62175 Q37543	V20464 Q23297 Q75297 Q762176 Q25444 T05556 T35520 T66412 V01700 V73801	V10339 V10362 V68520 Q76213 V81384 V81384 Q47927 Q47927 X55273 X55273 V44430 V64539 V64539 V64539	T48239 V12197 V21543 V53491 X53491 X53491 X53294 V18130 V18130 V18130
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p-PSDB; w09025.

Nucleic acids encoding nicotinic acetylcholine receptor sub-units used in screening to determine the effect of drugs on the receptor placed in screening to determine the effect of drugs on the receptor placed in screening to determine the effect of drugs on the receptor placed in the interpretation of the alpha-7 subunit (w09025) of the human neuronal nicotinic acetylcholine receptor (nAcha). Host cells, esp. mammalian cells or amphibian occytes, carrying alpha-7 nucleic acids, opt. in combination with other alpha and/or beta subunit nucleic acids (see also T48232-38, T48240-41), express recombinant nAcha subunits useful for identifying cpds. that modulate the activity of human nAchas.

Sequence 1876 BP; 369 A; 553 C; 531 G; 423 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SIBI-) SIBIA NEUROSCIENCES Elliott KJ, Harpold MM; WPI; 97-065463/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-DEC-1996.
07-JUN-1996; U09775.
07-JUN-1995; US-484722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neuronal nicotinic acetylcholine receptor alpha
Neuronal nicotinic acetylcholine receptor; nACh, neurotransmitter;
ligand-gated receptor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T48239 standard; DNA; 1876
T48239;
09-APR-1997 (first entry)
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10.3
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8438
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Q73500
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밁 밁 δõ 유 ŠÕ Query Match 27.8%; Score 127; DB 1; Best Local Similarity 100.0%; Pred. No. 2.2e-13; Matches 127; Conservative 0; Mismatches 0; 121 CTGCACG 127 441 CTGCACG 447 381 321 بــ GGCCGCAGGCCCAGGCCGACAGCCGAGACGTGGAGCGCGCCGGCTCGCTGCAGCT 60 GCCCCCAGGCCCAGGCCCACCAGCCGAGACGTGGAGCGCGCCGGCTCGCTGCAGCT 380 0 Gaps

V12197 standard; cDNA; 1876 BP V12197; 14-MAY-1998 (first entry)

Human neuronal nicotinic acetylcholine receptor alpha-7 subunit cDNA. Human; neuronal nicotinic acetylcholine receptor; alpha-7 subunit; brain tissue; screening; NAChR; antibody; ds.

Homo sapiens.

Location/Qualifiers 73. .1581

WO9420617-A2

/product= "neuronal nicotinic acetylcholine receptor alpha-7 subunit"

Length 1876;

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FITTER SON KEN CONTRACTOR OF THE FITTER OF T
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Best Local
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Sequence 1876 BP; 369 A; 553 C; 530 G; 423 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-MAY-1994 (first entry)
Lipopolysaccharide induced protein gene.
Macrophage; induced; lipo-polyasaccharide;
antiinflammatory; trypanocidal agent; antii
activation; cytotoxicity; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q51543 standard;
Q51543;
24-MAY-1994 (fin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human neuronal nicotinic acetylcholine receptor subunits and DNA also transformed cells useful for screening cpds. which modulate activity of the receptor Claim 8; Page 78-79; 99pp; English.

The present sequence encodes a human neuronal nicotinic acetylchor receptor (NAChR) subunit. The cells expressing the alpha and/or lanches subunits may be used in a method of screening compounds to the compound to the compounds to the compounds to the compound to the compound
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(SIBI-) SIBIA NEUROSCIENCES INC.
Elliott KJ, Ellis SB, Harpold MM;
WPI; 94-303024/37.
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08-MAR-1993; US-028031
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                                                                                                                                                                                                                                                                                                                                                                         /note- "Intron 1 is only (represented by (N)40 in estimated length ca. 5400
/note "Intron 3 is only partially sequenced (represented by (N)40 in the sequence estimated length ca. 1000 bp"
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Pred. No. 2.2e-13;
Pred. No. 2.2e-13;
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25-MAR-1999.
17-SEP-1998; U19419.
09-JUN-1998; US-093972.
17-SEP-1997; US-059160.
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Query Match
Best Local S
Matches 146
                                                      Human adenosine Al receptor antisense oligonucleotide fragment. Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma chonic obstructive pulmonary disease; leukemia; hepatic cancer; breast cancer; lung cancer; melanoma; hepatic metast
                                                                                                                                                                                                                                                                                        X53491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The polypeptide induced in macrophages by lipopolysaccharide stimulates cell prolification (esp. when costimulated with II-4) promote activation, cytotoxicity, and mobilisation of LAK cells; promote recruitment of suppressive peritoneal exudate cells; promote generation of immunocompetent lymph node cells (LNC) and have trypanocidal and trypanolytic activity. The human and murine sequences are given in (051543-45), peptide fragments able to generate antibodies are given in (R51951-61) sequence 3861 BP; 542 A; 1241 C; 1292 G; 658 T;
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11-NOV-1993.
28-APR-1993;
30-APR-1992;
(INNO-) INNOG
WO9913886-A1.
                                         prostate cancer;
                                                                                                                                                                                                                                                                   05-JUL-1999 (first entry)
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Devos K, Fransen L,
WPI; 93-368796/46.
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146; Conserv
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53.3%;
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Pred. No. 0.000
0; Mismatches
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UNIV

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RESULT
x53491/c
ID x534
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AC y54
AC y64
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CC directed against at least 2 mRNAs selected from target genes, coding and conon-coding regions of RNAs corresponding to target genes, gene coding target genes, gene coding target genes, gene coding target genes, gene coding the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one common describes associated with one common describes genes as sociated with one common describes genes as sociated with one coding proteins associated with one compared the section of the antisense oligonucleotides (specifically x55180-271) can be used for the antisense coding uncleotides (specifically x55180-271) can be used for the antisense coding conditions. Typical diseases and conditions conditions are those associated with impaired respiration and inflammation, concluding lung diseases, pulmonary vasoconstriction, inflammation, allergic rininits, acute asthma, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary distress syndrome, pain, cystic fibrosis, pulmonary cancer, pulmonary vasoconstriction, emphysema, chronic obstructive commonary distress syndrome, pain, cystic fibrosis, pulmonary carcer, hepatocellular carcinoma, kidney cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, pencreatic concers as well as all types of cancers which may metastasize or have metastasized to the lungs, including breast and prostate cancer.

20 Sequence 114955 Bp; 6071 A; 29417 C; 36712 G; 21328 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108466 GGCGGCGCTGGCTCSNNNDNNGGCGGGGGGGGGGGGCGCCTGGCTSNNNDNNGGCGGGG
Human adenosine Al receptor antisense oligonucleotide fragment Antisense oligonucleotide; multiple target; antisense treatment in the respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis;
                                                                                                                                                                                                                                    X53491;
05-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                           X53491 standard; DNA; 114955 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 37; 120pp; English. The specification describes antisens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antisense
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGCGCCCTGGCSNNNDNNGGCGGGGGGGGGGCGGCCTGGSNNNDNNGGCGGGGGGGG
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156; Conserv
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Pred. No. 0.0002;
3; Mismatches 227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS Discubsure; Page 37; 120pp; English.

CC The specification describes antisense oligonucleotides (X52869-X55271)

CC directed against at least 2 mRNAs selected from target genes, coding and

CC initiation codons, genomic flanking regions, intron-exon borders, the

CC initiation codons, genomic flanking regions, intron-exon borders, the

CC frend, the 3'-end and the juxta-section between coding and non-coding

CC regions and all segments of RNAs encoding proteins associated with one

CC or more diseases, conditions or mixtures. The antisense oligonucleotides

CC may be derived from sequences X5572-74. These multiple target

CC oligonucleotides (specifically X55180-271) can be used for the antisense

CC are those associated with impaired respiration and inflammation,

CC allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,

CC allergic rhinitis, acute asthma, allergies, asthma, impeded respiration,

CC respiratory distress syndrome, pain, cystic fibrosis, pulmonary

CC unmonary disease (CODD), and cancers such as leukemias, lymphomas,

CC cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic

CC cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic

CC metastases, as well as all types of cancers which may metastasize or have

CC metastases and the lungs, including breast and prostate cancer.

21328 T;

SQ Sequence 114955 BP; 6071 A; 29417 C; 35712 G; 21328 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 14.3
Best Local Similarity 35.1
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     104935 CVGCNNHNNNSCGGCCGGCCGGCCGCCCCCGGCCCNNHNNNSGGCCVGCGGNN 104876
                                                                                                                                                                                                                                                                                                                                                     136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-SEP-1998; U19419.
09-JUN-1998; US-093972.
17-SEP-1997; US-059160.
(UYEC-) UNIV EAST CAROLINA.
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                                                                                                                                                                                                                 CCVGGCCVGCGGNNHNNNSGCCCVGGCCVGCGGNNHNNNSCGCCCVGGCCVGCGGNNHNN
                                                                                                                                                                                                                                                                                                                                 GAGACTGGGGGTGGAGGTGCCCGGAGCGTACCCAGCGCCGGGAGTA-----CCTCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCTGGCCTTGGGCAGCCCCTGGCCAGAGGCGGAGGGCCGAGAGCCCGCTCGGTG
CCVGCGGNNHNNNSGGCGCGCCCVGGCCVGCCGNNHNNNSCGGCGCCCCVGGCCVGCCG 104636
                                                                                  TCTGTGGCCGCAGGCGCAGGCCGGCGACAGCCGAGACGTGGAGCGCGCCGGCTCGCTG
                                                                                                                             NSGCGCCCVGGCCVGCGGNNHNNNSCGCGCCCVGGCCCVGCGGNNHNNNSGCGCGCCCVGG
                                                                                                                                                     HNNNSVGGCCVGCGGNNHNNNSCVGGCCVGCGGNNHNNNSCCVGGCCVGCGGNNHNNNSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.3%; Score 65.2; D
35.1%; Pred. No. 0.00
tive 49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.2; DB 1;
No. 0.00075;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 114955
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Q23296 standard; DNA; 1281 BP
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       New isolated nucleic acid encoding the new human cytokine Tango-77 used to inhibit inflammation and to screen for specific modulators

1. Used to inhibit inflammation and to screen for specific modulators

2. Example 5; Figure 3; 226pp; English.

2. X02956-X03048 and X22310-X22304 are overlapping BAC genomic sequences

3. X02956-X03048 and X22310-X22304 are overlapping BAC genomic sequences

3. X02956-X03048 and X22310-X22304 are overlapping BAC genomic sequences

3. X02956-X03048 and X22310-X22304 are overlapping BAC genomic sequences

3. X02956-X03048 and X2310-X22304 are overlapping BAC genomic sequences

3. X02956-X03048 and X2310-X22304 are overlapping BAC genomic sequences

3. X02956-X03048 and X2301-X22304 are overlapping BAC genomic sequences

3. X02956-X03048 and X2301-X22304 are overlapping BAC genomic sequences

3. X02956-X03048 and X2301-X22304 are overlapping BAC genomic sequences

3. X02956-X03048 and X2301-X22304 are overlapping BAC genomic sequences

3. X02956-X03048 and X2301-X22304 are overlapping BAC genomic sequences

3. X02956-X03048 and X22301-X22304 are overlapping BAC genomic sequences

3. X02956-X03048 and X22301-X22304 are overlapping BAC genomic sequences

3. X02956-X03048 and X22301-X22304 are overlapping BAC genomic sequences

3. X02956-X03048 and X22301-X22304 are overlapping BAC genomic sequences

3. X02956-X03048 and X22301-X22304 are overlapping BAC genomic sequences

3. X02956-X03048 and X22301-X22304 are overlapping BAC genomic sequences

3. X02956-X03048 and X22301-X22304 are overlapping BAC genomic sequences

3. X02956-X03048 and X22301-X22304 are overlapping BAC genomic sequences

3. X02956-X03048 and X22301-X22304 are overlapping BAC genomic sequences

3. X02956-X03048 and X22304 are overlapping BAC genomic sequences

3. X02956-X03048 and X22304 are overlapping BAC genomic sequences

3. X02956-X03048 and X22304 are overlapping BAC genomic sequences

3. X02956-X03048 and X22304 are overlapping BAC genomic sequences

3. X02956-X03048 and X22304 are overlapping BAC genomic se
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CIGGGGGIGGAGGIGCCCGGAGCGIACCCAGCGCCGGGAGIACCICCCGCICACACCICG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCTGCAGTTCCCTGGGTGGCCGCCGAGACGCTGGCCCGGGCTGGAGGGATGGCGGGGCG 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 GGCCTTGGGCAGCCCTGGCCTGGCCAGAGGCGCGGAGGCCGAGAGCCCGCTCGGTGGAGA 85
                                                                                                                                                                                                        Human IL-1ra BAC contiguous DNA sequence 19.

Human IL-1ra BAC contiguous DNA sequence 19.

Tango-77; human: IL-1ra: cytkine superfamily; inflammation: inhibiti interleukin-1 receptor: IL-1R; regulation: asthma: rheumatoid arthrit chronic myelogenous leukaemia; psoriasis; inflammatory bowel disease:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      846 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
14.0%; Score 64; DB 1; Length 319
Best Local Similarity 51.3%; Pred. No. 0.0023;
Matches 176; Conservative 0; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 factors; treatment; IL-1 receptor complex; BAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  326 CAGGCGCAGGCCCGGGCGACAGCCGAGACGTGGAGCGCCCCGG 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            681 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            847 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JUL-1998; US-091650.
04-AUG-1997; US-054646.
(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    its receptor complex.
                                                                                                                                                                      BB
                                                                                                                                              (02974/c
ID X02974 standard; DNA; 3198
                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-AUG-1998; U16102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 99-153692/13
                                               Ob 104575 NNNSC 104571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of IL-1 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an X;
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RESULT Q23296/c

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New recombinant Herpes Simplex Virus vaccines - rendered

Tavinlent by deletion of ICP 34.5 gene encoding active gene prod.

Bicclosure; Fig 1: 78pp; English.

Disclosure; Fig 1: 78pp; English.

Disclosure; Fig 1: 78pp; English.

Cof infected virus-1 (MGH-10) was isolated from a recurrent facial vesicle and passaged a maximum of four times in cells in culture.

Viral DNA was prepd. from virons that accumulated in the cytoplasm.

Cof infected vERO cells (Kieff et al., J. Virol., 8, 125-132 (1971)).

The BamHI SP junction fragments contg. the domain of the gene that specified ICP34.5 were cloned into a pUCIB plasmid using HSV-1(F) sequences as probes in colony blot hybridisation. Further subclonings were done to facilitate sequencing of different regions of the gene. HSV may be rendered avirulent by removing the ICP34.5 gene from the viral genome. The modified HSV genome is useful for eliher does not establish latent infections or which cannot be reactivated from a latent state.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V18130 standard; DNA; 11820 BP.
V18130;
04-SEP-1998 (first entry)
Human chromosome 19 derived USF2 gene sequence.
Hydronephrosis gene; HNG gene; USF2 gene; renal disease; renal aplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       713 cegecescos de constante de 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 CGAGAGCCCGCTCGGTGGAGTGGAGGTGCTGCCCGGAGCGTACCCAGCGCCGGGA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 593 GGGGCICCGGCGCCCCCCCCCCGCGCGCCCAGGCGCAGGCGCGCAGGTGCTCCG 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 GCCTGGAGGGATGGCCGGGGGGGGGGGGGGGGGGGGGGCTCGTCACGTGGAGAGGC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184
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28-JUL-1992 (first entry)
HSV-1 (MOH-10) ICP34.5 gene.
Herpes simplex virus; avirulent; vaccine; immunisation; ss.
Herpes simplex virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 60.6; DB 1; Length 1:
Pred. No. 0.0098;
0; Mismatches 174; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           305 GCCGAGGTGCCTCTGTGGCCGCAGGCGCAGGCCCGGGCG 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  556 C;
                                                                                                                                                                                                                          Location/Qualifiers
134. .893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 A;
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Best Local Similarity 48.7%;
Matches 165; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    19-MAR-1992.
10-SEP-1991. U06532.
10-SEP-1990; US-579834.
(ROIZ/) ROIZMAN B.
ROIZMAN B;
                                                                                                                                                                                                                                                                                                                                          /*tag=
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P-PSDB; R21707.
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vesical-ureteral reflux; pelvi-ureteral junction obstruction; multicystic renal dysplasia; renal agenesis; hydronephrosis; yon Mayer-Rokitansky-Kuester disorder; bifid ureter; ss.
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    TTTTTTTTTCKETC
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Best Local Similarity
Matches 183; Conser
                           misc_rna
                                                                                                                                      04-AUG-1995 (first entry)
HSV L/ST region.
HSV; junction-spanning transcript;
                                                                                                                                                                                                3/c
076213
                                                                     misc_binding
                                                                                                                                                                                                                                                                                                                               1014
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09-OCT-1997;
09-OCT-1996;
                                                                                                                             Herpes simplex virus
                                                                                                                                                                                     076213;
                                                                                                                                                                                                                                                                                                                                                                                      1074
                                                                                                                                                                                                                                                                                                                                                                                                                                              1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translocation partner to this gene on chromosome 6 is the hydronephrosis gene (HNG) product. The HNG gene can be used as a starting point to design suitable compounds or techniques for the treatment of renal diseases or disorders, or nucleotide probes for diagnosing cells involved in renal diseases or disorders. A protein or a fragment encoded by HNG gene can be used as a starting point for preparing suitable antibodies for diagnosing cells involved in renal diseases and disorders. The products and method can be used to treat or diagnose renal diseases and disorders selected from vesical-ureteral reflux, uni or bilateral pelvi-ureteral junction obstruction, multicystic renal dysplasia, hydronephrosis, von Mayer-Rokitansky-Kuester disorder and bifid ureter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydronephrosis gene - useful to treat or diagnose renal diseases and disorders, e.g. vesical-ureteral reflux, pelvi-ureteral junction obstruction, multicystic renal dysplasia or renal agenesis Disclosure; Fig 6A-B; 73pp; English.

This DNA encodes a USF2 gene derived from human chromosome 19. A translocation partner to this gene on chromosome 6 is the hydronephrosis
                                                                                                 cata_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG
Fryns JPGJ, Groenen PMA, Van De Ven WJM;
WPI; 98-240833/21.
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                                                                                                                                                                                                                                                                                             TGCCTCTGTGGCCGCAGGCGCAGGCCCGGCGACA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGATACGGGAGCCGCTCGCGCTGATCACGGGGACA
                                                                                                                                                                                                                                                                                                                                        CGGGGCGCGGGCACGGCCGGGCCGG----
                                                                                                                                                                                                                                                                                                                                                                                                            GGGATGGCGGGGGGGGGGGGGGGGGGGGCTCGTCACGTGGAGAGGCGCGCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGCTCACACCTCGGGCTGCAGTTCCCTGGGTGGCCGGAGACGCTGGCCCGGGCTGGA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGCTCGGTGGAGACTGGGGGGGGAGTGCCCGGAGCGTACCCAGCGCCCGGGAGTACCTC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGGTAGAGCCTGGCCTTGGGCAGCCCCTGGC--CTGGCCAGAGGGCGCGAGGCCGAGAGCC
                                                                                                                                                                                                  standard; DNA; 12001
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                           /*tag= b
/note= "ICP4
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220. .;
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                                                                                                              Location/Qualifiers
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P; 745 A;
                                                                                                                           type
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                                      binding
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Pred. No. 0.018;
0; Mismatches 1
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                                                                                                                                        L/ST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GGATCTTACCTGGCGGCGGCAGCAGCGG
                                                                                                                                                                                                                                                                    920
                                                                                                                                       therapy; virucide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     683 T;
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Key 5'UTR

Location/Qualifiers

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Best Local Similarity
Matches 164; Conserv
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An HSV-specific junction-spanning transcript (L/ST) maps at the 5 and to the b repeat sequences of HSV DNA at approx. 3 and 125 kb, and extends into the c repeat sequences of HSV DNA. Compounds that inhibit HSV L/ST synthesis may be used as anti-HSV virucides. The HSV-1 DNA sequence in the region of the L/STs is given in 076213.
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08-DEC-1994.

20-MAY-1994; U

20-MAY-1993; U
                                                                                                                                                                                                                                                                                                                                                                                   v60339;
04-DEC-1998 (first entry)
04-DEC-1998 (first entry)
cDNA sequence of fibroblast growth factor-2 (FGF-2).
Fibroblast growth factor-2; FGF-2; leaderless protein;
export; angiogenesis; restenosis; treatment; tumour; in
cell proliferation; diabetes; retinopathy; infection;
cell proliferation; diabetes; atherosclerosis; ss.
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(CIBL-) CIBLEX CORP.

Baird A, Florklewicz RZ;

WPI; 98-495377/42.

Inhibiting export of leaderless protein with agent that inhibits binding to transporter protein - especially for treating angiogenesis and restenosis by preventing export of fibroblast
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    for inhibiting HSV L/ST s

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(DAND ) DANA FARBER CANCER
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26-FEB-1997; US-807014.
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Pred. No. 0.03;
0; Mismatches 161
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Chaim 2: Pages 53-54; 116pp; English.

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23-JUL-1997; U12904.
26-JUL-1996; US-690473.
(ARCH-) ARCH DEV CORP.
Leopardi R, Rolzman B;
WPI; 98-130697/12.
P-PSDB; W40200.
Use of herpes simplex virus ICP4 polypeptide - usiblocking apoptosis in cells, production of protein Disclosure; Fig 2; 63pp; English.
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protein number 4; ICP4; alpha-4; cell apoptosis;
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47.7%;
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16-APR-1997; US-843659.
(ARCH-) ARCH DEV CORP.
Leopardi R, Roizman B;
                                  Use of herpes simplex virus U(s)3 polypeptide - for developing products for modulating apoptosis in cells and for identifying compounds which act as stimulators or inhibitors of apoptosis Example 2; Pages 60-63; 85pp; English.

This is the nucleotide sequence of Herpes simplex virus ICD4 used the method of the invention as modulators of apoptosis. The method and products can be used to identify compounds which modulate (stimulate or inhibit) apoptosis in cells. They can be used to immortalise cells for the study of these cells or for growing cell
in large numbers for the productions used for stimulating apoptosis in cel with a MSV infection.
                                                                                                                                                                                                                                                                                                                                              The nucleotide sequence of the Herpes simplex virus ICP4 Herpes simplex virus ICP4; HSV ICP4; modulator; apoptosistimulation; inhibition; HSV infection; ss.
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V68520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The herpes simplex virus (HSV) alpha-4 gene encodes infected cell protein number 4 (ICP4). Both the alpha-4 gene and ICP4 can be used to block cell apoptosis. Similarly the administration of an agent that inhibits ICP4 or the alpha-4 gene can induce apoptosis in HSV infected cells. This can be used for the immortalisation of cells, production of proteins, gene therapy, or inhibition of cell death induced in vivo. They can also be used for production of therapeutics comprising inhibitors of HSV ICP4 function, useful for treating HSV function. Sequence 4257 BP; 412 A; 1768 C; 1663 G; 414 T;
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172; Conserv
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08-DEC-1994; U05770.

20-MAY-1993; US-065146.

~~ WAY-1993; CANC
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             Disclosure: Page 38-44; 64pp; English.
An HSV-specific junction-spanning transcript (L/ST) end to the b repeat sequences of HSV DNA at approx.
and extends into the c repeat sequences of HSV DNA that inhibit HSV L/ST synthesis may be used as anti-
virucides. The HSV-1 DNA sequence in the region of
                                                                  SCHAILEL F., WPI, 95-022825/03.

Herpes Simplex Virus (HSV) specific junction for inhibiting HSV L/ST synthesis, in the
                                                                                                 (DAND) DANA FARBER CANCER
           ls given
                                                                                                                                                                              misc_rna
                                                                                                                                                                                                        misc_rna
                                                                                                                                                                                                                                  misc_binding
                                                                                                                                                                                                                                                                         04-AUG-1995 (first entry)
HSV L/ST region.
HSV; junction-spanning transcript;
                                                                                                                                                                                                                                                                                                       Q76213;
Q76213;
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12001 BP;
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370. :372
                                                                                                                                                                                                       /note= "ICP4
229
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                                                                                                                                                                                               Serine/threonine protein kinase inducing axon extension and DNA encoding it - and antisense DNA inhibiting axon extension and useful for treatment of nervous system disorders.

Claim 1; Page 43-52; 84pp; Japanese.
Claim 1; Page 43-52; 84pp; Japanese.
The present sequence encodes a serine/threonine protein kinase (STPK) protein. STPK induce axon extension. The STPK protein and nucleic acid protein. STPK induce axon extension. The STPK protein and nucleic acid may be used for screening candidate drugs for treatment of neurological disorders such as Alzheimer's disease, senile dementia, and disorders such as Alzheimer's disease, senile dementia, and sisorders such as Alzheimer's disease, senile dementia, and the antisense DNA may be used for diagnosis of neurological disorders. The antisense DNA may be used in the treatment of neurological disorders.

Sequence 5228 BP; 936 A; 1826 C; 1519 G; 947 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding a serine/threonine protein kinase. Serine/threonine protein kinase; STPK; axon extension; neurological disorder; Alzheimer's disease; senile demen
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05-NOV-1998.
05-NOV-1998.
23-MAR-1998.
28-APR-1997: JP-124798.
28-APR-1997: JP-124798.
(HELL') HELLX RES INST.
MULIAMATSU M, NOGUCHI T, Shirasawa T, Tokumitsu Mpuramatsu M, Noguchi T, Shirasawa T, Tokumitsu WPI; 99-024050/02.
P-PSDB: W67642.
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137; Conservative
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New polynucleotide encoding PACE endo-peptidase - used for e.g.

Treducing blood pressure

Claim 1; Figure 1; 81pp; English.

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16-SEP-1993.
09-MAR-1993; U02147.
09-MAR-1992; US-84862
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(CHIR) CHIRON CORP.
Barr PJ, Klefer MC;
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WPI; 93-303473/38.
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Search completed: September 18, 1999, 00:34:06 Job time: 19006 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

## ALIGNMENTS

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NID VERSION	ACCESSION	DEFINITION	LOCUS	AI357868/c	RESULT 1
g4109489 AI357868.1	AI357868	qv13b02.x1	AI357868		
94109489 NI357868.1 GI:4109489	TR:Q69340 Q69340 ORF1, ORF2, AND ORF3. ;, mRNA sequence	1d8 Homo sapiens cDNA clone 1	641 bp mRNA EST 15-FEB-1999		

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Matches
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                                                                                             AGCGGCGAGGTGCCTCTGTGGCCGCAGGCGCAGGCCCGGGCGACAGCCGAGACGTGGAGC
                                                                                                                                                                                                          GGCGCTGGCCGCGTCG 437
                                                                                                                                                                                         GCGCCGGCTCGCTGCAGCTCCGGGACTCAACATGCGCTGCTCGCCGGGAGGCGTCTGGCT
                                                                                                                                                     GGCGCGCGGGGGCGGGGGGGGGGGCGCGCGCTTAAAGGCGCGCGAGCCG 301
                                                                                                                                                                                                                                                                       GGAGTACCTCCCGCTCACACCTCGGGCTGCAGTTCCCTGGGTGGCCGCCGAGACGCTGGC 181
                        Tumor Gene Index
Unpublished (1997)
On Aug 21, 1998 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert Length: 1681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 641)
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                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ert Length: 1681 Std Error: 0.00 primer: -40UP from Gibco h quality sequence stop: 90. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Robert_Strausberg@nih.gov
Procurement: Christopher Moskaluk, M.D., Ph.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Organ: kidney; Vector: pCMV-SPORT6; Site_1: Sal
Site_2: NotI; Cloned unidirectionally. Primer: Oligo
Average insert size 1.2 kb. Life Technologies catalog
11524-014"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:1981419"
/clone_lib="NCI_CGAP_Kid8"
/tissue_type="renal cell tumor"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                      16.9%;
                                                                                                                                                                                                                                                                                                                                                      Score 77.4; DB 45;
Pred. No. 0.0017;
0; Mismatches 193;
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                 43 GGCCTGGCCAGAGGCGGAGAGCCCGCTCGGTGGAGACTGGGGGGTGGAGGTGCC 102
TGGCCGACGAGACGCTGGCCCGGGCTGGAGGGATGGCGGGGCCGGGGGCCGGGGGCC
                                                                                                                                                          Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
This clone is available royalty-free through
IMAGE Consortium (info@inage.lln1.gov) for fu
Insert Length: 276 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq30a12.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1934014 3' similar to gb:X59268 TRANSCRIPTION INITIATION FACTOR IIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: -40UP from Gibco
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
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Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: mixed (see below); Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAp purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
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/clone="IMAGE:1934014"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Pooled human melanocyte,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares_NhHMPu_S1"
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                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                               Score 74.2; DB 45;
pred. No. 0.005;
0; Mismatches 167;
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further information
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GCCCGCTCGGTGGAGACTGGGGGTGGAGGTGCCCGGAGCGTACCCAGCGCCGGGAGTACC
                                         GGGAGAGGTAGAGCCTGGCCTTGGGCAGCCCTGGCCAGAGGCGCGAGAGGCCGAGA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACAGCCGAGACGTGGAGCGCGCCGGCTCGCTG
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Macke, J., Smallwood, P. and Nathans, J.
Adult Human Retina cDNA
Unpublished (1996)
On May 5, 1995 this sequence version replaced g1:797995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: jeremy_nathans@qmail.bs.jhu.edu
Clones from this library are NOT avail
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BACKWARD: GAGGTGGCTTATGAGTATTTC!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FORWARD: CTTTTGAGCAAGTTCAGCCTGGTTAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              725 North Wolfe Street, Baltimore, MD 21205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dr. Jeremy Nathans, Dept. of Molecular Biology and Genetics
Johns Hopkins School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                   /note="Organ: eye; Vector: lambda gt10; Site_1: EcoRI; Site_2: EcoRI; The library used for sequencing was a sublibrary derived from a human retina cDNA library. Inserts from retina cDNA library DNA were isolated, randomly primed, PCR amplified, size-selected, and clor into lambda gt10. Individual plaques were arrayed and used as templates for PCR amplification, and these PCR products were used for sequencing."
                                                                                                                                                                                                                                                                                                                                  /clone_lib="Human retina cDNA randomly
/sex="mixed (males and females)"
/tissue_type="retina"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                  'lab_host="E. coli strain K802"
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/db_xref="taxon:9606"
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cches 244;
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AI285778/c
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733 GGGGG 737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: Mark Raffeld, M.D.

CDNA Library Preparation: Stratagene, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 National Cancer Institute, Cancer Genome
Tumor Gene Index
Unpublished (1997)
On Jan 17, 1998 this sequence version rep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI285778 459 bp mRNA EST 03-FEB-1999 qu56b02.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1968747 3'similar to 9b:x59268 TRANSCRIPTION INITIATION FACTOR IIB (HUMAN);
                                                                                                                                                                                                                                                                                                                    Insert Length: 1167
                                                                                                                                                                                                                                                                                                                                                             www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 400)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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AI285778
                                                                                                                                                                                                                                                                                          primer: -40UP from Gibco
                                                                                                                                                                                                                                                                    quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (301) 496-1550
/db_xref="taxon:9606"
/clone="IMAGE:1968747"
/clone=lib="NCI_CGAP_Lym6"
/tissue_type="mantle_cell lymphoma"
/tissue_type="mantle cell lymphoma"
/lab_host="SOLR (Stratagene, kanamycin resistant)"
/note="Organ: lymph node; Vector: pBluescript SK:;
EcoRI; Site_2: XhOI; Cloned unidirectionally. Princolligo dT. Average insert size 0.8 kb. Non-amplified
                                                                                                                                                                                                 'organism="Homo sapiens"
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RESULT
W15723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W15723 1461 bp mRNA EST 10-SEP-1996 mb53c01.rl Soares mouse p3NMr19.5 Mus musculus cDNA clone. TMAGE: 333120 5' similar to gb:L04538 Mouse amyloid precursor-like protein mRNA, complete cds (MOUSE); mRNA sequence. W15723
                                                                                                         Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. La
                      This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                             Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                            Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                         1 (bases 1 to 1461)
Marra, M., Hiller, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston.
                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                            Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                 W15723.1 GI:1290109
                                                                                                                                                                                                                                                                                                                                                                                  house mouse
primer: ETPrimer
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REFERENCE
AUTHORS
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SOURCE
ORGANISM
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AI469170/c
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NID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126;
                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mamma. Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 457)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project Tumor Gene Index
Unpublished (1997)
On Mar 20, 1998 this sequence version replaced gi:2979737
                                                                                                                                                                                                                                                                  AI469170 457 bp
ta19d04.x1 NCI_CGAP_1
similar to gb:X59268
Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                     mRNA sequence.
                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                            AI469170.1
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="19.5 dpc total fetus"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pr773D (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco Rimer [5'
was primed with a Not I - oligo(dT) primer [5'
was primed with a Not I - oligo(dT) primer [5'

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone_lib="Soares mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                            GI:4331260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.8%;
                                                                                                                                                                                                                                                               D MRNA EST 09-MAR-1999
Lym5 Homo sapiens cDNA clone IMAGE:2044519 3'
3 TRANSCRIPTION INITIATION FACTOR IIB (HUMAN);,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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Robert\_Strausberg@nih.gov

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RESULT 7
AI525191/c
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ORIGIN
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Best Local
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                                                                                                                                                                                                                   GGGGCNNNCGGGGGNCCACCCCATTCCTCCCC
                                                                                                                                                                                                                                                                                                    GTGGAGCGCCGGCTCGCTGCAGCTCCGGGACTCAACATGCGCTGCTCGCCGGGAGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       al Similarity
169; Conserv
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 547)
                                                                                                                    promrna-9.G12.r
AI525191
                                                                                                                                                AI525191
                                                                                        AI525191.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue Procurement: Mark Raffeld, M.D.
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                                                                                        GI:4439326
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Pred. No. 0.084;
0; Mismatches 223;
                                                                                                                                mRNA
Homo
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                                                                                                                             5', mRNA
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                               Mammalia;
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Leroy Hood
University of Washington
Department of Molecular

Biotechnology,

Box 357730,

University

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                                                                                                                                                                                                                                                                                                                                                                                                                           GGGGGCGNGCGGCNTGAGGGGGGAGCCNG
                             Prostate Cancer Expression Profiling Unpublished (1999)
On May 7, 1998 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Washington
Department of Molecular Biotechnology,
Mashington, Seattle, WA 98195
  Contact:
                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 635)
Huang,G.M., Ng.W., Farkas,J., Chen,L., Liang,H.A., (Yu,J. and Hood,L.
                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                            AI525004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prostate Cancer Expression Profiling by cDNA Sequencing Analysis Unpublished (1999)
On May 18, 1998 this sequence version replaced g1:3136577.
                                                                                                                                                                                     AI525004.1
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Fax: 5106280108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Guyang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leroy Hood
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Guyang Matthew Huang
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                                                                                                                                                                                                                              .B11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: Prostate; Vector: pBluescript; Directional cDNA library was constructed using Lambda ZP II kit (Stratagene). mRNA was extracted from a fresh prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumor tissues (Urology Department, University
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/db_xref="taxon:9606"
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.r bvtumor
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Pred. No. 0.11;
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                           version replaced
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                                                      by cDNA Sequencing
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                                                                                   Gordon, D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCAAGCGNGCNGGGGGNCANGGAGNGNGNCCNGGNNGNGGGGCCNGGGGTTAAGNGGGGG
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                                                                          Mus musculus
Eutharia; Netazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 1208)
1 (bases 1, Kucaba, T., Lacy, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                      g1309579
W29297.1
                                                                                                                                                                                                                                                                                                                                                       M29297 1208 bp mRNA EST 11-SEP-1996 mb99e03.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:337564 5' similar to gb:703750_rna2 Mouse single stranded DNA binding protein p9 mRNA, complete (MOUSE);, mRNA sequence
                                                                                                                                                                                                                                                                                       EST
Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project
                                                    Unpublished (1996)
On Sep 1, 1995 thi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA library was constructed using Lambda ZP II kit (Stratagene). mRNA was extracted from a fresh prostate tumor tissues (Urology Department, University of Washington)."

Washington)."

a 69 c 312 g 94 t 85 others
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/note="Organ: Prostate; Vector: pBluescript; Directional
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Pred. No. 0.
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                                                                                                                                                                                                                                                                               AGGCGCAGGCCGGGCGACAGCCGGAGCGTGGAGCGCGCCGG 368
                                                                                                                                                                                                                                                                                                     Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 1075)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
                                                                                                                                 g1309566
W29419.1
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mb98hll.rl Soares mouse
mAGE:337509 5', mRNA se
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Tel: 314 286 1800
Fax: 314 286 1810
Theising, B., Wylie, T., Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of MedicineP
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
                                                                                                         nouse mouse
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/db_xref="taxon:10090"
/clone="IMAGE:337564"
                                                                                                                                 GI:1309566
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Pred. No. 0.33;
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              GCGCGCGCGCGCTCCTTAAAGGCGCGCGAGCCGAGCGGCGAGGTGCCTCTGTGGCCGCA
                                                                                                                                                                     TGCAGTTCCCTGGGTGGCCGCCGAGACGCTGGCCCGGGCTGGAGGGATGGCGGGGCGGGG
                                                                                                                                                                                                                                                                                                  GGGGTGGAGGTGCCCGGAGCGTACCCAGCGCCGGGAGTACCTCCCGCTCACACCTCGGGC
                                                                                                                                                                                                                                                                                                                                                   CTTGGGCAGCCCCTGGCCTGGCCAGAGGCGCGAGAGCCCGAGAGCCCGCTCGGTGGAGACTG
                                        TCAACATGCGCTGCTCGCCGGGAGGCGTCTGGCTGGCGCTGGCCGCGTCGC 438
                                                                                       GGCGCAGGCCCGGGCGACACCCGAGACGTGGAGCGCGCCGGCTCGCTGCAGCTCCGGGAC 387
                                                                                                                   196;
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4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Sep 1, 1995 this sequence version replaced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMAGE Consortium MGI:218909
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                          13.48;
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                                                                                                                                                                                                                                                                                                                                                                                          Score 61.4; DB Pred. No. 0.35;
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                                                                                                                                Matches 100;
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299 CCGAGCGGCGAGGTGCCTCTGTGGCCGCAGGCGCAGGCCCGGGCGACAGCCGAGACGTGG 358
                                                                                                                                                                                                     239 AGAGGCGCGGGGGGCGGGGGGGGGGGGGCGCGCCCCGGCTCCTTAAAGGCGGCGCGAG 298
                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information
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Fax: 314 286 1810
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Nov 8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGI:218996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Mayne State University)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="19.5 dpc total fetus"
/dev_stage="19.5 dpc total fetus"
/lab_host="19.5 dpc total fetus"
/lab_host="19.5 dpc total fetus"
/note="vector: pf773b (Pharmacia) with a modified
/note:"vector: pf773b (Pharmacia) with a modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 61; DB 2
Pred. No. 0.4;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 26;
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TITLE
JOURNAL
COMMENT
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                         Query Match
Best Local Simi
Matches 171;
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1 (bases 1 to 453)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

The WashU-HHMI Mouse EST Project
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lx
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mg64cl2.rl Soares mouse embryo NbMEl3.5 14.5 Mus musculus cDNA AAO08005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800 Fax: 314 286 1810
                         Similarity 47.071; Conservative
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                                                                                                                                   1153
                                                                                                                                                                                                                                                                                                                               /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/map="22; 21"
                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:437782"
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                       Pred. No. 0.51
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1161)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
wateraton.R.
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W41959.1
EST.
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                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information
                                                                                                                                                                                                                                                                        Contact: Marra M/Mouse EST Project
WashIn-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Id
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mc68bl0.rl Soares n
clone IMAGE:353659
                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                       The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                       Waterston, R.
                                                                                                                                                                 Seq primer: ETPrimer
                                                                                                                                                                                  MGI:225459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        house mouse.
                                                                                                                                                                                                                                                                                                                                                     Apr 14, 1993 this sequence version replaced gi:716741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82
                                                                                                                              quality sequence stop: 370 Location/Qualifiers
/organism="Mus musculus"
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/db_xref="rtaxon:1099"
/map="7; 883A09; 13; 13q12.2-13q12.3"
/clone="INAGE:353659"
/clone_lib="Scares mouse embryo NbME13.5 14.5"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:1326461
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14.5

Mus musculus

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146 321

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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                          AI468375
tg58d01.x1 |
similar to
Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Michael J. Br
                                                                              Tumor Gene Index
Unpublished (1997)
                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 403)
                                                                                                                                                                                                                                                sequence.
AI468375
                                                                 On Mar 10, 1998 this sequence version
                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                           Homo sapiens
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M.Fatima Bonaldo.
751 c 470 g
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="embryo"
/dev_stage="13.5-14.5
                                                                                                                                                                                                                                                                  NCI_CGAP_Fr28 Homo sapiens cDNA clone IMAGE:2112961 3' contains element MSR1 repetitive element .....
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Ph.D., Michael
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ACCESSION NID

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Best Local Similarity
Matches 116; Conserv
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                                                                                                                                                                                                                                                                                                                          NNNNNNNCNCCCCCCCCCC
                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
Macke, J., S
Adult Human
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 859)
Macke, J., Smallwood, P. and Nathans, J.
                                                                                         Homo sapiens
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52d7 Human
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                                                                                                                                                                                                 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"Organ: prostate; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_PT22 was prepared, and so circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from a pool of 5,000 clones made from the same library (cloneIDS 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo. " 179 c 77 g 52 t 53 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          r: -40UP from Gibco.
Location/Qualifiers
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/clone_lib="NCI_CGAP_Pr28"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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/lab_host="DH10B"
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Search completed: September 17, 1999, 21:28:10 Job time: 14274 sec
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Best Local Similarity 49.3%;
Matches 103; Conservative
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                                                                                          643 GGGGGGGNGGGGGGGGGGGNNGNGGGNGGG 615
                                                                                                                                340 GGCGACAGCCGAGACGTGGAGCGCGCGCGG 368
                                                                                                                                                                  280 CTCCTTAAAGGCGCGCGAGCCGAGCGGCGAGGTGCCTCTGTGGCCGCAGGCGCAGGCCCG 339
                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                      FORWARD: CTTTTGAGCAAGTTCAGCCTGGTTAAGT
BACKWARD: GAGGTGGCTTATGAGTATTTCTTCCAGGGTAA
Seq primer: GGGTAAAAAGCAAAAGAATT.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dr. Jeremy Nathans, Dept. of Molecular Biol
Johns Hopkins School of Medicine
725 North Wolfe Street, Baltimore, MD 21205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1996)
On May 9, 1995 this sequence version replaced gi:803988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: jeremy_nathans@qmail.bs.jhu.edu
Clones from this library are NOT available.
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Dr. Jeremy Nathans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 410 955 4678
Fax: 410 614 0827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="E. coli strain K802"
/note="Organ: eye; Vector: lambda gt10; Site_1: EcoRI;
Site_2: EcoRI; The library used for sequencing was a
sublibrary derived from a human retina cDNA library.
Inserts from retina cDNA library DNA were isolated,
randomly primed, PCR amplified, size-selected, and cloned
into lambda gt10. Individual plaques were arrayed and
used as templates for PCR amplification, and these PCR
products were used for sequencing."

352 c 112 g 161 t 93 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'clone_lib="Human retina cDNA randomly primed sublibrary"
'sex="mixed (males and females)"
'tissue_type="retina"
'dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 59.8; DB 26; Length 859; Pred. No. 0.61;
                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 106; Indels
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Title: Perfect s Sequence:

score:

US-08-956-518A-95

OM nucleic

nucleic search, using sw model

Scoring table:

679419 seqs,

1590154680 residues

Potabase :

GenEmbl:\*

gb\_p12:\*
gb\_pr1:\*
gb\_pr2:\*
gb\_pr3:\*
gb\_ro:\*

gb\_pat:\* gb\_om:\*

\*: 40\_d

gb\_st:\*

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1 (bases 1 to 641)
Gault, J., Robinson, M., Berger, R., Drebing, C., Logel, J., Hopkins, J., Moore, T., Jacobs, S., Meriwether, J., Choi, M.J., kim, E.J., Walton, K., Buiting, K., Davis, A., Breese, C., Freedman, R. and Leonard, S. Genomic organization and partial duplication of the human alpha7 genomics 52 (2), 173-185 (1998)

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2 (bases 1 to 641)
Leonard, S., Gault, J.,
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      , Logel, J., Drebing, C., Robinson, M., Berger, R., Hopkins, J. and Freedman, R.
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X14112 Herpes simp
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Y08223 H.sapiens M
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M31051 Human ornit
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Homo sapiens a
AF029839
Submitted (15-OCT-1997) Psychiatry, University of Colorado Health Sciences Center, 4200 E. 9th Ave., Denver, CO 80262, USA Location/Qualifiers
                                                                                                           Gault, J., Robinson, M., Berger, R., Drebing, C., Logel, J., Hopkins, J., Moore, T., Jacobs, S., Meriwether, J., Choi, M.J., Kim, E.J., Walton, K., Buiting, K., Davis, A., Breese, C., Freedman, R., and Leonard, S. Genomic organization and partial duplication of the human alpha7 neuronal nicotinic acetylcholine receptor gene Genomics 52 (2), 173-185 (1998)
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                                           Breese, C., Davis, A., Direct Submission
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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299; Conservative
Vector: pGEM-5Zf(-)
Clones are available from the UK MRC Human Genome Mapping Project
Resource Centre, Hinxton, Cambridgeshire CB10 1RQ, UK. See URL:
http://www.hgmp.mrc.ac.uk/ for details
or contact: biohelp@hgmp.mrc.ac.uk.
1. .291
                                                                                                                  Submitted (16-CCT-1995) The Sanger Centre, Hinxton, Cambridgeshire, CB10 1RQ, England. E-mail contact: humquery@sanger.ac.uk 2 (bases 1 to 291)
Cross,S.H., Charlton,J.A., Nan,X. and Bird,A.P.
Purification of CpG islands using a methylated DNA binding column Nat. Genet. 6 (3), 236-244 (1994)
                                                                                                                                                                                                                                                                                        Homo sapiens
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CpG island; genomic
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MacDonald, M., Huckle, E., Wilkinson, P. and Micklem, G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218;
                                                                                                                                       Clones are available from the UK MRC Human Resource Centre, Hinxton, Cambridgeshire CI http://www.hgmp.mrc.ac.uk/ for details or contact: biohelp@hgmp.mrc.ac.uk.

Location/Qualifiers
                                                                                                                                                                                                                                         2 (bases 1 to 298)
Cross, S.H., Charlton, J.A., Nan, X. and Bird, A.P.
Purification of CpG islands using a methylated
Nat. Genet. 6 (3), 236-244 (1994)
                                                                                                                                                                                                                                                                                                   Submitted (16-OCT-1995) The Sanger CB10 1RQ, England. E-mail contact:
                                                                                                                                                                                                                                                                                                                                                                                                                              z60646.1 GI:1032750
CpG island; genomic Msel fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H.sapiens
read cpg2:
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MacDonald,M., Huckle,E., Wilkinson,P. and Micklem,G.
                                                                                                                                                                                                                                                                                                                                                                      Primates; Catarrhini; Hominidae; Homo
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/db_xref="taxon:9606"
/sex="male"
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95 c
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/tissue_type="blood"
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nes 6;
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humquery@sanger.ac.uk
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GCCTGGTGGCCGCGCCATGACAGCGGCTCGGGACTGGCTCTTTTCCGCGCCCCTCCCG
                                                                                           CAGGCCGCCACACAGCTCCCCGCAGAGGCCTCGGTGCCCCTTGCCATTTTCCAGCCCTAC 47517
                                       TCCGACTAGAGTTGAGGCATCAGGGAGAGGCGGGAGGCTGGGAGAGCGCCGCGAGAGGTCC
                                                                  TCCCACGAGGGTCACGGCGGCGGGGAGAGGTGGAGCCGCGAGAGCTCGGCCGGGGGCCCC
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Direct Submission
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Submitted (08-SEP-1998) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
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Waterston, R.H.
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/db_xref="taxon:9606"
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Waterston, R.H.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 192439)
Waterston,R.H.
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Homo sapiens clone NH0497C14, WORKING DRAFT SEQUENCE, 4 unordered
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NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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/db_xref="taxon:9606"
/clone="NH0497C14"
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5353: gap of unknown length
20005: contig of 14652 bp in length
20023: gap of unknown length
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                                                                                                                    Score 154.8; DB 35; Length 192439; Pred. No. 8.1e-24; 0; Mismatches 67; Indels 4; G
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1 CAGGCCGCCACATAGCT-CCCGCCAAGTCCTCGGTGCCCCTTGCCATTTTCCAGCCGCG- 59

Conservative

Score 146.4; DB 35; Pred. No. 4.5e-22; 0; Mismatches 71;

Indels

5

Gaps

4:

Length 178307;

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                                                                                                                                                                                                                                                                                                                     MO 63108, USA

On Mar 13, 1999 this sequence version replaced gi:4138780.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 3 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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Waterston, R.H.
Direct Submission
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Waterston, R.H.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HTG; HTGS_PHASE1
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11181: gap of unknown length
11182 57066: contig of 45885 bp in length
57067 57084: gap of unknown length
57085 178307: contig of 121223 bp in length
Location/Qualifiers
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1. .178307
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/db_xref="taxon:9606"
/clone="NH0102005"
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                 47.5%;
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Human R kappa B mRNA,
U08191 S79520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adams, B.S., Leung, K.Y., Hanley, E.W. and Nabel, G.J. Cloning of R kappa B, a novel DNA-binding protein that recognizes the interleukin-2 receptor alpha chain kappa B site New Biol. 3, 1063-1073 (1991)
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U08191.1 GI:476273
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1 (bases 1 to 5281)
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CHARLES ALLOCA PELAIRALYDLAVLKKKVKEKEEKKKKKKKKKKKIKTIKSEAE

DLAEPLSSTEGVAPLSQAPSPLAIPAIKEEPLEDLKPCLGINEISSSFFSLLLEILLL

ESQASLPMLEERVLDWQSSPASSLNSWFSAAPNWAELVLPAALQYLAGESBAVPSSESP

FVERKKTQOWKLLGQSQDNEKELAALFQLWLETKOQAFCKQENEDSSDATTPVPRVR

TDYVVRPSTGEEKRVFQQGERYXYSQPHKAFTFRWHGFESVVGPYWGVFDKETSLNKA

REHSLLRSDRPAYVTILSLVRDAARLFQLWLETKDGAFCKQENEDSSDATTPVPRVR

TDYVVRPSTGEEKRVFGQGERYXYSQPHKAFTFRWHGFESVVGPYWGYFDKETSLNKA

REHSLLRSDRPAYVTILSLVRDAARLFNGEGTRAEICELLKDSQFLAPDVTSTQVNT

VYSGALDRLHYEKDPCYKYDIGKKLWIYLHRDRSEEFERHIQAQAAAKAKRALQOK

PKPPSKVKSSSKESIKVLSGGPSQFSQAWGSLSDSSWPTPVTPVTPTTPALPAIPISP

PVSAVNKSGPSTVSEPAKSSGVLLVSSPTMPHLGTMLSPASGTAPSGAAKRYCY

HSGSAGLSQVEVVAQPSLPAVPQQSGGPAQTLPQMPAGPGIRVPATATQTKVVPQTVM

ATVPVKAQTTAATVQRPGPGQTGLTVTSLPATASPVSKPATSSPGTSAPSASTAAVIQ

NVTGQNIKGVATTGGLGVKPQTGNSIPLTATNERIQGKDVLRLPPSSITTDAKGQTV

LRITPDMMATLAKSQVTTVKLTQDLFGTGGNTTGKGISATLHVTSNPVHAADSPAKAS

SAAPSSTPGTTVVKYTPDLKPTEASSSAFRLMPALGVSVADQKGKSTVASSEAKPA

***TATTTOTTTVKYTTPDLKPTEASSSAFRLMPALGVSVADQKGKSTVASSEAKPA

***TATTTTGTTTVKYTTPDLKPTEASSSAFRLMPALGVSVADQKGKSTVASSEAKPA

***TATTTTGTTTVKYTTPDLKPTEASSSAFRLMPALGTSATGTTGCHATATGTTTT

***TATTTTGTTTTVKYTTPDLKPTEASSSAFRLMPALGTSATGTT

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/protein_id="AAA17871.1"
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/db_xref="GI:476274"
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/db_xref="taxon:9606"
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X15819
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Direct Submission
Submitted (13-JUL-1989) An G., Washington State University
Pullman, Washington 99164-6340, U S A
                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence of rice nitrate reductase Plant Mol. Biol. 13 (6), 731-733 (1989)
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Location/Qualifiers
/db_xref="SWISS-PROT: p16081"
/tams1ation="MAASVQPRQFGHLEPGSAPVRGAASSNGAKAYPPANGIPRRADS
PVRGCGFPPLVSPPRKPPBOSODDEEEQEDWRELYGSHLQLEVEPPVRDARNEGTA
DAWTERNPSLIRLTGKHPLNCEPPLAELMHHGFITPAALHYVANHGAVPRGDWSTWTV
DVTGLVKRPHKLTMDELVNGFPAKDEIVTLVCAGNRRKEQNMYQTVGFNWGAAGVST
SVWRGARLRDVLRRGGIMPSKGGALWVCFEGAEDLPGGGGSKYGTSIRGWALDPSKG
SVWRGARKBULTRGGENGFPVRAIIPGCIGGRWYKWVKRIIVTTAESDNYYHYKDNRVL
IMLAXMQNGEPLLPDHGFPVRAIIPGCIGGRWYKWVKRIIVTTAESDNYYHYKDNRVL
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RIQTVPASISNREQLLAPPKQSPLLL"
1908 c 1336 g 1165 t
                                                                                                                                                                                                                                                                                          /organism="Oryza sativa"
/strain="Japonica M201"
/db_xref="taxon:4530"
                                                                                                                                                /product="nitrate reductase apoenzyme"
/protein_id="CAA33817.1"
/db_xref="PID:g295825"
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                                                                                                                                                      Resource Centre, Hinxton, Cambridgeshire CB10 http://www.hgmp.mrc.ac.uk/ for details or contact: biohelp@hgmp.mrc.ac.uk.
Location/Qualifiers
                                                                                                                                                                                                                                                                 Submitted (16-OCT-1995) The Sanger Centre, Hinxton, Cambridgeshire, CB10 1RQ, England. E-mail contact: humquery@sanger.ac.uk 2 (bases 1 to 171)
Cross,S.H., Charlton,J.A., Nan,X. and Bird,A.P.
Purification of CpG islands using a methylated DNA binding column Nat. Genet. 6 (3), 236-244 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HS165H1F 171 bp DNA
H.sapiens CpG island DNA genomic Msel fragment,
forward read cpg165h1.ftla.
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1 (bases 1 to 171)

1 (bases 1, Huckle, E., Wilkinson, P. and Micklem, G.
                                                                                                                                                                                                                    Clones are available from the UK MRC
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             /tissue_type="blood"
/clone_lib="CGI-1"
/clone="165h1"
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/number=2
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                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                           'dev_stage="adult"
                                                                                           /sex="male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:1028387
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                                                                                                       CCCACGAGGGTCACGGCGGCGGGGAGAGGTGGAGC 94
                                                                                       CCCAGGAGAGTGGAGGCTGCAGGAAGAGGCGGNTC 160
                                                                                                                                             CAGGCCGNCACACCTCCCGCCAAGACCT-GGTGCCCCTTGCCATTTTCCAGCCGCGCT 125
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HS51D8R
H.sapiens CpG
                                                                                                                                                                                                                                                                                                                                                                                                                          Resource Centre, Hinxton, Cambridgeshire http://www.hgmp.mrc.ac.uk/ for details or contact: biohelp@hgmp.mrc.ac.uk.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 180)
Cross, S.H., Charlton, J.A., Nan, X. and Bird, A.P.
Purification of CpG islands using a methylated
Nat. Genet. 6 (3), 236-244 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (16-OCT-1995) The Sanger Centre, Hinxton, Cambridgeshire, CB10 1RO, England. E-mail contact: humquery@sanger.ac.uk
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Primates; Catarrhini; Hominidae; Homo.
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Clones are available from the UK MRC
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                                                                                                                                                                                                                                                                                              /tissue_type="blood"
/clone_lib="CGI-1"
/clone="115g2"
a 57 c 58 g
                                                                                                                                                                                                                                                                                                                                                                       /sex="male
                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                         'dev_stage="adult"
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Pred. No. 0.1;
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Cross, S.H., Charlton, J.A., Nan, X. and Bird, A.P.
Purification of CpG islands using a methylated DNA binding column
Nat. Genet. 6 (3), 236-244 (1994)
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CB10 1RQ, England. E-mail contact: humquery@sanger.ac.uk
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macDonald,M., Huckle,E., Wilkinson,P. and Micklem,G
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261392
Submitted (16-MAY-1998) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63 SUBMITTED BY: WUGSC Genome Sequencing Center
                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 142123)

Kalicki,J. and Burkhart,J.

The sequence of Homo sapiens PAC clone DJ0630C24

Unpublished (1998)

2 (bases 1 to 142123)
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                                                                       Direct Submission
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/clone_lib="CGI-1"
/clone="51d8"
a 61 c 71 g
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                                         63108, USA
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mailto:sapiens@watson.wustl.edu
                      St. Louis MO 63108, USA http://genome.wustl.edu/gsc
                                                                  Washington University
                                                                                         Department of Genetics
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

Pieter de Jong and coworkers at Roswell Park Cancer Institute, using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor. For furth details, see http://bacpac.med.buffalo.edu/The clone is available from Genome Systems, Inc. This clone was derived from human PAC library RPCI-4, http://www.genomesystems.com). Genetics For further prepared by

VECTOR: PCYPAC2
NEIGHBORING SEQUENCE INFORMATION:
The actual start of this clone is at base position 1 of DJ0630C24;
actual end is at 142123 of DJ0630C24.

# This clone contains STS sWSS3567 (NID:g1916499)

This clone contains a transposon, has be deleted from the submitted Location/Qualifiers from base 123435-124772, which

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 /rpt_family="MER2_type"
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                           /rpt_family="L1"
7175. .7409
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/clone_lib="RPCI-4"
/clone="DJ0630C24"
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/rpt_family_"Alu"
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8. .18095
e="match to EST AA065302 (NID:g1929302)"
                  family="MIR"
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                                                                           family="Retroviral"
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                        Mangel,L.

Direct Submission
Submitted (12-AUG-1997) Mangel L., Medical Genetics and Virology,
University of Cologne, Institute of Genetics, Weyertal 121,
Cologne, 50931, GERMANY
Revised by [3]
                                                                                                                                                                                                                                   HSCGG16P5. 2837 bp DNA PRI 13-NOV-1998 Homo sapiens DNA for (CGG)n trinucleotide repeat region, isolate CL16-1 (Chr.16).
2 (bases 1 to 2837)
Mangel,L.
                                                                                                         Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2837)
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Frankia sp.
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                                                                                                                                                                                                                                                            Kong,R., Xu,X. and Wolk,C.P.
Direct Submission
Submitted (18-JUL-1997) MSU-DOE Plant Research Laboratory, Michigan
State University, E. Lansing, MI 48824, USA
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Actinomycetales; Frankineae; Frankiaceae; Frankia.
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/note="transcribed region"
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/chromosome="16"
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                                                  GGCTACCGCCGGCGGGGTCGGAAGCAGCCACACCGGGCCGGGGTCGCGGGTCGCGGCCG
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/tagislation="MAELGYEGIDELRGKIVAGEYAPDTVLPTLVELMARYQASRET/translation="MAELGYEGIDELRGKIVAGEYAPDTVLPTLVELMARYQASRETVRAIGQLETEGLVQAIRRRGTVVARRPDRSKIVRPRQVFRDSLGYLMARDSGDWRELFRARAIGQLETEGLVQAIRRRGTVVLRIVRLFRDFQAAQRQAAVSYLPSDITRGFSVEFYERJAGAFAPTDVBGLALHFGTPVLRIVRIGGTAIEQLRTGPGGLYDRLEELGGELWMDEELSAEAAAPTDVBGLALHFGTPVLRIVRIGGTAIEQLRTGPGGLYDRLEELGGELWMDEELSAEAAAPTDVBGLALHFGTPVLRIVRIGGTAIEQLRTGPGGLYDRLEELGGELWMDEELSAEAAAPTDVBGLTGAEAARFTRI
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ptssggvayvgmlraalavlleveaaggplpaamppavlslgtwtlaalgngaddgng
                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MTOGAPGVPARGPGGGRGLASSLRHALRRGLRHPLRRACVTVC VGSSPGYCGTASMRGYMVMAVNILKGGSSKTTSSAFLAHALAERGGGDVLLVDADPGG SAARMASLAEMLPVILLAHRDLHRRLPGIVGDRYSTIVIDTPPMEDHRGIVISANRA AGVVANTLAFMIELDRLPFVWSALDEVAAVREAPFAVAALLTRTVPRAASTGVVRDV VVSGGHRVLDAMVPRRESYAQAYGAPVVVGPHYRAVAEELLTLGAAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uvib provinces (6909. .7706) complement (6909. .7706) /note="orf3; similar to Alcaligenes eutrophus megaplasmid /note="orf3 para-like partition protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /T-A-101-14PSSRPDRGHPVVAAELDEQMEIAAGRRAPFTMIGDWVALSGID/TARSIation="MPSSRPDRGHPVVALEGID"/TARSIAtion="MPSSRPDRGHPVALEGID"/TARSIAtion="MPSSRPDRYLAQLVELGAIEVR"/TARSIAGGMRARNYLVHGSPSDDYAGARSLHEWYQRRRAEADPEPSRSPFQRTTARPAETRETPAQPVVRSSGLPESAPADLGSPPQRTGTKTKNNKTKNTTTPARTRKAPAPKPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="regulatory protein"
/protein_id="AAB88412.1"
/db_xref="PID:g2662455"
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/db_xref="PID:g2662457"
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'protein_id="AAB88411.1"
'db_xref="prD:926562454"
'db_xref="GI:2662454"
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db_xref="PID:g2662456"
db_xref="GI:2662456"
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protein_id="AAB88413.1"
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Search completed: September 17, 1999, 22:03:03	3693 CGCGACCCGTCCGGCGGGGGAGCTGGTGGGCGTGGGCCAGGCGCACGAGCA 3750	233 TGGCCCTCTATCTTCCAGGAGAACCAGGAGCCACAGCCGCGGCTCACGCCCCACCGCA 290	3633 GCACCGCTCGGAGCGTCGGACCGGTCTCGCCGGCGGGGGGGG

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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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# ALIGNMENTS

VERSION	NID	ACCESSION		DEFINITION	LOCUS	N83152	RESULT 1
N83152.1 GI:1441866	g1441866	N83152	clone K4329 5' similar to R KAPPA B(NON-EXACT), mRNA sequence.	K4329F Human fetal heart, Lambda ZAP Express Homo sapiens cDNP	N83152 170 bp mRNA EST 02-APR-1996		

KEYWORDS

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RESULT 2
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ID HSM01
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TITLE
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Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                               Homo sapiens mRNA; EST DKFZp586B2218)
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Seq primer: GAAATTAACCCTCACTAAAGGG
Locatton/Qualifiers
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Tel: 4169788758
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University of Toronto
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On Apr 14, 1993 this sequence version replaced g1:502850.
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Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 170)
Liew, C.C.
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                                                                                                       sequence
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/lab_host="E. coli XL1-Blue"
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
XhoI; mRNA was purified from human fetal hearts (8-10
weeks). cDNA was synthesized using a XhoI-Oligo dT
adaptor primer. EcoRI adaptors were ligated, followed by
digestion with XhoI for directional cloning into
predigested lambda ZAP Express."

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/db_xref="taxon:9606"
/clone="K4329"
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90,
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Last updated, Version
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   Eutheria;
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Matches 154
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                                                                                                                                                                                                                                                                                                                                                          183
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                                                                                                                                                                                                                                                                                                                                                    -CGTCCATCTTCGACAAGAACCACGAGCGA
                                                                                                                                                                                                                                                                                                                                                                              CCCTCTATCTTCCAGGAGAACCAGGAGCCA 265
                                                                                                                                                                                                                                                                                                                                                                                                         CCGCCGGAGATGAGGGGAAGATGTCCGTGTCAGGGCTCAAGGCCGAGCTGAAGTTCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                          CCGCCGGAGGTGAGGGGAAGATGTCCATGTCAGGGTTCAAGGCCAAACCGAAGTTACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGTGACGGCGCCCGGGCCCGGCTCCCCTTCCGCGCCCCGGCTCCCCTTCCGCGCCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCGGGGAGAGGTGGAGCCGCGCGAGAGCTCGGCC---GGGGGCCCCCGCCTGGTGGCCGCGC
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 335)

Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., Bult,C.J., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
                                                                                                                                                                                                                                          AA333244 335 bp mRNA EST 21-APR-1997 EST37317 Embryo, 8 week I Homo sapiens cDNA 5' end similar to similar to interleukin-2 receptor, alpha chain, kappa B binding
                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                         protein, mRNA sequence,
AA333244
                                                                                                                                                                                            AA333244.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S. Wiemann,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="586 (synonym: hutel). Vector pSportl; host DH10B; sites NotI + SalI/MluI" /dev_stage="adult" /tissue_type="uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/clone="DKFZp586B2218"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
                                                                                                                                                                                            GI:1985508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 81.2; DB 50
Pred. No. 5.4e-09;
D; Mismatches 33
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Genome Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 54;
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COMMENT
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AA407437
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                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                    SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                KEYWORDS
                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                       ERSION
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  JOURNAL
                                        TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weldman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., Pinke, D., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kin, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Pillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

L. Nature 377 (6547 Suppl.), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCCCTCTATCTTCCAGGAGAACCAGGAGCCA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCCGCCGAGATGAGGGGAAGATGTCCGTGTCAGGGCTCAAGGCCGAGCTGAAGTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCCGCCGGAGGTGAGGGGAAGATGTCCATGTCAAGGCTTCAAGGCCAAACCGAAGTTACT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GG-CGTCCATCTTCGACAAGAACCACGAGCGA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hg1/hg1.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 37
96026280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On May 18, 1995 this sequence version replaced gi:811121.
Other_ESTs: THC185696
Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                              MASCULUS
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                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 416)
Ro,M.S.H., Threat,T.A., Horton,J.H., Wang,X, Cui,Y.,
Pryor,E., Paris,J., Wells-Smith,J., Fujiwara,H., Yot
                                                                                                                                                                                                                                                                                                                                   AA407437 4
EST00734 Mouse
Unpublished (1997)
                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                         g2065649
                                        Systematic analyses
                                                                Nakashima, H.
                                                                                                                                                                                                            house mouse.
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                                                                                                                                                                                                                                                                                                           416 bp mRNA EST 26-AUG-1998 Mouse 7.5 dpc embryo ectoplacental cone cDNA library cDNA clone C0002B08 3', mRNA sequence.
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/clone_11b="Embryo, 8 week I"
/dev_stage="embryo, 8 wks"
/note="Organ: Embryo, 8 weeks; Vector: pBluescript SK-;
/note="Organ: Site_2: XhoI"
Site_1: EcoRI; Site_2: XhoI"
94 c 88 g 69 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="ATCC (inhost):134920"
                                                                                                                                                                                                                                                     GI:2065649
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                                             of mouse
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, Rockville,
                                             genes
                                             expressed in
                                                                                 Fujiwara, H., Yots
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                                             embryo implantation
                                                                                    Yotsumoto, S. and
                                                                                                                                                                        Mammalia;
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                                                                                                           Wang, X.,
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ORIGIN
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Best Local S
Matches 84
                                                                                    TITLE
                                                                                                                                                                                  AUTHORS
                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 CGGGACTGGCTCCTTTTCCGCGCCCCCCCCGGG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 CCTCGGTGCCCCTTGCCATTTTCCAGCCGCGTCCCACGAGGGTCACGGCGGGGGGAGAG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCTCCCCCCCTGTGGGGGGAACCTCCCCGTCGGTGTTCCCCCCGCCGGGTCCGCCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGGAGCCGCGAGAGCTCGGCCGGGGGGCCCCGCCTGGTGGCCGCGGCCATGACAGCGGCT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGGCCGCGTTNTCCGCGCGCGCCCCCCCCCG
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EST02243
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                                                                                                                                Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 328)
1 (bases 1 to 328)
1 (Ko,M.S.H., Threat,T.A., Horton,J.H., Wang,X, Cui,Y.,
Pryor,E., Paris,J., Wells-Smith,J., Fujiwara,H., Yot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human 28S ribosomal RNA gene.
Seq primer: M13 Forward.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        musculus
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Unpublished (1997)
On Sep 12, 1996 th
                                                                                                                      Nakashima, H.
                                                                                                                                                                                                                                                                                                                                                                                                AA407004.1
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                                                                                          Systematic analyses
                                                                                                                                                                                                                                                                                                                                     house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KO MSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     328 bp mRNA EST Mouse 7.5 dpc embryo ectoplacental cone cDNA clone C0019805 3', mRNA sequence.
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/dev_stage="embryonic day 7.5 pos'
/lab_host="DH10B"
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                GI:2067158
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      replaced g1:1393284
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                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 213)

Ko,M.S.H., Threat,T.A., Horton,J.H., Wang,X, Cui,Y., Wang,X., Pryor,E., Paris,J., Wells-Smith,J., Fujiwara,H., Yotsumoto,S.
                                                                                                                                                                                                                                                                                                                                    AA410084 213 bp
EST01971 Mouse 7.5 dr
musculus cDNA clone (
Contact: Ko MSH
                   Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1392981.
                                                                                       Systematic analyses
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Human ribosomal DNA complete rep
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/db_xref="taxon:10090"
/clone="C0019B05"
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/dev_stage="embryonic day 7.5 pos
/lab_host="DH10B"
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/strain="C57BL/6J"
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dpc embryo ectoplacental cone cDNA library Mus
e C0016B12 3', mRNA sequence.
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Center for Molecular Medicine Wayne State University

Genetics

Contact: Ko MSH

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Best Local Similarity
Matches 83; Conserv
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                                                                                 BukaryOta; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 268)
1 (Dases 1 to 268)
FOOM.S.H., Threat, T.A., Horton, J.H., Wang, X., Cui, Y., Wang, X., Pryor, Paris, J., Wells-Smith, J., Fujiwara, H., Yotsumoto, S.
       Unpublished (1997)
On Sep 12, 1996 th
                                                          Systematic analyses
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5047 Gullen Mall, Detroit, MI 48202
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Mouse 28S ribosomal RNA
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/dev_stage="embryonic day 7.5 pos
/lab_host="DH108"
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/strain-"C57BL/6J"
/db_xref-"Taxon:10090"
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Contact: Ko MSH
Center for Molecular Medicine
Wayne State University
5047 Gullen Mall, Detroit, MI
Tel: 3135776708
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Mouse 28S ribosomal RNA
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Pryor,E., Paris,J.,
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On Sep 12, 1996 th
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KO,M.S.H., Threat,T.A.,
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/strain="C57BL/6J"
/db_xref="ATCC (inhost):1363477"
/db_xref="taxon:10090"
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'dev_stage="embryonic day 7.5 postconception"
'lab_host="DH10B"
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                                                                               this sequence
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                                                                                                                       of mouse genes
                                                                                                                                                   Wells-Smith,J.,
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Pred. No. 3.7;
0; Mismatches
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                                                                                                                                                             Horton, J.H.,
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Fujiwara,H., Yot:
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CDNA library
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Query Match
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                                                                                                                                                                                                                 Mus musculus
Eukharyota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukharyota; Metazoa; Chordata; Craniata; Vertebrata; Musniae; Mus.

1 (bases 1 to 325)
1 (bases 1 to 325)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
                                                                                                                                                                 Theising,B., Wylie,T., Lennon,G., Soares,B., Waterston,R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI317247 325 bp mRNA EST 17-DEC-1998 u136c11.yl Soares mouse urogenital ridge NMUR Mus musculus cDNA clone IMAGE:1853396 5' similar to TR:004892 004892 CYTOCHROME P450
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Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                        Unpublished
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                                               WashU-HHMI Mouse EST Project
                                                                   Contact: Marra M/Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                           house mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="ATCC (inhost):1363168"
/db_xref="taxon:10090"
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Strain="C57BL/6J"
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'dev_stage="embryonic day 7.5 postconception"
'lab_host="DH10B"
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                                                                                                                     1998 this sequence version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTCGGTGCCCCTTGCCATTTTCCAGCCGCGTCCCACGAGGGTCACGGCGGCGGGAGAG
Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine
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                                                                     Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R. Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
                                                                                                                                            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 371)
Marra,M., Hiller,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
                                                                   Unpublished
                                                                                                                                                                                                            Mus musculus
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                            LIKE_TBP ;, mRNA sequence.
AI508264
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                                                                                                                                                                                                                                               house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustr.equ
This clone is available royalty free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                I508264 371 bp mRNA EST 12-MAR-1999 h66603.y1 Soares mouse placenta 4NbMP13.5 14.5 Mus musculus cDNA cone_IMAGE:455909 5′ similar to TR:004892 004892 CYTOCHROME P450
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/tissue="pe="urogenital ridge (embryonic)"
/dev_stage="fetal, mixture of 11.5 and 12.5 dpc"
/lab_host="DH10B"
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/map="12; 12, 40.8cR from WI-4263; 21q"
/clone="TWAGE:1853396"
                                        1998 this sequence version replaced gi:3138778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
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Pred. No. 3.8;
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                                                                                                                                                                                                                                             AA407075
EST02080
                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutherla; Rodentia; Sciurognathi; Muridae; Murinae;
1 (Dases 1 to 374)
KO,M.S.H., Threat,T.A., Horton,J.H., Wang,X, Cui,Y.,
Pryor,E., Paris,J., Wells-Smith,J., Fujiwara,H., Yot
                                                                                                                                                                                                           AA407075
                     Nakashima, H.
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     Systematic analyses
                                                                                                                           Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty free through LINL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4444 Forest Park Parkway, Box
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               correct orientation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                  374 bp mRNA EST Mouse 7.5 dpc embryo ectoplacental cone cDNA clone C0017C05 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

135 c 127 g 50 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Soares mouse placenta 4NbMP13.5 14.5"
/sex="unknown"
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/map="15 q22-qter; 21q"
/clone="IMAGE:455909"
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/dev_stage="adult"
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                                                                                                                                                                             GI:2066995
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of mouse genes expressed in
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Pred. No. 4.8;
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                              Fujiwara,H., Yotsumoto,S.
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embryo implantation
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                                Yotsumoto, S.
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                83;
                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 376)
1 (bases 1 to 376)
Ko,M.S.H., Threat,T.A., Horton,J.H., Wang,X., Cui,Y., Wang,X., Pryor,E., Paris,J., Wells-Smith,J., Fujiwara,H., Yotsumoto,S.
                                                                                                                                                                                                                Musculus
AA407297
                                                                                                                                                                                                                                       AA407297 376 bp
EST02294 Mouse 7.5 dp
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Seq primer: M13 Forward.
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On Sep 12, 1996 this
Unpublished (1997)
On Sep 12, 1996 th
                                                                                                                                       Mus musculus
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                                        Systematic analyses of mouse
                                                                                                                                                                                                 g2067209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 313577620
                                                                                                                                                                                   AA407297.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: embryo; Vector: pSPORT1 (
S1te_1: Not1; Total RNAs
ectoplacental cone of 7.5-dpc embryos.
double-stranded cDNA was synthesized fi
an Oligo(dT) primer. The library was co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="ATCC (inhost):1363695"
/db_xref="taxon:10090"
/clone="C0017C05"
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'lab_host="DH10B"
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dev_stage="embryonic day 7.5 pos
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Pred. No. 5.3;
0; Mismatches
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sequence version
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                                       genes expressed in
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replaced gi:1393088
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                                        embryo implantation
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CDNA library Mus
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AA407662
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EST01743
                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 271)
Ko,M.S.H., Threat,T.A., Horton,J.H., Wang,X, Cui,Y.,
Pryor,E., Paris,J., Wells-Smith,J., Fujiwara,H., Yot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: msko@cmb.biosci.wayne.edu
Human 28S ribosomal RNA gene.
Seq primer: M13 Forward.
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5047 Gullen Mall, Detroit, MI 48202
Tel: 3135776708
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1393367
                                                                                                                                                                                 Mus musculus
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                                                       Systematic analyses
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                                                                                                                                                                                                                                                                                             271 bp mRNA
Mouse 7.5 dpc embryo
cDNA clone C0013E08 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="ectoplacental cone"
/dev_stage="embryonic day 7.5 pos
/lab_host="DH10B"
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/db_xref="taxon:10090"
/clone="C0019G01"
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                                                       of mouse genes expressed in
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Pred. No. 5.3;
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Contact: Ko

FEATURES

Seq primer: M13 Forward

Location/Qualifiers

/strain="C57BL/6J" /db\_xref="ATCC (inhost):1364262" /db\_xref="taxon:10090" //lone="C0013E08"

clone\_lib="Mouse 7.5 dpc embryo ectoplacental

/organism="Mus musculus"

Email: msko@cmb.biosci.wayne. Mouse 28S ribosomal RNA

Fax: 3135776200

Center for Molecular Medicine and Genetics Wayne State University 5047 Gullen Mail, Detroit, MI 48202

source

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88 GTGGAGCCGCGAGAGCTCGGCCGGGGGGCCCCGCCTGGTGGCCGCCGCCATGACAGCGGCT 147
                                                                                                                                                      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 316)
Ko,M.S.H., Threat,T.A., Horton,J.H., Wang,X, Cui,Y., Wang,X.,
Pryor,E., Paris,J., Wells-Smith,J., Fujiwara,H., Yotsumoto,S.
                                                                                                                                                                                                                                                                                                                                                                   316 bp mRNA EST 26-AUG-1998 Mouse 7.5 dpc embryo ectoplacental cone cDNA library MuscDNA clone C0016C02 3', mRNA sequence.
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                                                                                                                                 embryo implantation
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Best Local s
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Wayne State University 5047 Gullen Mall, Detr Tel: 3135776708
                                              Contact: Ko MSH
Center for Molecular Medicine and Genetics
                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 373)

Ko,M.S., Threat,T.A., Horton,J.H., Wang,X, Cui,Y., Wang,X., Pryor,E., Paris,J., Wells-Smith,J., Fujiwara,H., Yotsumoto,S.
                                                                                               Unpublished (1997)
On Sep 12, 1996 this sequence version
                                                                                                                                                        Systematic analyses of mouse genes
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Seq primer: M13 Forward.
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Email: msko@cmb.biosci.wayne.edu
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/db_xref="taxon:10090"
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dev_stage="embryonic day 7.5 postconception"
lab_host="DH10B"
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REFERENCE AUTHORS

COMMENT

Unpublished (1997) On Sep 12, 1996 this sequence

Center for Mole Wayne State University

for Molecular Medicine

and Genetics

version replaced gi:1392824

TITLE JOURNAL

Systematic analyses

of mouse genes expressed in

SOURCE ORGANISM

house mouse AA407690.1

KEYWORDS

ERSION CCESSION DEFINITION

GI:2066888

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/tissue\_type="ectoplacental cone"
/dev\_stage="embryonic day 7.5 postconception
/lab\_host="bH108"

/sex="unknown"

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                                                                                                                                                             Fax: 3135776200
Email: msko@cmb.biosci.wayne.edu
Human ribosomal DNA complete repeating unit
Seq primer: M13 Forward.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 641)
2 (bases 1 to 641)
Leonard,S., Gault,J., Logel,J., Drebing,C., Robinson,M., Berger,R.,
Breese,C., Davis,A., Hopkins,J. and Freedman,R.
Direct Submission
                                           Gault, J., Robinson, M., Berger, R., Drebing, C., Logel, J., Hopkins, J., Moore, T., Jacobs, S., Meriwether, J., Chol, M.J., Kim, E.J., Walton, K., Buiting, K., Davis, A., Breese, C., Freedman, R. and Leonard, S. Genomic organization and partial duplication of the human alpha7 neuronal nicotinic acetylcholine receptor gene Genomics 52 (2), 173-185 (1998) 99000837
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                                                                                                                                                                                                                                                                                                                     Gault,J., Robinson,M., Berger,R., Drebing,C., Logel,J., Hopkins,J., Moore,T., Jacobs,S., Meriwether,J., Choi,M.J., Kim,E.J., Walton,K., Buiting,K., Davis,A., Breese,C., Freedman,R. and Leonard,S. Genomic organization and partial duplication of the human alpha7 neuronal nicotinic acetylcholine receptor gene Genomics 52 (2), 173-185 (1998)
                                                                                                                                                                                  Leonard,S., Gault,J., Logel,J., Drebing,C., Robinson,M., Breese,C., Davis,A., Hopkins,J. and Freedman,R. Direct Submission Submitted (15-cCT-197) Psychiatry, University of Colorad Sciences Center, 4200 E. 9th Ave., Denver, CO 80262, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 689)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (15-OCT-1997) Psychiatry, University of Colorado Sciences Center, 4200 E. 9th Ave., Denver, CO 80262, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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               ø
             alternative splicing"
a 210 c 196 g
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192 c 163 g
                                                              /note="RACE product A/C/D" <1. .>689
                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="15"
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/chromosome="15"
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                                          note="alpha 7 neuronal nicotinic receptor mRNA; used in
                                                                                                            /map="15q14"
                                                                                          clone-"CHRNA7-DR2"
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                                                                                                                                                                                                                                             1 CTCATTTCAGATTACAAGTGGACACCTGAGTCAGCAGGACCTGGAATCCCAGATGAGAGA 60
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                                reading frame on V00667 J01428
92938
V00667.1 GI:2938
                                             MINCO1 491 bp DNA PLN Neurospora crassa ATPase proteolipid like gene and reading frame on complementary strand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (03-NOV-1988) to the EMBL/GenBank/DDBJ 2 (bases 1 to 3093)

Kanamoto,R., Yoshimura,M., Hayashi,S. and Oka,T. Nucleotide sequence of a pseudogene for rat ornit Nucleic Acids Res. 17 (1), 463 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat ornithine decarboxylase pseudogene. x13417
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dentia; Sciurognathi; Muridae; Murinae; Rattus.
(bases 1 to 3093)
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                                                                                                                                                                                                                                                                                                                                                                      /note="ornithine decarboxylase pseudogene region"
683 c 623 g 930 t
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Pred. No. 0.2;
0; Mismatches 46;
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Pred. No. 9.7e-33;
0; Mismatches 2
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84
1 TTAACCACAGATAATGAAAC......GCATTTTCAGGTAGGATCAT 84
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                                                                   RESULT 1
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                                                                                                                                                                                                                               Score
A1655990 501 bp m
tt42c03 x1 NCI_CGAP_GC6 H
mRNA sequence.
A1655996 g4739969
A1655990.1 GI:4739969
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A1631518
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                                                                 EST 04-MAY-1999 sapiens cDNA clone IMAGE:2243428
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A1286133 q101c05.x
AA475853 vh12g4 x
AA475853 vh2g4 x
AA47588 wa99a01.x
AU056388 wa99a01.x
AU056388 AU056388
D47311 RICS12666A
H47049 yo20g08.s1
AA36072 EST69641
AA398114 zt58692.s
AA553441 nk77d07.s
AA553441 nk77d07.s
AA553441 nk77d07.s
AA572984 nm33d12.s
AU051905 AU051905
A1622332 486040C11
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T40435 ya01b06.s2
R09085 yf21g09.r1
T80555 yd06a07.r1
T80555 yd06a07.r1
T80555 yx08d12.r1
H998196 yx37h04.s1
H99885 yx37h04.s1
H95856 yx3608f12.r1
H95856 md85a10.r1
W54506 md85a10.r1
W62896 md85a10.r1
W77761 zd69c04.r1
AA003956 mg79d09.r
AA010721 ze22a07.r
AA0107721 ze22a07.r
AA010762 mi32099.r
AA01475 mi32090.r
AA01743 zm87b06.r
AA01743 zm87b06.r
AA01743 zm87b06.r
AA017475 mi3209.r
AA314075 EST185927
AA334011 EST39913
AA344752 EST50683
AA334011 EST39513
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W52861 zc03e02.r1
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W52861.1
                                                                                                   zc03e02.rl Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA IMAGE:321242 5' similar to gb:X70297 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-7 CHAIN (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                        60;
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index
Unpublished (1997)
On Jun 5, 1998 this sequence version replaced g1:3188057
                                                                                                                                                           W52861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D.,
R. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: (301) 496-1550
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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       sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1459064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "
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                                                         GI:1350351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="TMAGE:2243428"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                     53.8%;
                                                                                                                                                         560 bp
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Pred. No. 0.00066;
0; Mismatches 3;
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
Homo sapiens
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On Jan 24, 1995 this sequence version replaced
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@wateon.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1753 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH.
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(Pharmacia) with a modified polylinker; Site_1:
| Site_2: Eco RI; 1st strand cDNA was primed with
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'tissue_type="parathyroid_tumor"
'dev_stage="adult"
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db_xref="GDB:1258900"
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Pred. No. 0.07
0; Mismatches
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                                                                                                                                                           Homo sapiens cDNA clone IMAGE: 1408049
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Tumor Gene Index 
Unpublished (1997)
                                                                                                                                                                                                          AI286133 457 bp mRNA EST 27-JAN-1999 q101c05:x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855208 3' similar to 9b:m74525 UBIQUITIN-CONJUGATING ENZYME
                      NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 457)
                                                                                         Eukaryota;
                                                                                                                                             EST.
                                                                                                                                                                                                E2-17 KD (HUMAN);, mRNA sequence.
                                                                                                              Homo sapiens
                                                                                                                                                         AI286133.1 GI:3924366
                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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Unpublished (1997)
On Jan 9, 1998 this
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D
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1 (bases 1 to 487)
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Library Preparation: M. Bento Soares, Ph.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1408049"
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                                                                                                                                                                                                                                                                                                                                                                                                           37.6%;
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Pred. No. 5.
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                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 549)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                       Unpublished On Nov 29, 1
                                                                                                                                                                                                                                                                                                      Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA475853 549 bp mRNA
vhl2904.rl Soares mouse mammary
IMAGE:875286 5', mRNA sequence.
AA475853
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Seq primer: -40UP from Gibco
High quality sequence stop: 370.
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Insert Length: 787 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On Jan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17,
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/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
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High quality sequence stop: 462.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48;
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wa99a01.x1 NCI_CGAP_GC6
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                                                                                                                                                                                                                                                                                                                                mRNA sequence.
                Email:
                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 420)
                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                              Ā1631518.1 GI:4682848
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D.,
                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                   Unpublished (1997)
                                                                                                                     Tumor Gene Index
                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T 3'); double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/map="14; 17"
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/strain="C57BL/6J"
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/dev_stage="4 weeks"
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Homo sapiens cDNA clone IMAGE:2304264
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     Ph.D., Michael
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High quality sequence stop: (
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Sequencing by: Washington University Genome
DNA Sequencing: WCI-CGAP clone distribution
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AU056388 Oryza sativa mature leaf Nipponbare Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa
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                             Email: tsasaki@abr.affrc.go.jp
pROJECT ='RGP'.
                                                                                                                                                 Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
2-1-2 Kannondai,Tsukuba
                                                                                                                                                                                                                                           On May 18, 1998
                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AU056388.1
                                                                 Tel: 0298-38-7441
Fax: 0298-38-7468
                                                                                                                                                                                                                                                             Rice cDNA from mature leaf Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                         Japan 305
                                                                                                                                                                                                                                                                                                     l (bases 1 to 567)
Ramamoto, K. and Sasaki, T.
                                                                                                                                                                                                                                                                                                                                           Poaceae;
                                                                                                                                 Ibarak:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               quality sequence stop: 372.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                               Kannondai, Tsukuba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from the same library (cloneIDS 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. " 57 c 73 g 146 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made
                                                                                                                                                                                                                                                                                                                                             Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note-"vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH108"_____
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'clone="IMAGE:2304264"
Location/Qualifiers
1. .567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.6%;
                                                                                                                                                                                                                                                 this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 28.2; D. Pred. No. 50; O; Mismatches
                                                                                                                                                                                                                                                   version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 420;
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                                                                                                                                                                                                                                                   gi:3138441.
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BASE COUNT
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ACCESSION
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D47311
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Matches 43
                                                                                                                            Query Match
Best Local
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                                               235 CAAGCTGCTGCTGATAAGTTTGCTGCAAAAATATGCCTTCTAACATCATTCAGAG 289
                                                                         20 CAACCACCATCGGTTAAATTTGATGCAAAAATATTGCATCTACCAGCATTTTCAG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 TITCAGGT 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 AGATTAGGAGTTATCCACCATTCTTAATAGTTGAAGCAAAAGGAGATAAACTAACCGGAT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 CATCAGGT 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 AGATAATGAAACAACCACCATCGGTTAAATTTGATGCAAAAATATTGCATCTACCAGCAT 68
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                                                                                                                                                                                                                                                                                                                                                                                                          National Institute of Agrobiological Resources Rice Genome Research Program 2-1-2 Kannondai, Tsukuba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Oryza.

1 (bases 1 to 362)
Sasaki.T., Miyao,A. and Yamamoto,K.
Rice cDNA from callus 1995
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RICS12606A Rice green
D47311
                                                                                                                                                                                                                                                                                                                                                    Fax: 0298-38-7468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ď47311.1
                                                                                                                                                                                                                                                                                                                                                                                 Japan 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Takuji Sasaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa
                                                                                                             Similarity 69.38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                      113
                                                                                                                                                                                                                                                                                                 1: tsasaki@abr.affrc.go.jp
quality sequence stop: 277.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  0298-38-7441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                           /organism="Oryza sativa"
/organism="Oryza sativa"
/strain="Nipponbare"
/db_xref="taxon:4530"
/clone_lib="Rice green shoot"
/note="Green shoot (8 days old)"
a 64 c 81 g 104 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI:701020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="520537_1A"
/clone_11b="01yza sativa mature leaf Nipponbare"
/tissue_type="mature leaf"
111 c 127 g 142 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="Nipponbare"
/db_xref="taxon:4530"
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                                                                                                                         33.1%;
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                                                                                                                        Score 27.8;
Pred. No. 66;
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Pred. No. 55;
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                                                                                                          Mismatches
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                                                                                                                                       DB 21;
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Query Match
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BASE COUNT
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further i Possible reversed clone: polyT not found Insert Length: 685 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
Insert Size: 685
High quality sequence stops: 208
Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 17e1: 314 286 1800 Fax: 314 286 1810
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H47049.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 208
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The WashU-Merck EST Project
Unpublished (1995)
On May 18, 1995 this sequence version replaced g1:811216.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., RifKin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H47049

395 bp mRNA

396 pm mRNA

31-JUL-1995

9020908.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone
IMAGE:178526 3', similar to 9b:M74525 UBIQUITIN-CONJUGATING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 395)
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     114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer: SP6
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                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:178526"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="GDB:3840722"
                                                                                                                                                                                                                                                                                                                                                                                  'sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                               clone_lib="Soares adult brain N2b5HB55Y"
                                                                                                                                                                                                                                                                                                                                                                dev_stage="55-year old"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contact the
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Similarity

32.9%;

Score 27.6; D Pred. No. 75; 0; Mismatches

В

Length 395; Indels

Conservative

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26; 23;

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RESULT 1
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Query Match 32.9
Best Local Similarity 61.8
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 353)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
Insert Size: 464
High quality sequence stops:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4444 Forest Park Parkway,
Tel: 314 286 1800
Fax: 314 286 1810
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Location/Qualifiers
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                                                                                                                                                                          /lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
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/db_xref="GDB:3765840"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="20 week-post conception fetus"
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                                  32.9%;
         Score 27.6; Depred. No. 75; Open Mismatches
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

AL Nature 377 (6547 Suppl), 3-174 (1995)
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
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Fax: 3018699423
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62
                                                                                            /clone_lib="T-cell lymphoma"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-;
                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="ATCC (inhost):
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMAGE Consortium (info@image.llnl.gov) f.
Seq primer: -41ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        zt58e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726554
3' similar to gb:M74525 UBIQUITIN-CONJUGATING ENZYME E2-17 KD
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOMO Sapiens
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   32.9%;
nilarity 60.8%;
Conservative
                                                                                                                     115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        quality sequence stop: 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  est@watson.wustl.edu
                                                                                                                     ω
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                                                                                                                                                                                                                                                   /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(primer [5']
                                                                                                                                                                                                                         Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the
                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref-"taxon:9606"
/map-"13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="GDB:5923466"
                                                                                                                                                                                                                                                                                                                                                 'lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                   'sex="male"
                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                                                                                                                                                                          'clone="IMAGE:726554"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
                                                                                                             Eco RI sites of the modified pT773 vector. Library t through one round of normalization to Cot5, and was structed by Bento Soares and M. Fatima Bonaldo. "73 c 86 g 156 t
     0
                   Score 27.6;
Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  School of Medicine way, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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AA553441/c
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                           7 ACAGATAATGAAACAACCACCATCGGTTAAATTTGATGCAAAAATATTGCATCTACCAGC 66
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AAAGCAAAAAAAAAAGTAACATTGGGTGATTTATATGTAGATATAATACATATGGCAAC 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: -40m13 fwd. High quality sequence si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
On Apr 14, 1993 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tissue Procurement: L. :
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Eutheria; Primates;
1 (bases 1 to 493)
                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Stratagene,
                                                                                                                                                                   152
                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Robert_Strausberg@nih.gov
                                                                                                                                                                   þ
                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606",
/map="MMU16C3-C4 region; MMU16C3-C4 region; MMU16C3-C4 region:
/clone="IMAGE:101953"
/clone_11b="NCI_CGAP_Sch1"
/tissue_type="Schwannoma tumor"
/tissue_type="Schwannoma tumor"
/tissue_type="Schwannoma tumor"
                                                                                                                                                                                                                                                                                                                                                                                  1. .493
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ity sequence stop: 479.
Location/Qualifiers
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                                                                               32.9%;
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                                                              0,
                                                                              Score 27.6;
Pred. No. 73;
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                                                                Mismatches
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AA572984 g2347512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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Unpublished (1997)
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 496)
AU051905 567 bp
AU051905 Dictyostelium
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: L. J
Emmert-Buck, M.D., Ph.D.
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Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael
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                                                                                                                                                                                                                                                                                                                                                                                               129
                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pamp10; mRNA made from liposarcoma, cDNA made by oligo-dT priming. Non- directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:1061975"
/clone_11b="NCI_CGAP_L1p2"
/tlssue_type="11posarcoma"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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Pred. No. 83;
    discoideum SS
                      mRNA
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EST 26-MAR-1999
(H.Urushihara) Dictyostelium
                                                                                                                                                                                                                                                                                                                Length 496;
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AUTHORS
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Search completed: September 17, 1999, 21:28:20 Job time: 14284 sec
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                                                                                                                                                                                                                                                                                                                                                                                    218 TAATACAACCAACACCTCCATTTGAATCACATGAATAAATTTTACATTTATCAACTTGAC 159
                                                                                                                                                                                                                                                                  72 CAGGTAGGATCA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                    12 TAATGAAACAACCACCATCGGTTAAATTTGAAGCAAAAATATTGCATCTACCAGCATTTT 71
                                                                                                                                                                                                                  CATCTAATTTCA 147
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1 (bases 1 to 567)

2 (bases 1 to 567)

2 (bases 1 to 567)

3 (bases 1 to 567)

4 (bases 1 to 567)

5 (bases 1 to 567)

6 (bases 1 to 567)

7 (bases 1 to 567)

7 (bases 1 to 567)

8 (bases 1 to 567)

9 (bases 1 to 567)

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University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
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T = 'Dictyostelium discoldeum cDNA project in Japan'.
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/db_xref="taxon:44689"
/map="847612; 9: 9p23-9p24; 9q22.1-9q22.31"
/clone_lib="Dictyostelium discoideum SS (H.Urushihara)"
/dev_stage="slug"
/dev_stage="slug"
70 c 89 g 188 t 9 others
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Copyright (c) 1993 - 1998 Compugen Ltd.
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Leonard, S., Gault, J., Logel, J.,
Breese, C., Davis, A., Hopkins, J.
                                                                  Gault,J., Robinson,M., Berger,R., Drebing,C., Logel,J., Hopkins,J., Moore,T., Jacobs,S., Meriwether,J., Choi,M.J., Kim,E.J., Walton,K., Buiting,K., Davis,A., Breese,C., Freedman,R. and Leonard,S. Genomic organization and partial duplication of the human alpha7 neuronal nicotinic acetylcholine receptor gene (CHRNA7) Genomics 52 (2), 173-185 (1998)
                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutharia; Primates; Catarrhini; Hominidae; Homo.
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AB020752 Arabidops
L29769 Mouse hnRNP
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AC005283 Homo sapi
AC006453 Homo sapi
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AC00747 Homo sapi
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AL035423 Human DNA
AL031284 Homo sapi
AC004037 Homo sapi
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D50797 Schizosacch
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Z64354 S.pombe chr
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Submitted (03-DEC-1997) Psychiatry, University of Colorado Health
Sciences Center, 4200 E. 9th Ave., Denver, CO 80262, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                      Submitted (15-OCT-1997) Psychiatry, University of Colorado Health Sciences Center, 4200 E. 9th Ave., Denver, CO 80262, USA Location/Qualifiers
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Leonard, S., Gault, J., Logel, J., Drebing, C., Robinson, M.,
Breese, C., Davis, A., Hopkins, J. and Freedman, R.
Direct Submission
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/db_xref="taxon:9606"
/db_xref="dbEST:W03952"
/db_xref="dbEST:W73891"
/db_xref="fist":W73891"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="alpha-7 neuronal nicotinic acetylcholine receptor
precursor; intron included in 5' region"
1 503 c 469 g 481 t
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Genetics/IMAGE Consortium, LLNL"
/note="unprocessed mRNA with intron"
                                                                                       alternative splicing"
1 192 c 163 g
                                                                                                                                                4
                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="15"
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                                                                                                                             'note-"alpha 7 neuronal nicotinic receptor mRNA; used
                                                                                                                                                                                'clone-"CHRNA7-DR1"
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alpha
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Pred. No.
Score 49.8; DB 11;
Pred. No. 1.9e-07;
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6e-10;
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                  Length 641;
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AF036903
                                                                        KEYWORDS
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ORGANISM
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                                                                                                            VERSION
                                                                                                                                               ACCESSION
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Matches 51
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                                                     ORGANISM
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g3757807
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                                                                                                                               Homo sapiens (
AF029839
g3757794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (03-DEC-1997) Psychiatry, University of Colorado Health
Sciences Center, 4200 E. 9th Ave., Denver, CO 80262, USA
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leonard, S., Gault, J., Logel, J., Drebing, C., Robinson, M., Berger, R., Breese, C., Davis, A., Hopkins, J. and Freedman, R. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gault, J., Robinson, M., Berger, R., Drebing, C., Logel, J., Hopkins, J., Moore, T., Jacobs, S., Meriwether, J.; Choi, M.J., Kim, E.J., Walton, K., Buiting, K., Davis, A., Breese, C., Freedman, R. and Leonard, S. Genomic organization and partial duplication of the human alpha7 neuronal nicotinic acetylcholine receptor gene (CHRNA7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF036903 1712 bp mRNA PRI 16-OCT-1998 Homo sapiens alpha-7 neuronal nicotinic acetylcholine receptor mRNA, alternatively spliced, partial sequence.
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Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 1712)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 689)
                                                   Homo sapiens
                                                                        numan.
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                                                                                                                                                                                 AF029839
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/db_xref="taxon:9606"
/db_xref="dbEST:W52861"
/db_xref="dbEST:AA037389"
/chromosome="15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"alpha-7 neuronal nicotinic alternatively spliced" a 489 c 457 g 410 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /Clone_lib="Soares papathyroid tumor NbHPA library, Reseach Genetics/IMAGE Consortium, LLNL"
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                                                                                                              GI:3757794
                                                                                                                                                                  689 bp
alpha 7
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96.2%;
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                                                                                                                                                                                                                                                                                                                                                 Score 49.8; DB 11;
Pred. No. 1.8e-07;
0; Mismatches 2;
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                                                                                                                                                                  mRNA sequence.
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Sciences Center, 4200 E. 9th Ave., Denver, CO 80262, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 163403)

1 (bases 1 to 163403)

1 (cliniter, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Butenhoff, C., Champe, M., George, R.A., Harris, M.L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, M.L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Mazda, P., Kin, E., Levis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb. J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and Doyle, G., R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC007765 163403 bp DNA INV 09-JUN-1999 Drosophila melanogaster, chromosome 2L, region 23C1-23C5, Pl c. DS02190 and DS00906, complete sequence. AC007765 AC004375 AC003631 AC003632 AC003633 AC003634 AC003635 AC004154 AC002028 AC002976 AC002029 AC002977 AC002030 AC002031 AC002033 AC002033 AC002033 AC002034 AC002035
2 (bases 1 to 163403)

2 (clniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, Celniker, S.E., Agbayani, A., Chavez, C., Chew, M., Ciesiolka, L., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster
                                                                                                                                                                                                                    Sequencing of Drosophila chromosome 2L, Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC007765.1 GI:5030435
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    >689
    /note="alpha 7 neuronal nicotinic receptor mRNA; used alternative splicing"
    210 c 196 g 141 t

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Pred. No. 1.2e
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43; Conserv
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Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (09-JUN-1999) Berkeley Drosophila Genome Project, 164-121, Lawrence Berkeley National Laboratory, One Cyclotron Berkeley, CA 94720, US On Jun 9, 1999 this sequence version replaced gi:3293203 g1:3097820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Svirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. Rubin,G.M.
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AC006531
g4235137
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3 (bases 1 to 167525)
Bruce,D., Mundt,M., Doggett,N., Munk,C., Saunders,E., Robinson,D.,
Jones,M., Buckingham,J., Chasteen,L., Thompson,S., Goodwin,L.,
Bryant,J., Tesmer,J., Meincke,L., Longmire,J., White,S., Tatum,O.,
                                                                                                                                                                                                                                    Bruce, D., Mundt, M., Doggett, N., Munk, C., Saunders, E., Robinson, D., Jones, M., Buckingham, J., Chasteen, L., Thompson, S., Goodwin, L., Bryant, J., Tesmer, J., Meinoke, L., Longmire, J., White, S., Tatum, O., Campbell, C., Fawcett, J., Maltble, M., Bussod, M., Sutherland, R., Campbell, C., Fawcett, J., Maltble, M., Bussod, M., Sutherland, R.,
                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 167525)
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                                                                          Unpublished
                                                                                               Large Scale Sequence Analysis and Annotation with the Comparison Analysis (SCAN) System
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                                                                                                                                                                                              Sequencing of Human Chromosome 16p13.3
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/strain="y; cn bw sp"
/db_xref="taxon:7227"
/chromosome="2L"
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repeat_region 4533745419 /rpt_family="MER" repeat_region complement(4574946003)	_region 45220. 45336 /rpt_family="MLT"	misc_feature complement(403944226) /note="GRAIL 2 excellent exon, frame 2"	repeat_region complement(4.3625.43725) /ret family="MERRON"	repeat_region complement(40863 .41382)  /rot famil-"MFRA1"		repeat_region 38718. 38821	<pre>/note="GRAIL 2 excellent exon, frame 1" repeat_region complement(3802638318)</pre>	misc_feature 35856. 36026	repeat_region complement(3452034772)	repeat_region complement(34052 .34381)	<pre>/rpt_family="MIR" repeat_region 33206, .33361</pre>	<pre>repeat_region 32685, 32828</pre>	repeat_region 30282. 31394	<pre>/rpt_family="L1" repeat_region 29943 .30269</pre>	<pre>/rpt_family="MER2" repeat_region 29619, .29862</pre>	<pre>/rpt_family="Alu" repeat_region 28101 .28204</pre>	<pre>repeat_region complement(2716227453)</pre>	<pre>/rpt_family="MER" repeat_region 2679926960</pre>	<pre>repeat_region complement(2436525041)</pre>	repeat_region 23577. 23860	repeat_region complement(1820118458)	<pre>repeat_region complement(16599. 16853)</pre>	<pre>misc_feature complement(1460014851)</pre>		repeat_region complement(13201. 13294)	m m		/rpt_family="MIR"	repeat region 2396 2466	/clone="113K5"	source	lamos National Laboratory, MS M888, Lo	ission 06-FEB-1999) Center for Human Genome Studies,	
repeat_region 840/4. 84820 /pt_family="Li" repeat_region 85690. 85917 /rpt_family="Alu"	_region	region complement(8016880463) /rpt_family="Alu"	misc_feature complement(7986879993) /note="GRAIL 2 excellent exon, frame 2"	repeat_region complement(7953179812) /rpt_family="Alu"	repeat_region complement(7916, .78047)	repeat_region complementaly Air .77896)  /ref family="Alin"	repeat_region complementate exception exon, Irame 2"  /rnt family="alin"	on, trame		repeat_region complement(6936 excertent exon, irame 1"  /rnt family="MIP"	•	repeat_region 65464. 65742 Att	repeat_region 65034. Family="Ali"	repeat_region 64727. 64830	repeat_region 62540. 62679	repeat_region 6195860075 LI	repeat_region 61633. Grantly "LI"	repeat_region 61134. 65-11-07:	repeat_region 60534. 60842	repeat_region 58153. Serior 7	repeat_region 57272	repeat_region 56250.	repeat_region 55579	repeat_region 5493355231	repeat_region complement(38154442) /rpt_familv="MIR"	repeat_region complement(536654143)	at_region	/rpt_family="MIR" misc_feature 5232652469		_region	/rpt_fam _region	repeat_region 4850948629	reacure	rpt_family="Alu"

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x74464.1
                                                                                                                                                                     Delius,H.
Direct Submission
Submitted (06-AUG-1993) H. Delius, Deutsches
Krebsforschungszentrum, Abteilung ATV, Im Neuenheimer Feld 506,
6900 Heidelberg, FRG
                                                                                                                                                                                                                                                                                                      El gene; E2 gene; E4 gene; E gene; E
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Delius, H. and Hofmann, B.
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Human papillomavirus type 9
Viruses; dsDNA viruses, no R
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                                                                                                                Primer-directed sequencing of human Curr. Top. Microbiol. Immunol. 186,
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99315. .99414
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/rpt_family="L1"
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complement(86699. .86867)
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/gene="E6"
200. .646
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                                                /organism="Human papillomavirus type 9"
/db_xref="taxon:10621"
                                     clone="insert in BamHI site of pBR322"
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/db_xref="SWISS-PROT:P36801"
/translation="MYLTEQIMDRPKPRTVKELADTLVIPLIDLLIPCKFCNRFLSYF
ELLNFDHKCLQLIWTEEDLVYGLCSSCAYASAQLEFTHFFQFAVVGKDIETVEGTAIG
NICIRCRYCFKLLDLVEKLATCYKFEQFYKVRNSWKGLCRHCGSVE"
/trānslation="metlsarenalgetlmdlyesgredlgsgidhwgtlrgegillh
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rsppayafkkgpgnievvydgdpdnvmsytiwnfiyygtvndtwekvgghvdyfgayy
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AC007037/c
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                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 169891)
Waterston,R.H.
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AC007037.2 GI:4572700
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PFAKKSFWKVDLTERLSLDLDQYPLGRKFLFOAGLQTRKRPIKTSVKTSKNAKRRRT"
1 1393 c 1654 g 2024 t
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GDSTIVOGFVESSIVDVNIDEPDGLEVGRQETPSVEDVDFNSEDLLLDEGVEDFSGSQ
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                                                                                                                                                                                                                                                        169891 bp DNA HTG 07-APR-1999
ns clone NH0119H15, WORKING DRAFT SEQUENCE, 6 unordered
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                                                     g807669
L36962.1
                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                            glucocerebrosidase; metaxin; thrombospondin 3. Mus musculus (strain C57BL/6) brain cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                 MUSMRNA 1084 bp
Mus musculus metaxin
                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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On Apr 7, 1999 this sequence version replaced gi:4371308.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (06-MAR-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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terston,R.H.
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                                              Location/Qualifiers
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22865: contig of 15176 bp in length
22883: gap of unknown length
56499: contig of 33616 bp in length
56517: gap of unknown length
102994: contig of 46477 bp in length
103012: gap of unknown length
169891: contig of 66879 bp in length.
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                         SHGC-19832 G19509
SHGC-19839 G19514
SHGC-19839 G19514
SHGC-19837 G19513
SHGC4-1507 G01867
SHGC-19823 G19503
SHGC-19823 G19503
SHGC-19815 G194128
SHGC-19815 G194198
SHGC-36185 G30091
                                                                                                                                                                                                                                                                               Submitted (28-JAN-1998) Department of Genetics, Stanford Human Genome Center, 855 California Avenue, Palo Alto, CA 94304, USA (Dases 1 to 161326)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 161326)
                                                                                                                                                                          Submitted (08-NOV-1998) Department of Genetics, Stanford Human Genome Center, 855 California Avenue, Balo Alto, CA 94304, USA On Nov 9, 1998 this sequence version replaced g1:3694642.

Quality: Phrap Quality >=40 99.88 of Sequence;
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pwgspsgtlpalrtsdokvttypdkitthlerekynadydlsarggadtlafwstlee
kllpvlihtfwidaknyvevtrwyadkiftherekynadydlsarggadtlaflogehks
enebelekelyggarecitllsgreftggokfftgdapasldafvtshlallloaklpsg
kloahlrglhnicaycthilnlyffprdddevplprottaapeteeepyrrrtquisvl
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                                             91236164
4 (bases 1 to 100849)
4 (bases 1 to 100849)
Viskochil,D., Cawthon,R., O'Connell,P., Xu,G.F., Stevens,...,
Culver,M., Carey,J. and White,R.
The gene encoding the oligodendrocyte-myelin glycoprotein is embedded within the neurofibromatosis type 1 gene .
embedded within the neurofibromatosis type 1 gene .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A major segment of the neurofibromatosis type 1 gene: cDNA sequence, genomic structure, and point mutations [published appears in Cell 1990 Aug 10,62(3):following 608] cell 62 (1), 193-201 (1990) 90304909
                                                                                                                                                                                                                                                                                                                                            Identification and characterization of transcripts from the neurofibromatosis 1 region: the sequence and genomic structure EVI2 and mapping of other transcripts Genomics 7 (4), 555-565 (1990) 90353953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Mamma Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 100849)

Cawthon,R.M., Weiss,R.B., Xu,G., Viskochil,D., Culver,M., Stevens,J., Robertson,M., Dunn,D., Gesteland,R., O'Connel
                                                                                                                                                                                                      Cawthon, R.M., Andersen, L.B., Buchberg, A.M., Xu, G.F., O'Connell, P., Viskochil, D., Weiss, R.B., Wallace, M.R., Marchuk, D.A., Culver, M. Stevens, J., Jenkins, N.A., Copeland, N.G., Collins, F.S. and White, R. cDNA sequence and genomic structure of EVI2B, a gene lying within an intron of the neurofibromatosis type 1 gene genomics 9 (3), 446-460 (1991)
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Cawthon,R.M., O'Connell,P., Buchberg,A.M., Viskochil,
Weiss,R.B., Culver,M., Stevens,J., Jenkins,N.A., Cope
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91236164
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Brereton, A.,
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 Letcher,R., Odeh,H., Saulino,A.M.,
Nicholson,J., Mitchell,A.,
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Fountain,J.,

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/number=2 complement(2854232788) /gene="EVI2A"	/rpt_fa complem /gene=" /note=" /citati	/note="G00-125-901" /Gitation=[3] /number=1 _region	<pre>cy=04850</pre>		complement(1465825133) /gene="EVIZB" Complement(16738	/:pu_ramity="GF" complement(1465816737) /gene="EVIZB" /note="G00-125-901" /citation=[3]	/citation=[4] /citation=[4] /number=1 /region 12224. 12233	/number=1 complement(82668342) /gene="OMG" /note="GONG"	complement(74488265) /gene="OMG" /note="600-127-563"	complement(57617447) /gene="OMG" /note="G00-127-563" /citation=(4)		/db_xref=""" taxon: 9606" /map="17q11.2" <136919	Lake City, Utah 84112 telephone: (801) 585-3436.  Location/Qualifiers 1. 100849	<pre>tting author Robert Weiss may be con ss and telephone number: prona.med.utah.edu</pre>	(bases 1 to 100849)  Xu.G., O'Connell,P., Stevens,J. and White,R.  Characterization of human adenylate kinase 3 (AK3) cDNA and mapping of the AK3 pseudogene to an intron of the NF1 gene  Genomics 13 (3), 537-542 (1992)	<pre>6 (bases 1 to 100849) Weiss,R.B., Dunn,D., DiSera,L., Wheatley,W., Kimball,A., Rote,C., Cherry,J., Duval,B., Lee,R., Ferguson,M.W.J. and Gesteland,R.F. The Human Neurofibromatosis Type 1 locus: genomic sequence of the 3 region Unpublished (1992)</pre>	Brownstein, B.H. and Collins, F. A de novo Alu insertion results in neurofibromatosis type 1 Nature 353 (6347), 864-866 (1991) 92049738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (30-JUN-1998) to the DDBJ/EMBL/GenBank databases. Massaki Komatsu, National Institute of Neuroscience, Department of Neuromusclar Research; Ogawahigashi-machi 4-1-1, Kodaira, Tokyo 1878-8502, Japan (E-mail:komatsu@ncnaxp.ncnp.go.jp, Tel:+81-423-41-2711, Fax:+81-423-46-1742)
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Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 2638)
Romatsu,M. and Tsukahara,T.
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Komatsu, M. and Tsukahara, T.
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/gene="NF1"
/note="G00-120-231"
                                                                                                                                                                                                    NYYSSRYDDYDRYRRSRSRSYERRRSRSRSFDYNYRRSYSPRNSRPTGRPTRSRSHS
DNDRFKHRNRSFSRSKSNSRSRSKSQPKKEMKAKSRSASHTKTRGTSKTDSKTHYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                          /note="31 A
466 c
                                                                                                                                                                                       SGSRYEKESRKKEPPRSKSQSRSQSRSRSKSRSRSWTSPKSSGH"
                                                                                                                                                                                                                                    /translation="MSRYLRPPNTSLEVRNVADDTRSEDLRREFGRYGPIVDVYVPLD
FYTRRPRGFAYVQFEDVRDAEDALHNLDRKWICGRQIEIQFAQGDRKTPNQMKAKEGR
                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                       product="neural specific sr
protein_id="BAA35092.1"
                                                                                                                                                                                                                                                                                                                           /product-"neural
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                                                                                                                                                                                                                                                                 'db_xref="GI:4001720"
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                            Eukaryota; Metazoa; Chorvettheria; Primates; Cata:
1 (bases 1 to 297898)
Weiss, R.B., Dunn, D.W., A
                                                                                                                                                                                          AC004526
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Direct Submission
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Weiss,R.B., Dunn,D.M., Aoyagi,A., Banks,L., DiSera,L., Duval Hamil,C., Holmes,C., Korzeniowski,G., Mahmoud,M., Rose,R., Stokes,R., Stump,D., Yu,P., Zhou,L., Gitin,Y., Nelson,J. and
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/translation="MSRYLRPPNTSLFVRNVADDTRSEDLRREFGRYGPIVDVYVPLD
FYTRRPRGFAYVQFEDVRDAEDALHKLDRKWTCGRQIEIQFAQGDRKTPNMKAKEGR
NYYSSSRYDDYDRYRKSRSRSVERRRSRSRSRSRSKSFTRSTSRFTGRFRRSRSHS
DNDRFKHRNRSFSRSKSNSRSRSKSRSRSRSRSASHTKTRGTSKTDSKTHYK
SGSRYEKESRKKEPPRSKSQSRSGSRSRSRSRSRSRSRSRSHTSRSASHTK
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466 c 559 g 854 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="TLS-associated protein TASR-2"
/protein_id="AAC26715.1"
/db_xref="TD193327957"
/db_xref="G1:3327957"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="hematopoietic"
/cell_line="EML"
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odb_xref="taxon:10090"
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                                                                    Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
rimates; Catarrhini; Hominidae; Homo.
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g3924671
AC004943.1 G
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 141313)

Kozlowicz, A., McQuerry, Y. and Hotic, M.

The sequence of Homo sapiens PAC clone DJ0991G20

Unpublished (1998)

2 (bases 1 to 141313)
                                                                                                                                  Homo sapiens
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Direct Submission

Submitted (17-OCT-1998) Human Genetics, University of Utah, 20
2030 E., Rm 308, Salt Lake City, Utah 84112, U.S.A.

4 (bases 1 to 297898)

Weiss,R.B., Dunn,D.M., Aoyagi,A., Banks,L., DiSera,L., Duval,B.
Hamil,C., Holmes,C., Mahmoud,M., Rose,R., Stokes,R., Stump,D.,
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Direct Submission
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Hamil,C., Holmes,C., Mahmoud,M., Rose,R., Stokes,R., Stump,D.,
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/db_xref="taxon:9606"
/clone="23013,14502"
/chromosome="21"
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60770 c 62692 g 91988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The location of this clone is unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VECTOR: PCYPAC2
NEIGHBORING SEQUENCE INFORMATION:
Actual start of this clone is at base position 1 of DJ0991G20;
actual end is at 141313 of DJ0991G20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 one male donor.
The clone may be obtained either from Genome Systems,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone was derived from human PAC library RPCI-5, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from the company of the second company of the second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (http://www.genomesystems.com) or Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:sapiens@watson.wustl.edu
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SUBMITTED BY: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Sequencing Center Department of Genetics
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Submitted (12-JUN-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
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/clone="bJ0991G20"
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Search completed: September 17, 1999, 22:04:19 Job time: 16442 sec

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AA10375 mo25040. AA10377 mo25040. AA103787 mo25040. AA107857 mo49h08. D76888 MUSS1F01 m AA170084 ms52906. AA183839 mo95a04. AA184588 mt51c02. AA197755 mv03a06. AA517605 vb93d04. AA517665 vb3d040. AA51616 vl34e02. AA711653 vu27b09. AA755792 vv35d03. AA794314 vu77e08. AU066965 AU066965	C89442 C89142 MG AIZ55545 U155h01 T05021 EST02909 A1488647 EST2479 A1488637 EST2471 A1099847 34000 U1-R-C2 W10059 ma67d04 r AA027739 m114e011 AA027739 m143006 AA048492 mj30c08 AA061156 m1313c08	AI367541 qv93c12. AI655990 tt42c03.r1 W86937 zh60e03.r1 W76900 me58b02.r1 W85213 mf51b09.r1 W89656 mf81f04.r1 AA222672 mv99a05. AA388232 vb59c01. AA590415 vm16d07. AA719305 zh3sc02. AA719305 zh3sc02. AA792253 vn94a09.	Description  AA861176 ak66d w52861 zc03e02 W03952 za62c08 AA460018 zx49h AA844642 aj57a

RESULT 1 AA861176/c LOCUS DEFINITION

ACCESSION NID VERSION

AA861176 487 bp mRNA EST 04-JAN-1999
ak36099.s1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:1408049
3', mRNA sequence.
AA861176
g2953316
AA861176.1 GI:2953316

ALIGNMENTS

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W52861
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                                                                                                                                                                                                                                                                   W52861 EST 10-OCT-1996 zc03e02.rl Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321242 5' similar to gb:X70297 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-7 CHAIN (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                    l Similarity
51; Conserv
   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 560)
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                                                                                             W52861.1
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DNA Sequencing by: washington University Genome
Clone distribution: NCI-GGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: Robert_Strausberg@nih.gov cDNA Library Preparation: M. Bento
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Jan 9, 1998 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                 human
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                                                                                                                                                                                                                                                                                                                                                                                                                                 131
                                                                                                                                                                                                                                                                                                                                   72.5%;
ilarity 92.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker: Site_1: Not I; Site_2: ECO RI; Ist strand cD
was prepared from mRNA obtained from Clontech.
Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                 GI:1350351
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/db_xref="taxon:966"
/clone="IthAGE:1488049"
/clone_lib="Soares_testis_NHT"
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                                                                                                                                                                                                                                                                                                                                   Score 48.6; DB 39
Pred. No. 3.1e-07;
0; Mismatches 4
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                                Mammalia;
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                                                                                                                                                                                                                                                                                                                                                       TTTCAGTTCCAATTGCTAATCCAGCATTTGTGGATAGCTGCAAACTGTGATAT
                                                                                                                                                                              W03952 409 bp mRNA EST 19-APR-1996 za62c08.rl Soares fetal liver spleen lNELS Homo sapiens cDNA IMAGE:297134 5' similar to gb:X70297 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-7 CHAIN (HUMAN); mRNA sequence.
Eukaryota; Metazoa;
Eutheria; Primates;
1 (bases 1 to 409)
                                                            Homo sapiens
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Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (11fo@image.llnl.gov) for further i
Insert Length: 1753 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The WashU-Merck EST Project Unpublished (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jan 24, 1995 this sequence version replaced
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B (ampicillin resistant)"
/note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Site_2: Eco RI; 1st strand cDNA was primed with
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                                                                                                                        GI:1275817
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/tlasue_type="parathyroid tumor"
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/clone="IMAGE:321242"
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/db_xref="GDB:1258900"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.98;
                   Chordata; Craniata; Ven
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 48.2; DB 26;
Pred. No. 4.3e-07;
0; Mismatches 3;
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                                      Vertebrata; Mammalia;
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1 (bases 1 to 274)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. washu-Merck EST Project 1997
Unpublished (1997)
                                                                                                                                                                                                                                                                                                         AA450U18 274 bp mRNA EST 09-JUN-1997

zx49h09.s1 Soares_test1s_NHT Homo sapiens cDNA clone IMAGE:795617

3', mRNA sequence
                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Tel: 314 286 1800
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The WashU-Merck EST Project
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                      mRNA sequence
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/db_xref="GDB:1242055"
/db_xref="taxon:9606"
/clone="IMAGE:297134"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_lib="Soares fetal liver spleen lNFLS"
1996 this sequence version replaced gi:1393691
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                                                                                                                                                                                                                                                 GI:2184902
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94.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match
                                                                                                                              Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
cDNA Library Preparation: M. Ben
www-bio.llnl.gov/bbrp/image/image.html
                       CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                               On Jan 17, 1998
                                                                                                                                                                                                                                                                    Unpublished (1997)
                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 436)
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA844642 436 bp mRNA
aj57a12.s1 Soares_testis_NHT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4444 Forest Park 1
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA844642.1 GI:2931093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pT/T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: ECO RI; lst strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="IMAGE:795617"
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/db_xref="GDB:6038961"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.5%;
93.8%;
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Pred. No. 2.2e-05;
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                                                                                                                                 Bento Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                              Anatomy Project (CGAP),
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                                                                                                                                 Ph.D.,
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Insert Length:

497

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Error: 0.00

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REFERENCE
AUTHORS
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GANISM
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Best Local Similarity
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                                                                         Insert Length: 1828 Std Err
Seq primer: -400P from Gibco
High quality sequence stop: 3
                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.:
1 (Dases 1 to 396)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                              CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-blo.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                             Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher N
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
AI367541
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qv93c12.x1 NCI_CGAP_Ut2
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h quality sequence stop: 415.
                                                     quality sequence stop: 370
Location/Qualifiers
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96 c 103 g 122 t
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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93.8%;
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                                                                                                                                                                                                                                                                               Christopher Moskaluk, M.D., Ph.D.,
                                                                                                             Std Error: 0.00
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Pred. No. 2.2e-05;
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AI655990/c
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Query Match
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Unpublished (1997)
On Jun 5, 1998 this
                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: -40UP from Gibco High quality sequence stop: '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
AI655990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D.,
R. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (301) 496-1550
/note-"Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The drive was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257996-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by
                                                                                                                                                                                                /tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
                                                                                                                                                                                                                                             /clone="IMAGE: 2243428"
/clone_lib="NCI_CGAP_GC6"
                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT
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adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.5%;
93.8%;
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C
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Pred. No. 2.2e-05;
D; Mismatches 3;
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                                                                         this DNA was used as ion reaction. The driver
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Matches 45
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JOURNAL
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45; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1 Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chiasoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Le, M., Le, M., Le, N., Le, 
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clone IMAGE:416476 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vértebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Apr 14, 1993 this sequence version replaced gi:315330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert Length: 584
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       83
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107 c 115 g
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the and Eco RI sites of the modified pT773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo." 92 c 93 g 95 t 6 others
                                                                                                                                                                                                                      /lab_host**DH10B (ampicillin resistant)"
/note**Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
liver spleen lNFLS library. 1st strand cDNA was primed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="GDB:1324946"
/db_xref="taxon:9606"
/clone="IMAGE:416476"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone_lib="Soares_fetal_liver_spleen_infls_si"
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Pred. No. 2.2e-05
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                                                                                                                                                                                                                                                                                                                                                                                                                        WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1996)
On Apr 14, 1993 this sequence version replaced g1:716794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 560)
Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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              129
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                            M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="IMAGE:391659"
/clone_lib="Soares mouse embryo NbME13.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:1386942
                                                                                                                                                                                                               /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                          'sex-"unknown"
                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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85.48;
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ORGANISM
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W85213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lc
Fal: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Apr 18, 1995 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maria,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W85213 416 bp mRNA EST 12-SEP-1996 m£51bO9.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:408569 5', similar mentanti policias del musculus metaxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eutheria; Rodentia;
1 (bases 1 to 416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Theising, B., Wylie, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                   primer: -28M13 rev2 from Amersham
quality sequence stop: 375.
                    91
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Location/Qualifiers
                            complete cds (MOUSE);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
             M.Fatima Bonaldo.
                                                                                                                                                                                                 /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                             /clone_lib="Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:1397683
                                                                                                                                                                                                                                                                     _xref="taxon:10090"
one="IMAGE:408569"
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71.48;
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    replaced gi:775532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
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  BASE COUNT
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AUTHORS
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SOURCE
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DEFINITION
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W89656
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Best Local
                                                                                                                                                                                                                                                                                                                           source
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                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 492.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston,R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W89656.1 GI:1542182
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35; Conser
130
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                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/map="3 p24.2-p21.1"
/clone="IMAGE:420703"
                                                                                                                                                                note-"Vector:
                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                        'sex="unknown
                                                                                                                                                                                                                                                                                                                                      lon/Qualifiers
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Pred. No. 10;
0; Mismatches
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82 TGCTAATCCATACTTTTTGGATAGACGCCAAGAACTATGTGGAAGTGAC 130
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This clone is available royalty-free through LLNL;
IMAGE_Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/Mouse EST project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 517)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mf81f04.rl Soares mouse embryo NbMEl3.5 14.5 Mus musculus cDNA clone IMAGE:420703 5' similar to gb:L36962 Mus musculus metaxi mRNA, complete cds (MOUSE); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
'tissue_type="embryo"
'dev_stage="13.5-14.5dpc total fetus"
'lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                /clone_lib="Soares mouse embryo NbME13.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1996 this sequence version replaced g1:1404980
                                                                                                                                                                                                                           PT7T3D-Pac (Pharmacia) with a modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contact the
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BASE COUNT
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        TGCTAATCCATACTTTTTGGATAGACGCCAAGAACTATGTGGAAGTGAC 163
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                                                                        35,
                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: -28ml3 rev1 ET from Amersham High quality sequence stop: 443.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA222672 590 bp mRNA EST 12-MAR-1997 mv99a05.rl GuayWoodford Beler mouse kidney day 7 Mus musculus cDNA clone IMAGE:663152 5', similar to gb:L36962 Mus musculus metaxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 590)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Marrin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
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WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lc
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On May 9, 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The WashU-HHMI Mouse EST Project Unpublished (1996)
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                                                                                    Similarity
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                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:663152"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1995
                                                                                                                                                                                                                                                                           /dev_stage="juvenile (7 days old)"
/lab_host="SOLR (kanamycin resista
                                                                                                                                                                                                                                                                                                           /clone_lib="GuayWoodford Beier mouse kidney
/tissue_type="kidney"
                                                                                    39.7%;
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                                                                   Score 26.6; D
Pred. No. 10;
0; Mismatches
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Pred. No. 1
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AUTHORS
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ORGANISM
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KEYWORDS
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AA388232
LOCUS
                                                                                                                                              BASE COUNT
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JOURNAL
                                                    Matches
                                                                Query Match
Best Local
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                   18
High quality sequence stop: 445.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complete cds (MOUSE);, mRNA sequence.
AA388232
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                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   house mouse
                                                                                                                                               134
                                                 39.7%; ilarity 71.4%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mouseest@watson.wustl.edu
                                                                                                                                                                   constructed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Ko mouse embryo ll 5dpc'
                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="11.5dpc"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                  't1ssue_type="embryo"
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/clone="IMAGE:761280"
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/strain="C57BL/6J"
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                                               Score 26.6; DI
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0; Mismatches
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WashIngton University School of MedicineP
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1407058.
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Marra, M., Hiller, L., Allen, M., Bowles, M., Dietrich, N., Dub Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                             3'. The cDNAs were ligated to LL-Sal3A: 5'
GCTARTGACGTCGACTATCC 3' and LL-Sal3B: 5'
GCTARTGACGTCGACTATCC 3' and LL-Sal3B: 5'
GGATACTCGACGTCAAT 3'. The cDNAs were size-selected and amplified by long-range PCR using Ex Taq polymerase for 18 cycles. The PCR-amplifiable cDNA mixture went through one round of equalization and was digested with SalI/NotI and cloned into the SalI/NotI sites of the pSPORTI plasmid vector (Life Technologies). The library was
                                                                                                                                                                                                                                                                                                                                                     /note="Organ: embryo; Vector: psport1; Site_1:
Site_2: Not1; Total RNAs were extracted from 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bowles, M., Dietrich, N., Dubuque, T.,
Ko and Dr. Xiaohong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from 11.5 dpc
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TGCTAATCCATACTTTTTGGATAGACGCCAAGAACTATGTGGAAGTGAC

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RESULT 15
AA719305
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                                                                                                                                                    TGCTAATCCATACTTTTTGGATAGACGCCAAGAACTATGTGGAAGTGAC 192
AA719305 479 bp mRNA EST 30-DEC-1997 zh35c02.sl Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:414050 3' similar to contains L1.tl L1 repetitive element ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
WashUrHHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubudeisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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vm16d07.rl Knowles
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 545)
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153 c 137 g
                                                                                                                                                                                                                                                                                                                                                                                               o - UGGTUGACUGTUGACUGTTTTTTTTTTTTTTT-3'. cDNAs were cloned into the Noti/Sali sites of a pSPORT vector (I Technologies). Two different size selections: B1 (incorts) and no "
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: embryo; Vector: psport; Site_1: Not1; Site_2: SalI; Cloned unidirectionally from mRNA prefrom 800 blastocysts. Primer: SalI(dT): 5'-CGGTCGACCGTCGACCGTTTTTTTTTTTT-3'. CDNAs were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="embryo (pre-implantation)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="B6D2 F1/J"
/db_xref="taxon:10090"
/clone="IMAGE:990349"
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/tissue_type="blastocyst"
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71.48;
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Whes Solter mouse blastocyst B1 Mus musculus cD
10349 5' similar to gb:L36962 Mus musculus metax
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Pred. No. 10;
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Search completed: Job time: 14287 se

September 17, 1999,

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AUTHORS
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                                                                                                        TTTATTCTAGTTCCAATTGCTAATCCAGCATTTGTGGATAGCTGCAAACTGCGATATGTA 60
AGTTA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                             l Similarity 63.1
41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 479)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMAGE Consortium (info@image.llnl.gov) fo
seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 474.
Location/Qualifiers
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On Nov 6, 1997 thi
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AA719305
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                                                                                                                                                                                                                                                             124
                                                                                                                                                                                                                                                                                      3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and Conned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares
                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="IMAGE:414050"
/clone_llb="Soares_pineal_gland_N3HPG"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="GDB:1319321"
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Searched:

AF037646 Homo sapi U40583 Human alpha L37663 Mus musculu L31619 Rattus ratt S53987 nicotinic r x93604 B.taurus mR X52295 Chicken alp X68586 G.gallus mR X52296 Chicken alp G47584 Z5357\_1 Ze AF143847 Heliothis AC005890 Drosophil AC004326 Drosophil AC004326 Drosophil AC007291 Drosophil AC007291 Drosophil AC007291 Drosophil M33952 Rat neurona U21319 Caenorhabdi X15834 R.norvegicu U42976 Rattus norv AL035252 Human DNA

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Human a7 nicotinic acetylcholine receptor mRNA.
L25827
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Eukaryota; Metazoa; Chordata; Craniata; Vertebra
Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                      125827.1 GI:438616 nicotinic acetylcholine receptor alpha 7 subunit; transmembrane
                                                                                                    Doveette-Stamm, L., Monteggia, L.M.,
Lee, J., Tian, J. and Giordano, T.
Cloning and sequence of the human a
                                                                                                                                                                                                                                   Homo sapiens (library: Clontech HL1065b; ATCC 37433) fetus brain
                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                      cDNA to mRNA.
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M5541 Capra hircu
AF143846 Heliothis
AF045765 Homo sapi
AC007582 Drosophil
U62904 Gallus gall
AJ223978 Bacillus su
299120 Bacillus su
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2001795 Pan troglod
201594 M.musculus
238015 M.musculus
26004728 Drosophil
AC006447 Mus muscu
AC006447 Mus muscu
AC006447 Mus muscu
AC005557 Drosophil

Result

Vertebrata;

Mammalia;

18-AUG-1994

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/dev\_stage="fetus"

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Submitted (04-FEB-1993) M. Katz, Univ of Pennsylvania Medicine, Dept of Neuroscience, 36th & Hamilton Walk, Stemmler Hall, Philadelphia, PA 19104, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peng, X., Katz, M., Gerzanich, V., Anand, R. and Lindstrom, J. Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from the SH-SY5Y cell line and determination of pharmacological properties of native receptors and functional alpha 7 homomers expressed in Xenopus occytes Mol. Pharmacol. 45 (3), 546-554 (1994)
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1 (bases 1 to 2087)
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98.8%;
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line="SHSY-5Y"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecular cloning and chromosomal localiza 7-nicotinic receptor subunit gene (CHRNA7) Genomics 19 (2), 379-381 (1994)
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H.sapiens CHRNA7 mRNA,
Z23141
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DGVHCVPTPDSGVVCGRMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRCQ
DESEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFVEAVSKDFA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the human alpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Groot Kormelink, P.J. and Luyten, W.H.
Cloning and sequence of full-length cDNAs encoding the human neuronal nicotinic acetylcholine receptor (nAChR) subunits be and beta4 and expression of seven nAChR subunits in the human neuroblastoma cell line SH-SY5Y and/or IMR-32
FEBS Lett. 400 (3), 309-314 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H.sapiens mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                          Revised by author 22-JAN-1998
On Jan 25, 1998 this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (27-SEP-1996) P.J. Groot
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Foundation, Exp. Mol. Biol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 1509)
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HDEHLLHGGQÞÞEGDÞDLAKILEEVRYIANRFRCQDESEAVCSEWKFAACVVDRLCLM
AFSVFTIICTIGILMSAÞNFVEAVSKDFA"
3 454 c 434 g 347 t
                                                                                                                                                                                                                                                                                                                                                                       , 1998 this sequence version Location/Qualifiers
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VQHCKLKFGSWSYGGWSLDLOMQEADISGYIPNGEWDLVGIPGKRSERFYECCKEPYP
DVTFTVTMRRRTLYYGLNLLIPCVLISALALLVFLLPADSGEKISLGITVLLSLIVFM
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ANDSOPLTYYFSLSLLQIMDYDEKNOYLTINIWLOMSWTDHYLOWNYSEYPGYKTYRF
PDGQIWKPDILLYNSADERFDATFHINYLYNSSGHCQYLPPGIFKSSCYIDYRWFPFD
                                                                                                                                                  precursor"
                                                                                                                                                                                                                                                                      /ce11
                                                                                                                                                                                                                                                                                    /cell_type="neuroblastoma"
/cell_line="IMR-32"
                                                                           /db_xref="PID:e1246208"
/db_xref="PID:g2808624"
/db_xref="GI:2808624"
                                                                                                                                                                 /product="nicotinic acetylcholine receptor alpha7 subunit
                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                    /gene="nAChRA7"
                                                                                                                                                                                 'codon_start=1
                                                                                                                                                                                                 'gene="nAChRA7"
                                                                                                                              protein_id="CAA69697.1"
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Pred. No. 1.6e-2
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Turnhoutseweg 30, 1
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1 (bases 1 to 1876)
Elliott, K.J., Ellis, S.B., Berckhan, K.J., Urrutia, A., Chavez-Noriega, L.E., Johnson, E.C., Velicelebi, G. and Harpold, M.M. Chavez-Noriega, L.E., Johnson, E.C., Velicelebi, G. and Harpold, M.M. Comparative structure of human neuronal alpha 2-alpha 7 and beta 2-beta 4 nicotinic acetylcholine receptor subunits and functional expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and beta 2, alpha 3, alpha 4, alpha 7, beta 2, and beta 2, alpha 3, alpha 4, alpha 7, beta 2, and beta 2, alpha 3, alpha 4, alpha 7, beta 2, and beta 2, alpha 3, alpha 4, alpha 7, beta 2, and beta 2, alpha 3, alpha 4, alpha 7, beta 2, and beta 2, alpha 4, alpha 7, beta 2, and beta 2, alpha 4, alpha 4, alpha 7, beta 2, and beta 2, alpha 4, alpha 7, beta 2, and beta 2, alpha 4, alpha 7, beta 2, and beta 2, alpha 4, alpha 7, beta 2, and beta 2, alpha 4, alpha 7, beta 2, and beta 2, alpha 4, alpha 7, beta 2, and beta 2, alpha 4, alpha 7, beta 2, and beta 2, alpha 4, alpha 7, beta 2, and beta 2, alpha 4, alpha 7, beta 2, and beta 2, alpha 4, alpha 7, beta 2, and beta 2, alpha 4, alpha 7, beta 2, and beta 2, alpha 4, alpha 7, beta 2, and beta 2, alpha 4, alpha 7, beta 2, and beta 2, alpha 4, alpha 4, alpha 7, beta 2, alpha 4, alpha 4, alpha 4, alpha 4, alpha 4, alpha 4, alpha 5, alpha 4, alpha 4,
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Human nicotinic acetylcholine receptor alpha7 subunit precursor,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (28-JUN-1996) Kathryn J. Elliott, Inc., 505 Coast Blvd. So., La Jolla, CA 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Elliott, K.J.
Direct Submission
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67, 1800
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DGYHCVPTPDSGVVCGRMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRCQ
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                                                                                                                                                                                                                                                                                                                           73. .138
73. .1581
/translation="mrcspggywlalaasilhyslogeforklykelyknynplerpy
ANDSOPLTYYFSLSLLQIMDYDEKNOVLTTNIWLOMSWTDHYLOWNYSEYPGYKTYRF
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VQHCKLKFGSWSYGGWSLDLQMQEADISGYIFNGEWDLYGIPGKRSERFYECCKEPYP
                                                                                                                                                                                                                         /codon_start=1
/product="nicotinic acetylcholine receptor alpha7 subunit
precursor"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="SIBIA lambda gtll library #3 (M. Williams)"
/cell_line="IMR32"
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/db_xref="PID:g1458120"
/db_xref="GI:1458120"
                                                                                                                                                                                                                                                                                                                                                                                                                 cell_type="neuroblastoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
db_xref="taxon:9606"
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98.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens alpha AF029838
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Leonardy.S., Gault,J., Logel,J., Drebing,C., Robinson,M.,
Breese,C., Dayis,A., Hopkins,J. and Freedman,R.
Direct Submission
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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192 c 163 g
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<1. .>641
                                                                                                                                                                                            /note="alpha 7 neuronal nicotinic receptor
                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="15"
                                                                                                                                                                                                                                                        /clone="CHRNA7-DR1"
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No. 1.6e-20;
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2.4e-20;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1712)
                                                      Homo sapiens
                                                                                                                                    AF036903 1712 bp mRNA PRI 16-C
Homo sapiens alpha-7 neuronal nicotinic acetylcholine
mRNA, alternatively spliced, partial sequence.
                                                                                                   ĀF036903.1
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Eutheria; E
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/map="15q14"
/clone="CHRNA7-DR2"
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Homo sapiens alpha-7 no
precursor RNA, partial
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Leonard, S., Gault, J., Logel, J., Drebing, C., Robinson, M., Berger, R.,
Breese, C., Davis, A., Hopkins, J. and Freedman, R.
Direct Submission
                                                                                             Leonard, S., Gault, J., Logel, J., Breese, C., Davis, A., Hopkins, J. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             precursor RNA,
AF037646
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                                                         Submitted (03-DEC-1997) Psychiatry, Sciences Center, 4200 E. 9th Ave., I
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref-"taxon:9606"
/db_xref-"dbsST:W52861"
/db_xref-"dbsST:AA037389"
/chromosome-"15"
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Reseach Genetics/IMAGE Consortium, LLNL"
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1. .1836
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∕organism="Homo sapiens'
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97.7%;
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Pred. No. 2.6e-20;
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                                                                                                                   Drebing, C., Robinson, M., and Freedman, R.
                                                         , University of Colorado Health Denver, CO 80262, USA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1977)
1 (bases 1 to 1977)
1 Logel,J., Drebing,C., Barnhart,M., Antle,C. and Leonard,S.
Nucleotide Sequence and Transcript Size of the Alpha-7 Neuronal
Nicotinic Acetylcholine Receptor in Human Postmortem Brain
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U40583.1
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Health Sciences Center,
Denver, CO 80262, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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/Clone_lib="Soares fetal liver spleen
Genetics/IMAGE Consortium, LLNL"
/note="unprocessed mRNA with intron"
<1. .1836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="alpha-7 neuronal nicotinic precursor; intron included in 5' x 503 c 469 g 481 t
/db_xref="GI:1125077"
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ANDSQPLTVYFSLNLLQIMDVDEKNQVLTTNIWLQMSWTDHYLQMNVSEYPGVKTVRF
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                                                                                                                                                                                           /tissue_type="hippocampus"
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                                                                                                                                                                                                                                                                'clone="pBShalpha7"
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                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
ob_xref="taxon:9606"
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                                                                                                                                                                                                                             'sex="male"
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                                                                                                       product="alpha 7 neuronal
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region"
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 1848)
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Mus musculus (strain BALB/c, sub_species domesticus) neonatal brain
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                                                                                                                  /Translation="MCGRRGGIWLALAAALLHYSLOGEFQRRLYKELYKNYNPLERPY ANDSOPLTVYFSLSLLOIMYDEKNQVLTTNIWLQMSWTDHYLQWNMSEYPGVKNVRF PDGOIWKPDILLYNSADERFDATFHTWYLVNASGHCOYLPFGIKKSSCYIDVRWFPFD VQQCKLKFGSMSYGGGBLDLQMQEADISSYIPMEWDLMGIGKRNBKFYEGCKEPFD VQQCKLKFGSMSYGGGBLDLQMQEADISSYIPMEWDLMGIGKNBKFYEGCKEPFD DVTYTVTMRRRTLYYGLNLLIPCVLISALALLVFLLPADSGEKISLGITVLLSLTVFM LLVAEIMPATSDSVPLIAQYFASTMIIVGLSVVVTVVLRYHHDDDGGKWFWTRII LLVAEIMPATSDSVPLIAQYFASTMIIVGLSVVTVVVLRYHHDDDGGKWFWTRII
                                                        DESEVICSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFVEAVSKDFA'
                                                                           LLNWCAWFLRMKRPGEDKVRPACQHKPRRCSLASVELSAGAGPPTSNGNLLYIGFRGL
EGMHCAPTPDSGVVCGRLACSPTHDEHLMHGTHPSDGDPDLAKILEEVRYIANRFRCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="BALB/c"
/sub_species="domesticus"
/db_xref="taxon:10090"
/dev_stage="neonatal"
                                                                                                                                                                                                                                                                     /product="neuronal acetylcholine receptor subunit alpha /protein_id="AAC42053.1" /db_xref="pID:9790854" /db_xref="GI:790854"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="BALB/c"
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                                                                                                                                                                                                                                                                                                                                                                     'codon_start-1
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Pred. No. 6.2e-20;
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On Aug 27, 1998 this sequence version replaced gi:468919
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (06-APR-1994) Department of Psychiatry and Biobehavioral Sciences, University of California, 760 Westwood Plaza, Los Angeles, CA 90095-1759, USA (bases 1 to 2106)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (27-AUG-1998) The Salk Institute, Torrey Pines Road, La Jolla, CA 92037, USA
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Direct Submission
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1 (bases 1 to 2106)
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DESEVICSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFVEAVSKDFA"
3 554 c 533 g 546 t
                                                        LLVAEIMPATSDSVPLIAQYFASTMIIVGLSVVVTVIVLRYHHHDDDGGKMPKWTRII
LLNWCAWFLRMKRPGEDKVRPACQHKPRRCSLASVELSAGAGPPTSNGNLLYIGFRGL
                                                                                           /translation="MCGGRGGIWLALAAALLHVSLQGEFQRRLYKELVKNYNPLERPVANDSGPLTVYFSLSLLQIMYVDEKNOYLTHINTAQMSWIDHLUQMMSEYPGYKNYRFPDGQUWKPDILYNAADERDATEHTNYLVNASGHQQYLPGGIFKSSCYIDVRWFPPDVQQCKLKFGSWSYGGWSLDLQMQDADISSYIPMGEWDLMGIPGKRNEKFYECKKEPPDVGYCKLKFGSWSYGGWSLDLQMQDADISSYIPMGEWDLMGIPGKRNEKFYECKKEPPDVTYTYTMRRRTLYYGLNLLIPCVLISALALLVFLLPADSGEKISLGITVLLSLTVFM
                                                                                                                                                                                                                                                                subunit"
                                                                                                                                                                                                                                                                                                                                                     /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/cell_type="neuronal"
/dev_stage="adult"
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/db_xref="PID:g3478619"
/db_xref="GI:3478619"
                                                                                                                                                                                                                                                                          'product="nicotinic acetylcholine receptor alpha
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nicotinic :
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Location/Qualifiers
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 3030)
Seguela,P., Wadiche,J., Dineley-Miller,K., Dani,J.A. and
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DESEVICSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAÞNFVEAVSKDFA"
1756 c 801 g 775 t
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DVTYTVTMRRRTLYYGLNLLIPCVLISALALLVFLLPADSGEKISLGITVLLSLTVFM
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andsqpltyyfslsllqimdydeknqylttniwlqmswtdhylqwnmseypgyknyrf
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                                                                                                                                                                                                                                                                                                                                                                                                   /gene="nicotinic receptor alpha 7 subunit"
/note="This sequence comes from Fig. 1. Protein sequence is in conflict with the conceptual translation;
mismatch(469[R->P])"
                                                                                                                                                                                                                                                                                                                               /product="nicotinic receptor alpha 7
/protein_id="AAB25224.1"
/db_xref="pID:9264771"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Artiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; 1 (bases 1 to 1551)
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B.taurus mRNA for alpha7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Revised by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37075-Goettingen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Garcia-Guzman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Garcia-Guzman,M., Sala,F., S
Gutierrez,L.M. and Criado,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95346009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 1551)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  taurus
                 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 taurus.
                                                                                                                                                                            /gene="alpha7"
477 c 4
                                                                                               EAVCSEWKFAACVVDRLCLMAFSVFTILCTIGILMSAPNFVEAVSKQFA
                                                                                                                  HCAPTPDSGVVCGRVACSPTHDEHLLHAG
                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Bos taurus"
/db_xref="taxon:9913"
/dev_stage="adult"
                                                                                                                                WCAWFLRMKRPGEDKVRPACQHNERRCSLASVEMSAVAGPPATNGNLLYIGFRGLDTM
                                                                                                                                                               FTVSIRRTLYYGLNLLIPCVLISALALLVFLLPADSGEKISLGITVLLSLTVFMLLV
                                                                                                                                                                                                                                                                                        'product="alpha7 nicotinic acetylcholine receptor subunit"
'protein_id="caa63802.1"
'db_xref="PID:e218821"
'db_xref="PID:e218821"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1996 this sequence version 
Location/Qualifiers
                                                           'gene≖"alpha7"
                                                                                                                                                                                                                                                              'db_xref="PID:g110338'
'db_xref="GI:1103383"
                                                                                                                                                                                                                                                                                                                                                                                                                             'tissue_type="adrenal gland medulla'
                                                                                                                                                                                                                                               db_xref="SWISS-PROT:P54131"
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                                                                                                                                                                                                                                                                                                                                                                                             gene-"alpha7"
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                 429
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N (Abt. XI), Hermann-Rein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sala, S., Campos-Caro, A.,
                 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               replaced g1:1103382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JAN-1996
                                                                                                                EEVRYIAHRFRCQDES.
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;; Bovinae;
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Query Match Best Local Similarity

67.4%; 87.1%;

Score Pred.

67.4; No. 1

DB 3; .2e-14;

Length 1551;

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BASE COUNT
ORIGIN
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AUTHORS
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AUTHORS
TITLE
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GGA7NAREC
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MEDLINE
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                382 AGTGCTGATGAACGGTTTGATGCTACGTTCCACACCAATGTGTTAGTGAATTCTTCTGGG 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         442 CACTGCCAGTACCTCCCTCCAGGCA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 CATTGCCAGTACCTGCCTCCAGGTA 93
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Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves;
Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 2696)
Schoepfer,R., Conroy,W.G., Whiting,P., Gore,M. and Lindstrom,J
Brain alpha-bungarotoxin binding protein cDNAs and MAbs reveal
subtypes of this branch of the ligand-gated ion channel gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (12-APR-1990) Schoepfer R., The Salk Institute for Submitted (12-APR-1990) Schoepfer R., The Salk Institute for Submission Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGA7NAREC 2696 bp mRNA VRT 12-AUG-19
Chicken alpha7 subunit of nicotinic acetylcholine receptor.
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90315158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X52295.1 GI:63077 alpha7 subunit; nicotinic acetylcholine receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schoepfer, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        superfamily
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                                                                                                              /product="mature protein (AA 1-480)"
580 c 555 g 784 t
                                                                                                                                                                             deeeaicnewkfaasvydrlcimafsyftiictigilmsapnfyeayskdfa"
                                                                                                                                                                                                       DGVHCTPTTDSGVICGRMTCSPTEEENLLHSGHPSEGDPDLAKII
                                                                                                                                                                                                                       LLVAEIMPATSDSVPLIAQYFASTMIIVGLSVVVTVIVLQYHHHDPDGGKMPKWTRVI
LLNWCAWFLRWKRPGEDKVRPACQHKQRRCSLSSMEMNTVSGQQCSNGNMLXIGFRGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Gallus gallus"
/db_xref="taxon:9031"
/dev_stage="18 day old embryo"
/tissue_type="brain"
/clone_lib="8Ch"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .2696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="alpha7 subunit of nicotinic acetylcholine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="protein precursor (AA -21-480)"
codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="pCh29-3 and pCh34-1."
                                                                                                                                                                                                                                                                      ITFTVTMRRRTLYYGLNLLIPCVLISALALLYFLLPADSGEKISLG:
                                                                                                                                                                                                                                                                                  ID_xref="SWISS-PROT:P22770"

ID_xref="SWISS-PROT:P22770"

IRANS.LACTOR="MGLERIMLENLLARACLYRESLOGEFORKLYKELLKNYNPLERPY

UDSQPLTYYFTLSLMQLENDVDEKNOYLUTINIWLOMYWTDHYLOMNVSEYFGVKNYRE

UDSQPLTYYFTLSLMQLENDVDEKNOYLUTINIWLOMYWTDHYLOMNVSEYFGVKNYRFFD

USCHLWKPDILLYNSADERFDATFHTNYLVNSSCHCQYLDFGIFKSSCYLDYRMFPFD

OKCHLKFGSWTYGGWSLDLQMCEADISGYISNCEWDLYGIFGKRTESFYECCKEPYP
                                                                                                                                                                                                                                                                                                                                                                                                                               protein_id="CAA36543.1"
ib_xref="PID:g63078"
  57.8%;
80.0%;
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  Score 57.8; DB 4;
Pred. No. 4.3e-11;
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                     Length 2696;
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CACTGCCAATATCTGCCACCAGGCA 437
                    CATTGCCAGTACCTGCCTCCAGGTA 93
                                                               AGTGCTGATGAGCGCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTCTTCTGGG 68
                                                                                      68;
                                                                                      Conservative
                                                                                     0;
                                                                                     Mismatches
                                                                                      17;
                                                                                      Indels
                                                                                     0;
                                                                                    Gaps
                                                                           . 0;
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Search completed: September 17, 1999, 22:04:21 Job time: 16444 sec

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Polynucleotide seq
Human death associ
DNA sequence encod
ACV synthetase gen
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Maize Xa21 gene DT
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V274T variant huma
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GalR2 recept
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Best Local Similarity
Matches 84; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1996; U09775.
07-JUN-1995; US-48472.
(SIBI-) SIBIA NEUROSCIEN
Elliott KJ, Harpold MM;
WPI; 97-065463/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; W09025.

Nucleic acids encoding nicotinic acetylcholine receptor sub-units used in screening to determine the effect of drugs on the receptor lisclosure; Page 71-73; 108pp; English.

A DNA sequence (T48239) codes for the alpha-7 subunit (W09025) of the human neuronal nicotinic acetylcholine receptor (nAChR). Host cells, esp. mammalian cells or amphibian occytes, carrying alpha-7 nucleic acids, opt. in combination with other alpha and/or beta subunit nucleic acids (see also T48232-38, T48240-41), express recombinant nAChR subunits useful for identifying cpds. that modulate the activity of human nAChRs.

Sequence 1876 BP; 369 A; 553 C; 531 G; 423 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T48239;
15-SEP-1994.
08-MAR-1994; U02447.
08-MAR-1993; US-028031.
(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC (SIBI-) SIBIA NEUROSCIENCES INC.
                                                                                                                                                                               14-MAY-1998 (first entry)
Human neuronal nicotinic acetylcholine receptor alpha-7 subunit cDNA.
Human; neuronal nicotinic acetylcholine receptor; alpha-7 subunit;
brain tissue; screening; NAChR; antibody; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9641876-A1
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Neuronal nicotinic acetylcholine
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                                                                         WO9420617-A2.
                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                         V12197
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                                                                                                                                                                                                                                                                                                                                                                                              421
                                                                                                                                                                                                                                                                                                                                    481 CATTGCCAGTACCTGCCTCCAGGCA 505
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                                                                                                                                                                                                                                                         standard; cDNA; 1876 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                   Location/Qualifiers
                                                                                                     /product-
                                                                                                                     /*tag=
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                                                                                         "neuronal nicotinic alpha-7 subunit"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 83.4; In Pred. No. 5.6e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INC
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les 1;
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                                                                                                       acetylcholine
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Result No.

Match

Length

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Description

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Streptococcus Vector containing

1732 16636 2038 2038 11601 13058 8697 1569

Searched:

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311585 seqs, 125096042 residues

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Scoring table:

IDENTITY\_NUC

Sequence:

Perfect score:

US-08-956-518A-99 100

CTGTTTCTAGTGCTGATGAG......CTGCCTCCAGGTAAGCTGCA 100

Run

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nucleic search, using sw model

Copyright

GenCore version 4.5 (c) 1993 - 1998 Compugen Ltd

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Human herpesvirus-Lactobacillus bact

September 18, 1999, 00:34:33; Search time 425.19 Seconds (without alignments) 58.842 Million cell updates/sec

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes a human neuronal nicotinic acetylcholine C receptor (NAChR) subunit. The cells expressing the alpha and/or beta CNAChR subunits may be used in a method of screening compounds to identify any which modulate the activity of human neuronal NAChR. Subunit specific antibodies may be used to monitor the distribution and expression density of various subunits in normal vs diseased brain ctissues. Testing of single receptor subunits or specific receptor subunit combinations with a variety of potential agonists or antagonists provides information with respect to the function and activity of the individual subunits and should lead to the identification and design of compounds that are capable of very specific interaction with one or unwanted side effects than drugs identified e.g. screening with cells that express a variety of subtypes.

Sequence 1876 BP; 369 A; 553 C; 530 G; 423 T;
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Best Local
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                                                                                                                                                                                                                                                                                02-JUL-1998.
22-DEC-1997; U23405.
20-DEC-1996; US-771737.
(ABBO ) ABBOTT LAB.
Briggs CA, Gopalakrishnan M
Roch J, Sullivan JP, Touma:
WPI; 98-377593/32.
Nucleic acid encoding variant of human alpha? nicotinic acetyl-choline receptor sub-unit - used to identify modulators of the receptor, potentially useful for treating neuro-degeneration, cancer, affective disorders etc.

Claim 14; Fig 2; 44pp; English.

This sequence encodes the V247T variant of human alpha? nicotinic acetylcholine receptor (nAChR) subbunit of the invention. Cells containing the DNA are used to express the protein and to identify modulators of alpha? nAChR activity or cytoprotective agents, e.g. antisense compounds or antagonists that are potentially useful for treating neurodegeneration, enzyme dysfunction, affective disorders and immune dysfunction, such as cancer, post-herpetic neuralgia, diabetic neuropathy, osteoarthritis, Alzheimer's or Parkinson's diseases, kuru,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-OCT-1998 (first entry)
V274T variant human alpha7 nAChR coding sequence.
Alpha7 nAChR; alpha7 nicotinic acetylcholine receptor subunit; cancer; neurodegeneration; enzyme dysfunction; affective disorder; therapy; immune dysfunction; diabetic neuropathy; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human neuronal nicotinic acetylcholine receptor subunits and DNA also transformed cells useful for screening cpds. which modulate activity of the receptor Claim 8; Page 78-79; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V44687 standard; cDNA; 1590
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98.88;
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Pred. No. 5.
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AGTGCTGATGAGCGCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTCTTCTGGG

Query Match Best Local S Matches 68

Similarity

57.8%;

Conservative

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Score 57.8; D pred. No. 2.4e 0; Mismatches

8; DB 1; 2.4e-12; ches 17;

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Gaps

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TRESULT TO SUPPLY TO SUPPLY SU
New isolated neuronal alpha-bungarotoxin-binding protein DNA - used PT New isolated neuronal alpha-bungarotoxin-binding protein.

PT to screen cholinergic agents and other drugs which may affect ligand PT binding, ion channel or other activities of the protein.

PS Claim 1; Fig 2A-B; 18pp; English.

CC 2 CDNA clones (T59196 and T59197) respectively code for the alphal CS subunit (W12368) and alpha2 subunit (W12369) of chick neuronal CS claim 18-day embryo chick brain cDNA library using a probe (see also CC T59198) based on the N-terminal amino acid sequence of chicken CC brain AbbBP. The probe isolated partial clone pCh9-1, which can coded the N-terminal portion of alpha1. A subclone, pCh29-3 (ATCC 40641), was used to rescreen the library, yielding clone pCh31-1 (ATCC 40640), which encoded the entire alpha2 sequence.

CC A probe based on the C-terminal region of pCh31-1 was used obtain CC clone pCh34-1 (ATCC 40649), encoding the C-terminal portion of CC alpha1. The cDNA clones can be used as probes to identify further CC alpha1. The cDNA clones can be used as probes to identify further CC ABBP subunits, and in the recombinant prodn. of ABBP.

SQ Sequence 2765 BP; 790 A; 604 C; 571 G; 804 T;
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T59196;
17-JUN-1997
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Neuronal alpha-bungarotoxin |
ligand binding; ion channel;
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P-PSDB; W12368.
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28-SEP-1989;
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US-413947.
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71. .136
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137. .1510
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alpha 1; cholinergic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T59197 standard; cDNA; 2101 BP. T59197; 17-JUN-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; W12369.

New isolated neuronal alpha-bungarotoxin-binding protein DNA - used to screen cholinergic agents and other drugs which may affect ligand to screen cholinergic agents and other drugs which may affect ligand binding, ion channel or other activities of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         subunit (W12368) and alpha2 subunit (W12369) of chick neuronal alpha-bungarotoxin binding protein (ABBP). They were isolated from an 18-day embryo chick brain cDNA library using a probe (see also T59198) based on the N-terminal amino acid sequence of chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              binding, ion channel or other activities of the protein.

Claim 1; Fig 3A-B; 18pp; English.

2 cDNA clones (T59196 and T59197) respectively code for the alphal
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24-JAN-1991 (first entry)
Plasmid pZPCl3 encoding neuronal nicotinic acetylcholine receptor
beta 4 subunit.
Rat; nAchR; ss.
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(SALK ) SALK INST BIOLOGICAL STUDIES
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                                                                                                                                                                                                                                                                               9 AGTGCTGATGAGGGGCTTTGAGGGCCACATTCCAGACTAACGTGTTGGTGAATTCTTCTGGG 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACTGCCAATATCTGCCACCAGGCA 503
                                                                                                                                                                                                                   CATTGCCAGTACCTGCCTCCAGGTAAGCTGCA 100
                                                                                                                                                                                       TCCTGTCAATATTCCTCCAGGCATTTTGAA
                                                                                                                                                                                                                                                           AGTGCGGATGAAAGATTCGATGCAACATTTCACACAAATGTGCTGGTGAATTACTCTGGA 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp.
                                                                                                                                                                                                                                                                                                                              65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schoepfer RD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56. .145
/*tag= b
146. .1498
/*tag= c
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56. .14
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                                                                                                                                                                                                                                                                                                                            Score 48.8; DB 1;
Pred. No. 5.2e-09;
0; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein alpha2 subunit cDNA.
protein alpha 2; cholinergic;
                                                                                                                                                                                       519
                                                                                                                                                                                                                                                                                                                                                                   Length 2101;
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AGCATCCAGTGGCTGCCCCCTGCTA 499

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                                                                                                                                                                The sequence encodes a novel neuronal nicotinic acetylcholine receptor subunit, beta 4. Plasmid process. AFTC 67893) was isolated from a cDNA library in lambda ZAP II prepd. from rat the sequence of the cDNA in the region encoded by the 5th cexon is identical to that determined for the genomic clone with the exception of a sustn. at posn. 720 of a t for a c (this does not alter the AA sequence); this may be due to a polymorphism the rat strains used for the genomic library and the cDNA library, or could have resulted from a reverse transcriptase error during prepn. of the cDNA. A sequence, the core of which is 44 bp long is repeated three times at the beginning of the 3 UT region. The function of this remains unknown. The protein subunit can combine with the known subunits, alpha-2, 3, and -4, and beta-2 to form previously unknown unctional receptors. The new subunit is expressed in the central and peripheral nervous systems and in
                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
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Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polya_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_unit
                                                                                                                                                                                                                                                                                                                                                   beta 4 sub-unit and DNA sequences encoding them. Claim 11; Fig 3; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                  (SALK ) SALK INST FOR BIOL STUD.
Heinemann SF; Deneris ES; Duvoisin
                                                                                                                                                                                                                                                                                                                                                                                                                                            14-MAR-1989;
12-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-SEP-1990.
14-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_unit
                                                                                                                                                                                                                                                                                                                                                                              New neuronal nicotinic acetyl:choline receptor - compsns. contg
                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; R07143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NO9010648-A.
                                                                                                                                        Sequence
                                                                                                                                                is expressed in the central and peripheral nervous systems and policy cells.
                           415
  69
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                        AATGCCGATGGCACCTATGAGGTGTCTGTCTACACCAACGTGATTGTGCGTTCCAACGGC 474
                                        AGTGCTGATGAGGCGTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTCTTCTGGG
 CATTGCCAGTACCTGCCTCCAGGTA 93
                                                                                       Similarity
                                                                                                                                        2460 BP;
                                                                          Conservative
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/*tag= g
/number= 2
1683. .1726
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/*tag= f
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                                                                                       30.6%;
                                                                                                                                        519 A;
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                                                                                     Score 30.6;
Pred. No. 0.
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                                                                            Mismatches
                                                                                                                                         767 C;
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                                                                                                    Length 2460;
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X23530
ID X2
AC X2
AC X2
DT 17
DE Ma
KW P1
DS Ze
PN WC
PD 255
PF 17
PF 17
PF 17
PF 11
PF HU
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PT WG
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Matches
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                                                                                                                                                                                            31-JUL-1997.
24-JAN-1997, U01301.
27-SEP-1996; US-721837.
24-JAN-1996; US-5590494.
01-APR-1996; US-626046.
01-APR-1996; US-626685.
     Nucleic acid molecule encoding galanin receptor antagonists of which are useful to treat eating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human galanin receptor GĀLR2 cDNA.
Galanin receptor; GALR2; human; agonist; antagonist; pain;
eating disorder; Alzheimer's disease; diabetes; ischaemia;
obesity; bulimia; anorexia; nociception; cognitive disorder;
sensory disorder; motion sickness; hypertension; convulsion;
                                                                      P-PSDB; W24562
                                                                                                                            Weinshank RL;
                                                                                                                                                                               (SYNA-)
                                                                                                                                                                                                                                                                                                                                                            WO9726853-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New RRK polynucleotides and nucleic acid constructs - used for generating transgenic plants resistant to Xanthomonas Claim 12; Page 57-58; 67pp; English.

This invention describes a method for conferring disease resistance in plants. The invention describes the use of novel genes and proteins belonging to the Oryza longistaminata and Oryza sativa receptor cassava, maize and tomato are also described. The genes and proteins cassava, maize and tomato are also described. The genes and proteins can be used for enhancing resistance to Xanthomonas in a plant, preferably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T79976 standard;
T79976;
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WPI; 99-204431/17.
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17-JUN-1999 (first entry)
Maize Xa21 gene DT4 DNA fragment.
Xa21; receptor kinase-like protein; multigene family; RRK; rice; DT4;
Xa21; receptor kinase-like protein; maize; tomato; Xanthomonas; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  705
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13-AUG-1997; US-910386.
(REGC ) UNIV CALIFORNIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 GCCAGTACCTGCCTCCAGGTAAGCTG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 CTGATGAGCGCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTCTTCTGGGCATT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                           97-393326/36.
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                                                                                                                                               SYNAPTIC PHARM CORP.

k T, Forray C, Gerald
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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102. .1265
/*tag= a
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Pred. No. 0.23
0; Mismatches
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                                                                                                                                    Linemeyer D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immune disease; anxiety;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .23;
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GALR2 - agonists and disorders, pain and
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                                                                                                                                 Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PT Alzheimer's disease

PS Claim 56; Fig 10; 236pp; English.

CC This cDNA clone codes for a novel claimed galanin receptor subtype,

CC designated GALRZ (see W24562). It was isolated from a human heart

CC CDNA library using primers based on rat GALRZ CDNA (see T79975).

CC Also claimed are: (1) an isolated nucled acid molecule (1) encoding

CC addition in the third intracellular domain; (2) a purified GALRZ

CC protein; (3) a vector comprising (1); and (4) a cell comprising the

CC GALRZ by (claimed). GALRZ antagonists can be used to treat obesity,

CC data anorexia or pain, or to decrease nociception (claimed).

CC Aponists and antagonists can also be used to treat other disorders,

CC hypertension, convulsion/epilepsy diabetes, glaucome, reproductive

CC disorders, gastric and intestinal ulcers, inflammation, immune

CC disorders and anxiety. Antibodies can be used to detect the

CC presence of GALRZ on the surface of a cell, while transgenic

CC mammals can be used to detect the

CC varying levels of GALRZ activity (claimed).

Sequence 1365 BP; 184 A; 498 C; 424 G; 259 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 44
Galanin receptor protein GalR2 and encoding polynucleotide - useful for e.g. identifying GalR2 receptor agonists or antagonists to regulate physiological responses e.g. to treat obesity and diabetes This cDNA sequence encodes a novel human galanin receptor protein, GalR2. This protein is useful for screening drugs for agonist and antagonist activity, Galanin has effects such as antinociceptive activity, smooth muscle contraction, cardiovascular activity, pituitary hormone release, cognition and increased food intake and identified drugs can regulate physiological responses associated with the GalR2 receptor, e.g.
                                                                                                                                                                                                                                              11-DEC-1997
05-JUN-1997; U09787
03-JUN-1997; US-6650
05-JUN-1996; US-6650
                                                                                                                                                                                         (FARB ) BAYER CORP.
Bloomquist BT, Cornfield
WPI; 98-042189/04.
                                                                                                                                                                                                                                                                                                                                                                                                                           Human GalR2 receptor partial cDNA.
Galanin receptor; GalR2; disease; treatment; screening; activity;
antinociceptive activity; obesity; stroke; smooth muscle contraction;
cardiovascular activity; diabetes; anorexia; pituitary hormone release;
Alzheimer's disease; neuropathic pain; endocrine disorder; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1218
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                                                                                                                                                                                                                                                                                                                                                                                                                         transgenic animal;
                                                                                                                                                                                                                                                                                                                   /product= GalR2
/note= "par+:-
                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                               "partial coding region of galanin recepto"
                                                                                                                                                                                                       LJ, Heeja Y, McCaleb
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                                                                                                                                                                                                                                                                                                                                                                                                                       human;
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RESULT 10
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Best Local Similarity
Matches 44; Conserv
antagonists to treat continued in the first part of obesity or cognitive disorders treatment of obesity or cognitive disorders

Example 6; Fig 7A-B; 57pp; English.

This is the DNA sequence of the human GalR2 gene that codes for a novel galanin receptor, designated GALR2 (see W61386), that is a member of the G-protein coupled receptor family. It was isolated from an EMBL3 SP6/T7 human genomic library using as probe a partigenes sequence that had been amplified from genomic DNA by PCR usi primers (see V28298-99) based on transmembrane regions of sometostatin and sometostatin-related gene receptors. The human carry game was mapped to chromosome 17q25. The invention provide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antagonists could be used to treat obesity and diabetes by reducing appetite and food consumption, or to treat Alzheimer's disease, stroke, neuropathic pain and endocrine disorders, whilst agonists could be used to treat anorexic conditions. The proteins are also useful in determining GalR2 agonist or antagonist amounts in a solution (e.g. blood plasma or serum) or to develop antibodies for determining receptor acids are useful for developing probes for determining receptor axpression levels e.g. to identify diseased or abnormal states, or antisense nucleotides to selectively inhibit expression of the receptor gene. They can also be used in gene therapy to isolate homologous sequences from other species e.g. primates, and to create transgenic mammals, e.g. knockout animals or non-human animals with native receptor replaced with the human homologue.

Sequence 1083 BP; 139 A; 406 C; 322 G; 216 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1027
                                                                                                                                                                                                         (MERI ) MERCK & CO INC.
(UTTE-) UNIV TEXAS HEALTH SCI CENT SAN ANTONIO.
(UTOR ) UNIV TOKONTO.
KOLAKOWSKI LF, ODOWÓ B, Sullivan K;
WPI; 98-388039/33.
P-PSDB; W61386.
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18-DEC-1997; U23892.
27-DEC-1996; US-033851.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human galanin receptor Galanin receptor; GalR2
                                                                                                                                                                      New human galanin receptor, GALR2, - useful to idemantagonists to treat conditions involving galanin,
                                                                                                                                                                                                                                                                                                                                                                                                        exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                       intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pain; cognitive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GalR2 gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human;
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    useful to identify
volving galanin, e.g.

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ligand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 obesity; anorexia;
coupled receptor;
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for
                                                          a partial
PCR using
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Best Local Similarity
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18-DEC-1997; U23891.
27-DEC-1996; US-033851.
(MERI ) MERCK & CO INC.
(UYTE-) UNIV TEXAS HEALTH S
KOLAKOWSKI LF, Tan CP;
       novel galanin receptor, designated GALR2 (see W61402), that is a member of the G-protein coupled receptor family. It was isolated from an EMBL3 SP6/T7 human genomic library using as probe a partial gene sequence that had been amplified from genomic DNA by PCR using primers (see V45092-93) based on transmembrane regions of somatostatin and somatostatin-related gene receptors. The human GALR2 gene was mapped to chromosome 17925. The invention provides rat, human and mouse GALR2 sequences (see W61461-63). Also provided are nucleic acids encoding these novel receptor sequences and assays to identify ligands particular to murine GALR2. Such ligands may be useful therapeutically e.g. to treat obesity or cognitive disorders involving excess galanin or to treat pain or
                                                                                                                                                                                      obesity, pain or cognitive disorders
Example 6; Fig 7A-B; 56pp; English.
This is the DNA sequence of the human GALR2 gene
                                                                                                                                                                                                                                                                                                                                                                                                                               exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rat, human and mouse GALR2 sequences (see W61385-86 and W61388). Also provided are nucleic acids encoding these novel receptors and assays to identify ligands particular to human GALR2. Such ligands may be useful therapeutically e.g. to treat obesity or cognitive disorders involving excess galanin or to treat pain or anorexia involving insufficient galanin. Nucleic acids encoding GALR2 are useful in assays for GALR2 and to produce hybridisation probes to screen for similar receptors or for GALR2 in other species. Sequence 3390 BP; 571 A; 1132 C; 1025 G; 660 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human galanin
Galanin recept
                                                                                                                                                                                                                                                New mouse galanin receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2811 GCCAGGACGGCC
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                                                                                                                                                                                                                                                                   P-PSDB; W61462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 GCCAGTACCTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cognitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor;
                                                                                                                                                                                                                                 to treat conditions involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /number I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorder;
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2 gene; human; ligand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВP
                                                                                                                                                                                                                                                  GALR2,
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Pred. No. 1.2;
0; Mismatches
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                                                                                                                                                                                                                                                                                                           SAN ANTONIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G-protein
                                                                                                                                                                                                                                 useful to identify lving galanin, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        obesity;
coupled r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29;
                                                                                                                                                                                     that codes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor;
                                                                                                                                                                                                                                 agonists and for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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OPPRESENTATION OPPRES
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New galanin receptor, GALR2 - useful, e.g. to identify agonists and antagonists, therapeutically to treat conditions involving excess or insufficient galanin such as obesity sexample 6; Fig 7A-B; 57pp; English.

This is the DNA sequence of the human GALR2 gene that codes for a cover galanin receptor, designated GALR2 (see W49003); that is a conver galanin receptor, designated receptor family. It was isolated from an EMBL3 SP5/T7 human genomic library using as probe a partial gene sequence that had been amplified from genomic DNA by PCR using commandation of somatostatin and somatostatin-related gene receptors. The human of GALR2 gene was mapped to chromosome 17g25. The invention provides cat, human and mouse GALR2 sequences (see W49002-04). Also provided are nucleic acids encoding these novel receptor sequences can dassays to identify ligands particular to GALR2. Such ligands can useful therapeutically e.g. to treat obesity or cognitive consolving excess galanin or to treat pain or anorexia involving insufficient galanin. Nucleic acids encoding GALR2 are useful in assays for GALR2 and to produce hybridisation probes to screen for similar receptors or for GALR2 in other species.
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18-DEC-1997; U23890.

27-DEC-1996; US-033851.

(MERI ) MERCK & CO INC.

SULLIVAN K, TAN C;

WPI; 98-388037/33.

P-PSDB; W49003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human galanin receptor GAIR2 genomic DNA.
Galanin receptor; GalR2 gene; human; ligand;
pain; cognitive disorder; therapy; G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2871
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V32649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             V32649 standard; DNA; 3390 BP.
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screen for
3390 BP;
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/note= "contains
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Pred. No. 1.
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coupled receptor; ss.
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Query Match Best Local Similarity

26.6%;

Score 26.6; Pred. No. 1

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Length 3390

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RESULT 1
X25011/c
ID X250
AC X250
DT 05-J
DE Anth
KW ESJ2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SClaim 1; Page 706-713; 2084pp; English.

28 Claim 1; Page 706-713; 2084pp; English.

29 A computer readable medium has been developed which has recorded on it

20 A computer readable medium has been developed which has recorded on it

20 State 1 and 1
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Best Local S
Matches 42
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14-NOV-1997; US-06609.
06-MAY-1997; US-044031.
16-MAY-1997; US-046655.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Dillon PJ, Kunsch CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2811
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                                                                                                                                                                                                                                                                                                                                                                                                              4022 TIGGIGATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 99-045171/04.

New isolated Enterococcus faecalis polynucleotides and polypeptides

- used to develop products for the detection of Enterococcus and for
use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterococcus faecalis genome contig SEQ ID NO:114. 
Enterococcus faecalis; contig; detection; Enterococ vaccine; attenuation; computer readable medium; ds. 
Enterococcus faecalis.
   Anther-specific ESJ2A ESJ2A gene; promoter; transgenic plant; ss. Arabidopsis thaliana.
                                                                                                                                                     05-JUL-1999 (first entry)
                                                                                                                                                                                   X25011 standard; DNA; 5002 BP
X25011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9850555-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 CTGGGCATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 TTTCTAGTGCTGATGAGCGCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTCTT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGATGAGGGCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTCTTCTGGGCATT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGCTAAGTGCTTTCAGGCCACATCAACCGTCAGGATGCTGTCGCCTTGCGCCTTTGGGCCCT 2812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13574 BP;
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                                                             ESJ2A gene and promoter.
moter; pollen; anther dehiscence; male sterile;
                                                                                                                                                                                                                                                                                                                                                                                                              4031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4658 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 25.2; DE Pred. No. 6.5; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2376 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2922 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 13574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Key promoter

ocation/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cexample, expression of the RNase barnase causes cell ablation, while expression of a plant hormone alters the developmental fate cof a cell. Plants are produced that have phenotypically normal collections, within phenotypically normal anthers, but in which the anthers do not dehisce and thus do not release the pollen comparison. The system allows the female to be multiplied with the cartificial male sterility gene in the homozygous state, since the comparison of the plant produces viable pollen. The system is suited to crops which have high seed multiplication, large amounts of collen, and/or separate male and female inflorescences. These comparisons allow for easy collection of pollen from non-dehiscing conthers, facile self-pollination and the minimisation of the area cof plants that have to be self-pollinated manually. Such an collection crop is the monocot maize, but the system is also applicable to e.g. wheat, barley, rice, fodder grass, banana, palm, orchid, custeful in the avoidance or reduction of pollen allergens and compared the self-cutter of asthma caused by pollen release. Sequence 5002 BP; 1702 A; 793 C; 821 G; 1686 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 50
isolating neuroblastic cells from a population - by detecting the expression of the Sox1 gene in the cells and sorting the cells to isolate those cells expressing Sox1 bisclosure; Page 43-44; 60pp; English.

A method has been developed for isolating neuroblastic cells from a cell population. The method comprises: (a) detecting Sox1 gene expression in the cells; and (b) isolating those cells expressing Sox1. Also described is a method for producing a cell committed to the neuronal lineage, comprising: (a) transfecting a pluripotent stem cell with a genetic construct encoding Sox1 expression; (b) culturing the stem cells to differentiate into neural cells; and (c) isolating those neural cells produced. The present sequence represents mouse Sox1 cDNA. Detection of Sox1 expressing cells is important in diagnosing and treating cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Generation of male sterile plants by controlling anther dehisce Example 1; F1g 3; 34pp; English.

Example 1; F1g 3; 34pp; English.

This is the DNA sequence of the ESJ2A gene of Arabidopsis thali

The gene was isolated from an A. thaliana genomic library using

Brassica napus SAC66 cDNA as probe. The invention relates to tuse of the ESJ2A promoter to reduce dehiscence and create male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sterile plants for use in hybrid seed production. The promoter is used to drive expression of a further nucleic acid sequence that results in prevention or reduction of anther dehiscence. For
                                                                                                                                                                                                                                                                                                (MEDI-) MEDICAL RES COUNCIL.
Lovell-Badge R, Pevny LH, Sm
WPI; 99-095759/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nervous system; neurological disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse; Sox1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse Sox1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X16153 standard;
X16153;
                                                                                                                                                                                                                                                                                                                                                                                                                   07-JAN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 ATCTAGTCATTGTTATAACTTGGCCTTAGTTA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 TGTGCGTAGTTTGCTTGAGAGACCTAAAGGTATGGTCGAGAGTCATGTCTTTGGAAATTT 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 TTCTGGGCATTGCCAGTACCTGCCTCCAGGTA 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 TGTTTCTAGTGCTGATGAGCGCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                    GB-013469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neuronal stem cell gene; neuroblastic cell; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA to mRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.8%;
                                                                                                                                                                                                                                                                                                                       Smith A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 24.8; I
Pred. No. 6.6;
O; Mismatches
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Search completed: September 18, 1999, 00:34:34 Job time: 19034 sec

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SUMMARIES

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## ALIGNMENTS

ACCESSION NID		DEFINITION	LOCUS	W03952	RESOLUTION
W03952 g1275817	IMAGE: 297134 5' similar to gb: X/029/ NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-7 CHAIN (HUMAN);, mRNA sequence.	za62c08.rl Soares fetal liver spieen inFLS Homo sapiens CUNA Clone	W03952 409 bp mRNA EST 19-APR-1996		

SOURCE

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                                                                                                         W52861 EST 10-OCT-199 cC03e02.rl Soares_parathyroid_tumor_NbhPA Homo sapiens cDNA IMAGE:321242 5' similar to gb:X70297 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-7 CHAIN (HUMAN); mrna sequence.
                                                                    W52861.1 GI:1350351
                 Homo sapiens
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The WashU-Merck EST Project
Thoublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further;
Seq primer: mob.REGA+ET
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Fax: 314 286 1810
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1 (bases 1 to 409)

Hillier_L. Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rikin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
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went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."
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/clone_lib_"Soares fetal liver spleen lNFLS"
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/db_xref="GDB:1242055"
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L.2e-17;
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AI292581 93941988
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This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further j
Insert Length: 1753 Std Error: 0.00
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1 (bases 1 to 560)

Hillier_L, Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-Merck EST Project Unpublished (1995)
On Jan 24, 1995 this sequence
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                       128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases,
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/note="Organ: parathyroid gland; Vector: pT7T3D
/note="Organ: parathyroid gland; Vector: pT7T3D
(Pharmacia) with a modified polylinker; Site_1:
Site_2: Eco RI; 1st strand cDNA was primed with
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/db_xref="GDB:1258900"
/db_xref="taxon:9606"
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/tissue_type="parathyroid tumor"
/dev_stage="adult"
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Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C.,

Brokstein, P., Lewis, S. and Rubin, G.M.

BDGP/HHMI Drosophila EST Project

Unpublished (1997)

On Jun 18, 1996 this sequence version replaced g1:1366631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G. M. Rubin-Molecular and Cell Biology
University of Callfornia Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: http://www.fruitfly.org/EST, hit genomic sequence AC005890 plate: 155 row: B column: 6 High quality sequence stop: 465.
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha: Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                               AI520119 569 bp mRNA EST 16-MAR-1999 LD40102.3prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD40102 3prime, mRNA sequence.
AI520119
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                                    Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J.,
Brokstein,P., Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (1997)
On Jun 5, 1998 this sequence version replaced q1:
                                                                                                                                      Drosophila melanogaster
Eukaryota; Metazoa; Arthopoda; Tracheata; Hexapoda;
Eukaryota; Metazoa; Endopterygota; Diptera; Brachyce
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila..
1 (bases 1 to 569)
Transculla M Bondioto 1 Sufficient
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Contact: Harvey,
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/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/lab_host="DH5 - alpha"
/note="organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
/khoI; Sized fractionated cDNAs were directly ligated into
poT2. Plasmid cDNA library."
151 c 162 g 137 t
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/db_xref="taxon:7227"
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                                         1998 this sequence version replaced g1:3188811.
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.00071;
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Fax: 510 643 9947
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Email: http://www.fruitfly.edu
Email: http://www.fruitfly.edu
Email:
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1 (bases 1 to 689)
Huang, G.M., Ng, W., Farkas, J., Chen, L., Liang, H.A., Gordon, D., Yu, J. and Hood, L.

Yu, J. and Hood, L.

Prostate Cancer Expression Profiling by cDNA Sequencing Analys Unpublished (1999)
On May 18, 1998 this sequence version replaced gi:3138627.
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University of California Berkeley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plate: 401 row: A column: 2
High quality sequence stop: 494.
                                                                                                                                                                                                                                                                                           University of Washington Department of Molecular I Washington, Seattle, WA
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Fax: 5106280108
                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Guyang Matthew Huang
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                                                                                                                                                                                                                                                                                                                                                                                                   Leroy Hood
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                                                                                                                                                                                                huanggm@yahoo.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L_F07.r mynorm
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/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
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/db_xref="taxon:7227"
/clone="LD40102"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="974B10; 19; Chromosome
/clone_lib="mynorm"
                                                                                                                                                                location/Qualifiers
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WA 98195
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                                      11;
                                                                                                                                                                                                                                                                                                                                        Box 357730, University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST 22-MAR-1
5', mRNA sequence.
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directly ligated into
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ORIGIN
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                                                                                                                                                                                                                                                                                                           WARNING: There is evidence that suggests that the plate of this clone contains both human and mouse Thus, the origin of this clone is uncertain. This kept in mind should you use this clone.
                                                                                                                                                                                                                                              Seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. J
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Eutheria; Primates;
1 (bases 1 to 318)
                                                                                                                                                                                                                                                                 MAGE
                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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IMAGE:530279 5', mRNA
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                                                                                                                                                                                                                                  s clone is available royalty-free through LLNL
3E Consortium (info@image.llnl.gov) for further
primer: -28M13 rev2 from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                               314 286 1800
314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
/clone_lib="Stratagene fibroblast (#937212)"
/lab host="SQLR cells (kanamycin resistant)"
/note="Vector: pBluescript SK:, Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dT. WI38
cell line. Average insert size: 0.8 kb; Uni-ZAP XR Vector;
-5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3' adaptor
                                                                                                                                                           /organism="Homo sapiens"
/db_xref="GDB:3919790"
                                                                                                                           /clone="IMAGE:530279"
                                                                                                                                             /db_xref="taxon:9606"
                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1995 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Note="Organ: Prostate; Vector: pBluescript; Directional CDNA library was constructed using Lambda ZP II kit (Stratagene), mRNA was extracted from a frozen normal prostate tissue (Mayo Clinic)."

a 147 c 134 g 204 t 57 others
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59.78;
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Catarrhini; Hominidae;
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Pred. No. 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (#937212)
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Best Local S
Matches 41
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                                                                                                                                                                                                                                                     IMAGE Consortium (info@image.linl.gov) Seq primer: -40M13 fwd. from Amersham.
                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; MAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
WARNING: There is evidence that suggests that the 384-well parent
plate of this clone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should hept in mind should you use this clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Chissoe, S., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                 4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g1664253
AA112074.1
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 322)
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zm62h12.s1 Stratagene fibroblast (#937212) Homo
IMAGE:530279 3', mRNA sequence.
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/organism="Homo sapiens"
/db_xref="GDB:3919790"
                                                                                                                                       /clone="IMAGE:530279"
                                                                                                                                                                       /db_xref="taxon:9606"
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RESULT 8
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   BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marra, M., Hiller, L., Allen, M., Bowles, M., Dietrich, N., Dubudesel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA123934.1
                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1996)
On Apr 14, 1993 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                            IMAGE Consortium (info@image.llnl.gov)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 383.
rounds of normalization, and was constructed Soares and M.Fatima Bonaldo."
89 c 106 g 116 t
                                                (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT/T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two
                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:575356"
                                                                                /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                          clone_lib="Soares 2NbMT"
                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
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Pred. No. 6.4;
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RESULT 9
AA267622/c
LOCUS
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274 TTTGCTGCAACATTAAACACTCACGAGTGAGGGCTATCCACTGCCCATTGTCACTGTCTC 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 CTTC 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 CCTC 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 TTTGACGCCACATTCCACACTAACGTGTTGGTGAATTCTTCTGGGCATTGCCAGTACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  In (bases 1 to 139)

1 (bases 1 to 139)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Morris,M., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Moore,B., Cahallenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Cahallenberg,K., Steptoe,M., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced g1:1282817.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA267622
                                                                                                                                                                                                                                                                                                                                                                                                                                   Putative full length read vector to vector length is 241 seg primer: -28ml3 rev2 ET fro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA267622.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMAGE:721443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGI:446939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .rl Soares mouse lympn n
21443 5', mRNA sequence.
3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTPT3 vector. RNA provided by Dr. Bertrand Jordan. Library constructed and normalized by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                            /note-"Organ: lymph node; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
lst strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:721443"
                                                                                                        'lab_host="DH10B"
                                                                                                                                                                                                                             /tissue_type="lymph node"
/dev_stage="4 weeks"
                                                                                                                                                                                                                                                                     /sex="male"
                                                                                                                                                                                                                                                                                             /clone_lib="Soares mouse lymph node NbMLN"
                                                                                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:1904376
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Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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Pred. No. 7
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lymph
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               musculus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83
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BASE COUNT

Length

408;

0

Gaps 83

0

02-JAN-1998

Mammalia;

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Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 CTTC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 CCTC 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 TITGCTGCAACATTAAACACTCACGAGTGAGGGCTATCCACTGCCCATTGTCACTGTCTC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 TITGACGCCACATICCACACTAACGTGTTGGTGAATTCTTCTGGGCATIGCCAGTACCTG 83
                                                                                                                                                                                                                                                                                                       High quality sequence stop: Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1996)
On Nov 29, 1993 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vf44e03.rl Soares mouse NbMH
5', mRNA secure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eutheria; Rodentia;
1 (bases 1 to 408)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA422190.1
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                                                                                                                                                                                                                                                                                                                 primer: -28m13 rev2 ET from Amersham
h quality sequence stop: 356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                314 286 1800
314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                          mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43
                              provided by Dr. Minoru Ko, constructed and normalized
                                                                                                                                                           /dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="IMAGE:846652"
                                                                                                                                                                                         'tissue_type="heart"
                                                                                                                                                                                                                  'clone_lib="Soares mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ø
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Pred. No. 4.7;
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                                                                                                                                                                                                                   "HMdN
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                      by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           replaced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gi:637644
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                                                                                                                                                                                                                                                                                                                                                                        contact the
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 BASE COUNT
                                                                                                                                                                                                                                                               FEATURES
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTGCTGCAACATTAAACACTCACGAGTGAGGGCTATCCACTGCCCATTGTCACTGTCTC 280
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                                                                                                                                                                                                                                                                     Seq primer: -28m13 rev1 ET from High quality sequence stop: 162.
                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. La
                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                              Putative full length read
                                                                                                                                                                                                                                                                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston, R.
The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                    ector to vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            i (bases 1 to 178)
Marra,M., Hillier,L., Allen,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eutheria; Rodentia;
1 (bases 1 to 178)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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    /clone_lib="Stratagene mouse
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                                                                                                                                          'sex-"females"
                                                                                                                                                                                                              organism="Mus musculus
/strain="C57BL/6"
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                                                                                                                                                                  lone="IMAGE: 1209228"
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                                                     62 TTCTGGGCATTGCCAGTAC 80
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                                                                                  TGTTTCTAGTGCTGATGAGCGCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTC 61
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AU010910 Schizosaccharomyces pc
Schizosaccharomyces pombe cDNA
AU010910
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Eukaryota; Fungi; Ascomyce
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National Institute of Radiological
9-1, Anagawa-4-chome, Inage-ku, Chi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ûnpublished (1998)
On Jan 17, 1998 this sequence
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Morimyo, M. and Mita, K.
Identification of expressed sequence tags of Schizosaccharomyces
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l: morimyo@nirs.go.jp.
Location/Qualifiers
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                                                                                                                                              Conservative
                                                                                                                                                                                                                               /note-"Vector: M13mp19; The cDNA 11brary of Schizosaccharomyces pombe was prepared by cloning cDNA into the Smal site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)" 87 c 81 g 140 t 11 others
                                                                                                                                                                                                                                                                                                                                                                                             /organism="Schizosaccharomyces/strain="972"
                                                                                                                                                                                                                                                                                                                                                  /clone="spc10518"
/clone=11b="Schizosaccharomyces pombe late log phase cDNA"
                                                                                                                                                                                                                                                                                                                                        'sex="h minus"
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57.0%;
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Pred. No. 14;
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pombe late log phase cDNA
NA clone spc10518, mRNA sequence.
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348
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                            61 CITCIGGGC 69
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                                                                                       1 CTGTTTCTAGTGCTGATGAGCGCCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATT 60
TCCATGGGC
                                                          Source: IMAGE Consortium, LINL
This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.linl.gov) for further information.
Insert Length: 1122 Std Error: 0.00
Seg primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
Insert Size: 1122
High quality sequence stops:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R72681 374 bp mRNA EST 02-JUN-1999
y193d04.r1 Soares breast 2NbHBst Homo sapiens cDNA clone
IMAGE:156295 5' similar to SP:A47285 A47285 MILK FAT GLOBULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1995)
On May 9, 1995 thi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parsons, J., Rifkin, L., Rohlfing, T., Soares
Trevaskis, E., Waterston, R., Williamson, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hillier, L., Clark, N., Dubuque, T.,
Holman, M., Hultman, M., Kucaba, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eutheria; Primates;
1 (bases 1 to 374)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 275
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4444 Forest Park Parkway,
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'clone="IMAGE:156295"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'organism="Homo sapiens"
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lab_host="DH10B (ampicillin resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                clone_lib="Soares breast 2NbHBst"
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Pred. No. 21;
0; Mismatches
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                                                                                                                                                                                                175 CAAAGAAAGTGTCAGTC 191
                                                                                                                                                                                                                                                           69 CATTGCCAGTACCTGCC 85
                                                                                                                                                                                                                                                                                                                                                                      9 AGTGCTGATGAGGGCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTCTTCTGGG 68
      Mu28g03.x1 Soares 2NDMT Mus I
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 66.
Location/Qualifiers
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1 (bases 1 to 216)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and waters and waters are better the standard of the sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1394413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston, R.
The WashU-HHMI Mouse EST Project
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is clone is available royalty-free through LLNL;
AGE Consortium (info@image.llnl.gov) for further j
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone_lib="Stratagene mouse melanoma (#937312)"
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58.4%;
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IMAGE: 640756 3'
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   183
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                                69 CATTGCCAGTACCTGCC 85
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CAAAGAAAGTGTCAGTC
                                                          AATGCTGATGTGTGTTTATGCCACACTCCAAACTACAGACTCAGTACAATATTTCAAA 182
                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 314 265 1010
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
On Jun 5, 1998 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                 Conservative
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                                                                                                                                                                                                  provided by Dr. Bertrand Jordan. Library went through two Soares and M.Fatima Bonaldo."
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/clone="IMAGE:640756"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"/strain="C57BL/6J"
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199
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Pred. No. 24;
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D>+abase Searched: Scoring table:

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em\_est8:\*
em\_est9:\*

em\_est11:\* em\_est10:\* em\_est7:\* em\_est6:\*

em\_est15:\* em\_est16:\* em\_est17:\*

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Title: Perfect score:

US-08-956-518A-102 689

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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

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nucleic search, using sw model
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                                                                                                RESULT 1
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AA697326 HL02253.5

A1492967 gz47c02.x

A1192683 ge62d07.x

A1192883 ge62d07.x

A1192683 ge62d07.x

A11956428 z151c02.s

W6693.r1

A1395069 vb77d03.y

AA408177 EST02759

A10815986 AU067986

A1085561 cy68ad4.x

A1085561 cy68ad4.x

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A11462417 ub62e06.x

A1467007 ub78b04.x

A1467017 ub78b04.x

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A1467017 ub78b06.s

A1586795 486061606

A1493905 MEST4-D6.

A1443300 sa4dh11.y

W27222 2649 Human

D22064 RICC10276A

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D24866 RICC10350A
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AA33244 EST37317
AI292581 GH15518.5
AA861176 ak36d09.s
AA460018 zx49h09.s
AA460018 zx49h09.s
AA464642 aj57a12.s
AI367541 qv93c12.x
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W52861 zc03e02.rl
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                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 143;
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1 (bases 1 to 409)

1 (lases 1 to 40
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Fax: 314 286 1810
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                         W52861 560 bp mRNA 10-00T-139 ac03e0:11 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA IMAGE:321242 5' similar to gb:X70297 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-7 CHAIN (HUMAN);, mRNA sequence. W52861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 263.
Location/Qualifiers
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/db_xref="GDB:1242055"
/db_xref="taxon:9606"
/clone="IMAGE:297134"
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37
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                                                                                                                                                                                                                                               The WashU-Merck EST Project Unpublished (1995)
On Jan 24, 1995 this sequence
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Hilller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Parsons,J., Waterston,R., Williamson,A., Wohldmann,P. and
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Fax: 314 286 1810
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/lab_host-DH10B (ampicillin resistant)"
/note-"Organ: parathyroid gland; Vector: pT7T3D
/note-"Organ: pT7T3D
/note-"Org
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/clone="IMAGE:321242"
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/dev_stage="adult"
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Fax: 4169785650
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On Apr 14, 1993 this sequence version
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primer: GAAATTAACCCTCACTAAAGGG.
Location/Qualifiers
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59, Last upd
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/note="Vector: Lambda ZAP Express; Site_l: EcoRI; XhoI; mRNA was purified from human fetal hearts (8)
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/db_xref="taxon:9606"
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Pred. No. 2.1e-16;
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R KAPPA B(NON-EXACT), mF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pathobiology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          replaced gi:502850.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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sapiens cDNA
nRNA sequence.
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Ouery Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                        248 CATGACAGCGGCTCGGGACT------------GGCTCCTTTTCCGCGCCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                191 GCGGGGAGAGGTGGAGCCGCGAGAGCTCGGCC---GGGGGCCCCGCCTGGTGGCCGCGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available at the RZPD in Berlin Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
                                                                                                                                                                                                                                                                                                                                                          63 CGTGACGGCGGCTCCGGGCTCCCCTTCCGCGCCCCGGCTCCCCTTCCGCGCCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone from S. Wiemann, s
sequencing consortium of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No s1 sequence available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens m
DKFZp586B2218)
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                                                                                                                                                                                                                                             CGTCCATCTTCGACAAGAACCACGAGCGA
                                                                                                                                                                                                                                                                          CCTCTATCTTCCAGGAGAACCAGGAGCCA 377
                                                                                                                                                                                                                                                                                               CGCCGGAGATGAGGGGAAGATGTCCGTGTCAGGGCTCAAGGCCGAGCTGAAGTTCCTGG
                                                                                                                                                                                                                                                                                                                     CCGCCGGAGGTGAGGGGAAGATGTCCATGTCAGGGTTCAAGGCCAAACCGAAGTTACTGG
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Eukaryota; Metazoa;
Euthería; Primates;
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AA333244.1
                                                                                                                         AA333244 335 bp mRNA EST
EST37317 Embryo, 8 week I Homo sapiens cDNA 5',
similar to interleukin-2 receptor, alpha chain,
                                                                                                              similar to interleukin.
protein, mRNA sequence.
AA333244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="DKrZp58682218" /clone=lib="896 (synonym: hute1). Vector pSport1; host DH10B; Sites Not1 + Sal1/MluI" /dev_stage="adult" /tissue_type="uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                            GI:1985508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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8a D-82152 Martinsried, GERMANY
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Pred. No. 6.5e
0; Mismatches
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Ppa B binding
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Chordata; Craniata; Catarrhini; Hominida

Hominidae; Homo

Vertebrata; Mammalia;

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                       KEYWORDS
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Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., gocayne, J.D., klikness, E.F., Weinstock, K.G., Gocayne, J.D., white, O., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Man Wai, C., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man Wai, C., White, O., Sutton, R.A., Ciine, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Clayton, R.A., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.C., Liu, L.I., Manmaros, S.M., Merrick, J.M., Glodek, A., Gnehm, C.L., Liu, L.I., Marmaros, S.M., Merrick, J.M., Kelley, J.M., Kelley, J.C., Liu, L.I., Mayren, D.T., Pelligrino, S.M., Kelley, J.M., Kelley, J.M., Shirley, R., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Phillips, C.A., Fyriges, T.A., Cotleman, T.A., Collins, E.J., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Shirley, R.J., Shirley, R.J., Shirley, R.J., Shirley, R.J., Weissner, P.S., Olsen, H., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Kaymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Brilds, C., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Dillion, P.J., Fannon, M.R., Ros
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Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns that assessment of contact of cDNA sequence based upon 83 million nucleotides of cDNA sequence based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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for clone availability, additional sequence and ex
information related to this EST, please check the
information related to this EST, please check the
index (http://www.tigr.org/tdb/hgi/hgi.html)
seq primer: M13 Reverse.
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                                                                                                                                                                                                                                                  01-DEC-1998
AT292581 607 bp mRNA
GH15518.5prime GH Drosophila melanogaster head pOT2 Drosophila
melanogaster cDNA clone GH15518 5prime, mRNA sequence.
AT292581
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2 Medical Center Drive, Rockvil
                                                                                                                                                                   Ā1292581.1 GI:3941988
fruit fly.
Drosophila melanogaster
Enkarvota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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/db_xref="taxon:9606"
/dlone_lib="Embryo, 8 week I"
/clone_lib="Embryo, 8 wks"
/dev_stage="embryo, 8 wks"
/note="Organ: Embryo, 8 weeks; vector: pBluescript SK-;
/not
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TITLE
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                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            398 TACAACAGCGCGGATGAGGGATTCGATGGCACGTATCACACCAGCGTTGTGGTCAAACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              575 TGCGATATTGCTGATGAGCGCTTTGACGCCACATTCCACACGTGTTGGTGTGAATTCT 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       635 TCTGGGCATTGCCAGTACCTGCCTCCAGGCATATTCAAGAGTTCCTGCTACATCG 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C. Brokstein, P., Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Jun 18, 1996 this sequence version replaced gi:1366631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
htt genomic sequence AC005890
plate: 155 row: B column: 6
plate: 155 row: B column: 465.
High quality sequence stop: 465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCGGCAGTTGTCTGTACGTGCCCCCTGGTATCTTCAAGAGCACATGCAAGATGG
                                                                                                                                                                                                                                                                                                                                              AAU61176 487 bp mRNA EST 04-JAN-1999
ak36d09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1408049
3', mRNA sequence.
AA861176
                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCI-GAP 1 to 487)

1 (bases 1 to 487)

NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

On Jan 9, 1998 this sequence version replaced gi:937098.
                                                                                                                                                                                                                                                                                                               AA861176.1
                                                                                                                                                                                                                                                                                                    EST
                             Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
cDNA_Library_Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157
CDNA Library Arrayed by: Greg Lennon, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DH5 - alpha"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
/note="Organ: head; Vector cDNAs were directly ligated into
xho1; Sized fractionated cDNAs were directly ligated into
pOT1. plasmid cDNA library."
pOT2. 151 c 152 g 137 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="GH Drosophila melanogaster head pOT2"
/sex-"male and female"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                        GI:2953316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Pred. No. 0.017;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   607;
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FEATURES

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DEFINITION
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 96.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            459 CAGTTCCAATTGCTAATCCAGCATTTGTGGATAGCTGCAAACTGTGATAT 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             533 CAATTCCAATTGCTAATCCAGCATTTGTGGATAGCTGCAAACTGCGATAT 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
        Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41m13 fwd. ET from Amersham.
                                                                              Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1 Tel: 314 286 1800
                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 274)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.

WashU-Merck EST Project 1997

Unpublished (1997)
                                                                                                                                                 Contact: Wilson RK
                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                              AA460018 274 bp mRNA 
zx49h09.s1 Soares_testis_NHT Homo 
3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                  Eukaryota;
                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                       EST
                                                                                                                                                                                                                                                                                                                                                                                                   92184902
AA460018.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primer:
                                                                                                                                                                    12, 1996 this sequence version replaced gi:1393691.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand was prepared from mRNA obtained from Clontech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratories, Inc., and primed with a Not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:1408049"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            th: 758 Std Error: 0.00
-40ml3 fwd. ET from Amersham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 39;
                                                                                                          Louis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA clone IMAGE:795617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 487;
                                                                                                        MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing Center information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I - oligo(dT)
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                                                                                  FEATURES
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AUTHORS
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KEYWORDS
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AA844642/c
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
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Best Local
                                                                  source
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В Š

RESULT

FEATURES

/map="1; 1" /clone="IMAGE:1394398" /organism="Homo sapiens" /db\_xref="taxon:9606" Location/Qualifiers COMMENT

TITLE JOURNAL

REFERENCE

AUTHORS

ACCESSION

RSION

WORDS

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255 TICCAATIGCTAATCCAGCATTTGCGGATAGCTCCAAACTGGGATAT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            536 TTCCAATTGCTAATCCAGCATTTGTGGATAGCTGCAAACTGCGATAT 582
 Insert Length: 497 Std
Seq primer: -40m13 fwd.
High quality sequence st
                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
Tumor Gene Index
Unpublished (1997)
                                                           www-bio.llni.gov/bbrp/image/image.html
                                                                       CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                            Email: Robert_Strausberg@nih.gov CDNA Library Preparation: M. Bento Soares,
                                                                                                                                                                                                 Contact: Robert Stra
Tel: (301) 496-1550
                                                                                                                                                                                                                                                     ő
                                                                                                                                                   Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 436)
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g2931093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       436 bp mRNA aj57al2.sl Soares_testis_NHT 3', mRNA servence
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                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
primer: -40m13 fwd. ET from quality sequence stop: 415.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cD was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT)
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/db_xref="GDB:6038961"
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                                                                                                                                                                                                             Strausberg, Ph.D.
                                                                                                                                                                                                                                      this sequence version replaced gi:1900948
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                                Std Error: 0.00
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                Amersham
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                                                                                                                                                                                                                                                                                         Anatomy
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CDNA clone IMAGE:13
                                                                                                                                                          Ph.D.,
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                                                                                                          Sequencing Center
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                                                                                                                                                          Fatima
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ORIGIN

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BASE COUNT
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98
  Q
                                                         /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1; SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Site_2: NotI; Cloned unidirectionally.
Average insert size 1.85 kb. 11539-012" 86 c 97 g 115 t
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BASE COUNT
ORIGIN
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AI367541/c
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AUTHORS
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ORGANISM
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                                                                                                                                                 FEATURES
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qv93c12.x1 NCI_CGAP_Ut2
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AI367541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 396)
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                                                                                                                                                                                                                                                CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
                                                                                                                                                         Insert Length: 1828 Std Error:
Seq primer: -400P from Gibco
High quality sequence stop: 370.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. " 96 C 103 g 122 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/clone="IMAGE:1989142"
/clone_lib="NCI_CGAP_Ut2"
/tissue_type="moderately-differentiated endometrial
/tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
                                                                                                                  organism="Homo sapiens"
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RESULT 11
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Unpublished (1997)
On Jun 5, 1998 this sequence version replaced gi:3188057
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D.,
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Tel: (301) 496*1550
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                                                                                            Similarity
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                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="pooled germ cell tumors"
//ab_host="DH10B"
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/clone_11b="NCI_CGAP_GC6"
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pred. No. 0.87
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No s1 sequence available
This clone is available at the RZPD in Berlin
Please contact the RZPD: Ressourcenzentrum, HG
Berlin-Charlottenburg, GERMANY; Email: clone@1
                                                                                                                                                                                                                              Sequence 521
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GACCATGGCCGGGTCCGACACCGCGCCCTTCCTCAGCCAGGCGGATGACCCGGACGACGG
                   CGTCTCCGGGCGCACTTNCCTCGCCTGTGTTCGGNCCATCCTCCTTTCTCCAGCCTCCTC
                                                                                                      CAGGCCGCCACATAGCTCCCGCCAAGTCCTCGGTGCCCCTTGCCATTTTCCAGCCGCGCT 172
                                          TTCCAATTCCTAATCCAGCATTTGCGGATAGCTCCAAACTGGGATAT
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                                                                                                                                                                                                                              BP.;
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/Clonce="DKF2p(null)El31"
/Clone_1bb="(null) (synonym: hmcfl).
/Clone_1bb="(null) (synonym: hmcfl).
DH10B; Sites NotI + SalI"
/dev_stage="adult"
/tissue_type="breast cancer"
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3a D-82152 Martinsried, GERMANY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                        634
                                                                                                  574 CTGCGATATTGCTGATGAGCGCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTC 633
                                                                            244
304 CACGGGAGAGGTCCTGGGGTTCCTCCGGCCATTTACCAGAGCTCCTGCACCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            453
                    TTCTGGGCATTGCCAGTACCTGCCTCCAGGCATATTCAAGAGTTCCTGCTACATCG 689
                                                                      CTTCAATAATGCCGATGGCAACTACGAGGTGCGCTACAAGTCCAACGTGCTGATTTATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGAGGTGAGGGGAAGATGTCCATGTCAGGGTTCAAGGCCCAAACCGAAGTTACTGGCCTC
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                                                                                                                                                        69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G. M. Rubin-Molecular and Cell Biology University of California Berkeley 539 LSA, Berkeley, CA 94720-3200, USA Fax: 510 643 9947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BDGP/HHMI Drosophila EST Project
Unpublished (1997)
On Nov 20, 1997 this sequence ve.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins.
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 494)
Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C.,
Brokstein,P., Lewis,S. and Rubin,G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA697326

494 bp mRNA
HI02253.5prime HL Drosophila melanogaster head BlueScript
Drosophila melanogaster cDNA clone HL02253 5prime similar to
M20316: D.melanogaster acetylcholine receptor-related protein
complete cds, mRNA sequence.

AA697326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: http://www.fruitfly.org/EST, Plate: 22 row: E column: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Harvey, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ÃA697326.1 GI:2700255
                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                        124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quality sequence stop: 416.
                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                  /note-"Organ: head--brain & sensory organ; Vector: BlueScript SK; Site_1: EcoRI; Site_2: XhoI; Constructed using Stratagene ZAP-cDNA Synthesis kit. Oligo dT-primed and directionally cloned at EcoRI and XhoI in BlueScript SK(+/-)"

114 c 127 g 129 t
                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="HL Drosophila melanogaster
/sex="male and female"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Drosophila
/db_xref="taxon:7227"
/clone="HL02253"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                        'lab_host="SOLR"
                                                                                                                                                                        59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    this sequence version replaced gi:1172316.
                                                                                                                                                  Score 40.8; Di
Pred. No. 1.9;
0; Mismatches
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                                                                                                                                                      47;
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                                                                                                                                                                                          494;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                  258 GCTCGGGACTGGCTCCTTTTCCGCGCCCCCTCCCGCCGGAGGTGAGGGGGAAGATGTCCATG 317
                                                                                                                                                                                                138 GTCCTCGGTGCCCCTTGCCATTTTCCAGCCGCGCCCCCACGAGGGTCACGGCGGCGGGGA 197
               165
                                                                                   106 CCGGGGCCGGGGCCGGGGCCGGGGCCGGGGCCGGT-GCTGGGGGCCGGGGCCGCG
                                                                                                                                                           46
                                                                                                                                                           GGCCGCGCTGCCCCGGTTCGCGCCCTGCTCGCGCGCTCTCTTGAGGCGCCCGCGTCCGGGG 105
             ACTGGAGCCGGGGCCGGAGCCGGAGCCGGGGCCGGGGCCGGGGCCAGGACCGAG
                                                                                                                                                                                                                                     105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert Length: 908 Std Error:
Seg primer: -400P from G1bco
High quality sequence stop: 65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: (301) 496-1550
Email: Robert C+----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
On May 18, 1998 this sequence version replaced gi:3136536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                   /note-"Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /map="21q22.1-3"
/clone="IMAGE:2030018"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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/lab_host="DH10B"
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Best Local Similarity 53.3%;
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258 GCTCGGGACTGGCTCTTTTCCGCGCCCCTCCCGCGGAGGTGAGGGGAAGATGTCCATG 317
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Location/Qualifiers
1. .557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        db_xref-"taxon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
                                                                                                                                                                                                                       Score 39; DB 'Pred. No. 5.4;
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138 GTCCTCGGTGCCCTTGCCATTTTCCAGCCGCGCTCCCACGAGGGTCACGGCGGGGGGA 197
                                           128 CCGGGGCCGGGGCGGGCCGGGGCCGGGGCCGG-GGCTGGGGCCGGGGCCGG
                                                                                            AI192683 557 bp mRNA 29-OCT-1998 q62607.1 Soares_fetal_lung_NbHL19W Home Sapiens CDNA clone 1MAGE:1743565 3' similar to SW:CDNC_HUMAN P49918 CYCLIN-DEPENDENT KINASE INHIBITOR 1C ; contains MER22.b3 TAR1 repetitive element ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 557)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)
On Jan 14, 1998 this sequence version replaced gi:1797633.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 862 Std Error: 0.00
Seq primer: -40UP from Gibco
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                    from the same fetus as the fetal heart library, fetal heart NbHH19W."
193 c 242 g 60 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:1743565"
/clone_lib="Soares_fetal_lung_NbHL19w"
/dev_stage="19 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'lab_host="DH10B (ampicillin resistant)"
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187 ACTGGAGCCGGGGCCGGAGCCGGAGCCGGGGCCGGGGCCGGGGCCAGGACCGCG 246
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Search completed: September 17, 1999, 21:28:33 Job time: 14297 sec

Database :

Searched:

Sequence:

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Title:
Perfect score:
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                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                        Score
                   30
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Match
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1 ACCCACACAGGCATATT
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59.970 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GénCore version Copyright (c) 1993 - 1998
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        L25827 Human a7
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AUTHORS
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                                                              Doveette-Stamm,L., Monteggia,L.M., Donnelly-Roberts,D., Wang,M.T., Lee,J., Tian,J. and Glordano,T. Cloning and sequence of the human a7 nicotinic acetylcholine
                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                       nicotinic acetylcholine receptor alpha 7 subunit; transmembrane
                                                                                                                                                              Homo sapiens (library: Clontech HL1065b; ATCC 37433) fetus brain
                                                                                                                                                                                                              L25827.1
                                                                                                                                                                                                                                       L25827
                                                                                                                                                                                                                                         HUMA7NAR 1559 bp mRNA PRI Human a7 nicotinic acetylcholine receptor mRNA.
                       Dev. Res. (1993) in press
Location/Qualifiers
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282244 Homo sapien
AB008264 Arabidops
AC005207 Homo sapi
AC007541 Homo sapi
AF143846 Heliothis
AL023803 Human DNA
AL031736 Human DNA
AC004582 Human Chr
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L10077 Rat neurona
X57032 B. taurus mR
L35901 Human nicot
X89745 H. sapiens m
Y08421 H. sapiens m
X87629 H. sapiens m
X87629 H. sapiens m
X87629 Rat nicotin
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X13931 Homo sapien
AC006080 Homo sapi
AC007284 Homo sapi
X52295 Chicken alp
X58295 Chicken alp
X68586 G.gallus mR
AF055129 Homo sapi
AL022476 Human DNA
AC005539 Homo sapi
AC0005406 Homo sapi
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Z23141 H.sapiens C
L31619 Rattus ratt
S53987 nicotinic r
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Y08420 H.sapiens m
U40583 Human alpha
U62436 Human nicot
AF029838 Homo sapi
AF029839 Homo sapi
AF036903 Homo sapi
AF0367646 Homo sapi
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AC004517 Homo sapi
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[ bases 1 to 2087)
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H. sapiens mRNA for nicotinic acetylcholine receptor alpha7 subunit
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On Jan 25, 1998 this sequence version replaced gi:1702915.
Location/Qualifiers
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Submitted (27-SEP-1996) P.J. Groot Kormelink, Janssen Research
Foundation, Exp. Mol. Biol. Dept., Turnhoutseweg 30, B-2340 Be
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Groot Kormelink, P.J.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (13-NOV-1995)
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1 (bases 1 to 1977)

Logel, ... Drebing, C., Barnhart, M., Antle, C. and Leonard, S. Nucleotide Sequence and Transcript Size of the Alpha-7 Neuronal Nicotinic Acetylcholine Receptor in Human Postmortem Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Denver, CO 80362, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leonard,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jnpublished
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                                                                                    426 a
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                                                                                                                                 /protesin_id="AAA83561.1"
/db_xref="piD:g1125077"
/db_xref="gi:1125077"
/db_xref="gi:1125077"
/db_xref="gi:1125077"
/db_xref="gi:1125077"
/translation="mrcspggvwlalaaslihvslogeforklykelyknynplerpy ANDSOPLTVYFSLNLLOIMDVDEKNOVLITNIWLOMSWTDHYLOWNVSBYPGVKTVRF PDGQTWKPDILLYNSADERFDATFHTNVLVNPSGHCQYLPPGIFKSSCYIDVRWFPFD VQHCKLKFGSWSYGGWSLDLOWOEADISGYIPWGFWDLWGIPGKRSERFYECCKEPYP DVTFTYTWARRETLYYGLNLLIPCVLISALALLVFLLPADSGEKISLGITVLLSLTVFM LLVABIMPATSDSVPLIAQYFASTMIIVGLSVVVTYTYLQYHHHDPDGGKMPKWTRVI LLNWCAWFLKWKRPGEDKVRFACOHKORRCSLASVEMSAVAPPPASNGNLLYIGFRGL DGYHHVPTDNSGVVCGRMACSPTHDEHLLHGGOPPEGGDDLAKILEEVRYIANNEFRCO
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                                                                                                            1514. .1977
                                                                                                                                                                                                                                                                                                                                       /product="alpha 7 neuronal nicotinic acetylcholine
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/dev_stage="20 yr old adul
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1. .1977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                'sex="male"
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/clone_lib="Clontech lambda
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/db_xref="taxon:9606"
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o. 0.0051;
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81.1%;

Score 30; Pred. No.

DB 10; 0.0052;

Length 1977;

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CAGGCATATTCAAGAGTTCCTGCTACATCG

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3'UTR
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                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 1876)
Elliott, K.J., Ellis, S.B., Berckhan, K.J., Urrutia, A.,
Chavez Noriega, L.E., Johnson, E.C., Velicelebi, G. and Harpold, M.M.
Comparative structure of human neuronal alpha 2-alpha 7 and beta
2-beta 4 nicotinic acetylcholine receptor subunits and functional
expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (28-JUN-1996) Kathryn J. Elliott, SIBIA Neurosciences, Inc., 505 Coast Blvd. So., La Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Elliott, K.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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          Conservative
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                                                                                                                                                                                    /TIANSLATION="MRCSPGGYWLALAASLLHVSLQGEFQRKLYKELVKNYNPLERPV
/TIANSLATION="MRCSPGGYWLALAASLLHVSLQGEFQRKLYKELVKNYNPLERPV
ANDSQPLTVYESLSLLQIMDVDEKNQVLTTNIWLQMSWTDHYLQWNSEYPGYKTYRE
PDGQIWKPDILLYNSADERFDATFHYNYLVNSSGHCQYLPPGIFKSSCYIDVRWFPFD
VQHCKLKFGSWSYGGWSLDLQWQEADISGYIPMGEWDLVGIFGKRSERFYECCKEPYP
DVTFTVFMRRRTLYYGLNLLTPCVLLSALALLVFLLPAGBKISLGITVLLSLTVFM
LLVAEIMPATSDSVPLIAQYFASTMIIVGLSVVVTVLVLQYHHHDDDGGKWEKWTRVI
LLWAEIMPATSDSVPLIAQYFASTMIIVGLSVVENSAVAPPPASNGNLLYIGFRGL
DGVHCVPTPDSGVVCGRMACSPTHDEHLHGGQQPEDDDLLKILEBVRYIANFFRCQ
                                                                                                                /product="nicotinic acetylcholine
1582..1876
553 c 531 g 423 t
                                                                                                                                                                    DESEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFVEAVSKDFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 73. .138
73. .1581
                                                                                                                                                                                                                                                                                                                                       /protein_id="AAB40114.1"
/db_xref="PID:g1458120"
/db_xref="GI:1458120"
                                                                                                                                                                                                                                                                                                                                                                                             /product="nicotinic acetylcholine receptor alpha7 subunit
precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="KEalpha7.3"
/clone_lib="SIBIA lambda gtll library #3
/cell_line="IMR32"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell.
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                         81.18;
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         0,
                         Score 30;
Pred. No.
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                     DB 10;
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                                     Length 1876;
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                    Gault, J., Robinson, M., Berger, R., Drebing, C., Logel, J., Hopkins, J., Moore, T., Jacobs, S., Meriwether, J., Choi, M.J., Kim, E.J., Walton, K., Bulting, K., Davis, A., Breese, C., Freedman, R., and Leonard, S. Genomic organization and partial duplication of the human alpha7 neuronal nicotinic acetylcholine receptor gene Genomics 52 (2), 173-185 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens alpha
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 641)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (15-OCT-1997) Psychiatry,
Sciences Center, 4200 E. 9th Ave.,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leonard, S., Gault, J., Logel, J., Breese, C., Davis, A., Hopkins, J.
                                                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity
30; Conserv
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Leonard, S., Gault, J.,
                Gault, J., Robinson, M., Berger, R., Drebing, C., Logel, J., Hopkins, Moore, T., Jacobs, S., Meriwether, J., Choi, M.J., Kim, E.J., Walton, R. Buiting, K., Davis, A., Breese, C., Freedman, R. and Leonard, S. Genomic organization and partial duplication of the human alpha7 neuronal nicotinic acetylcholine receptor gene Genomics 52 (2), 173-185 (1998)
                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 689), Porcor B. Drebing, C., Logel, J., Hopki
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                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="alpha 7 neuronal nicotinic receptor mRNA; used alternative splicing" 192 c 163 g 135 t
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/note="RACE product A/B/C/D"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                689 bp
alpha 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 30;
Pred. No.
                                                                                                                                                                                                                                                                  neuronal
                                                                                                                                                                                                                                                                                   mRNA
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                                                                                                                                                                                                                                                                   nicotinic
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                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11;
. 0.0048;
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Denver, CO 80262, USA
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                                                                                                                                                                                                                                                                       receptor mRNA sequence.
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                                                                                             Hopkins, J., Walton, K.,
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REFERENCE
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BASE COUNT
ORIGIN
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Best Local
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JOURNAL
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                                                                           misc_feature
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Direct Submission

Direct Submission

Submitted (15-OCT-1997) Psychiatry, University of Colorado Health Submitted (15-OCT-1997) Psychiatry, Colorado Health Submitted (15-OCT-1997) Psychiatry, Colorado Health Sciences Center, 4200 E. 9th Ave., Denver, CO 80262, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF036903
g3757807
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                                                                                                                                                                                                                                                                                                                                                                                                      Gault, J., Robinson, M., Berger, R., Drebing, C., Logel, J., Hopkins, J., Moore, T., Jacobs, S., Meriwether, J., Chol, M.J., Kim, E.J., Walton, K., Buiting, K., Davis, A., Breese, C., Freedman, R. and Leonard, S. Genomic organization and partial duplication of the human alpha? neuronal nicotinic acetylcholine receptor gene (CHRNA?) Genomics 52 (2), 173-185 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF036903.1
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                                                                                                                                                                                                                                                              Submitted (03-DEC-1997) Psychiatry, Sciences Center, 4200 E. 9th Ave., I cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                  (bases 1 to 1712)

(bases 1 to 1712)

Leonard, S., Gault, J., Logel, J., Drebing, C., Robinson, M., Berger, R., Breese, C., Davis, A., Hopkins, J. and Freedman, R. Direct Submission
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
                         /note="alpha-7 neuronal nicotinic acetylcholine receptor;
alternatively spliced"
a 489 c 457 g 410 t
                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="dbEST:W52861"
/db_xref="dbEST:AA037389"
                                                                                                  Reseach
                                                                                                /clone_lib="Soares papathyroid tumor NbHPA library
teseach Genetics/IMAGE Consortium, LLNL"
                                                                                                                                      /clone="32124
                                                                                                                                                        'chromosome-"l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.1%;
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. 0.0049;
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8 CAGGCATATTCAAGAGTTCCTGCTACATCG 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (03-DEC-1997) Psychiatry, Sciences Center, 4200 E. 9th Ave.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leonard,S., Gault,J., Logel,J., Drebing,C., Robinson,M.,
Breese,C., Davis,A., Hopkins,J. and Freedman,R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gault, J., Robinson, M., Berger, R., Drebing, C., Logel, J., Hopkins, J., Moore, T., Jacobs, S., Meriwether, J., Choi, M.J., Kim, E.J., Walton, K., Buiting, K., Davis, A., Breese, C., Freedman, R. and Leonard, S. Genomic organization and partial duplication of the human alpha? neuronal nicotinic acetylcholine receptor gene (CHRNA?) g9000837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                           acetylcholine receptor subunit alpha 7 unit.
                                                                                                                                                                                                                                                                                                                                                                      /note="alpha-7 neuronal nicotinic acetylcholine receptor
precursor; intron included in 5' region"
503 c 469 g 481 t
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="unprocessed mRNA with intron"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Soares fetal liver spleen
Genetics/IMAGE Consortium, LLNL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="dbEST:W03952"
/db_xref="dbEST:N73891"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNA, partial sequence.
                                                                                                                                                                                                                                                                                 Score 30; DB; Pred. No. 0.0
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neuronal nicotinic
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                                                                                                                                                                                                                                                                               DB 11; 1
0.0052;
hes 0;
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0.0051;
hes 0;
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Denver, CO 80262, USA
                                                                                                                                                                                                                                                                                                            Length 1836;
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                                                                  JOURNAL
MEDLINE
REFERENCE
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
HSCHRNA7A
                                                                                                                                                                                   REFERENCE
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                  DEFINITION
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                                                                                                                                                                  AUTHORS
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (29-JUN-1993) BICE CHINI, CCIPE, Rue de la
                                                                                     7-nicotinic receptor subunit ge
Genomics 19 (2), 379-381 (1994)
                                               Chini, B.
                                                                                94245214
                                                                                                                Heinemann, S.
Molecular cloning and chromosomal
                                                                                                                                                 Chini, B., Raimond, E., Elgoyhen, A.B., Moralli, D.,
                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                  223141.1 GI:457736
alpha7 nicotinic receptor subunit; cholinergic receptor; CHRNA7
                                                                                                                                                                       Primates; Catarrhin1; Hominidae; 1 (bases 1 to 1555)
                                                                                                                                                                                                                                                                                                                                           H.Sapiens CHRNA7 mRNA,
                                                                                                                                                                                                                                                                                                                                                              HSCHRNA7A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 88.6
31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
Eukaryota; Metazoa; Chordata; Craniata;
Entheria; Rodentia; Sciurognathi; Murida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Orr-Urtreger,A., Seldin,M.F., Baldini,A. and Beaudet,A.L. Cloning and mapping of the mouse alpha 7-neuronal nicotinic acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (strain BALB/c, sub_species domesticus) neonatal brain
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487 /
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PDGQIMKPDILLYNSADEREDATFHINVLVNASGHCOYLPPOIFKSSCYIDYBWFFFFF
VOOCKLKFGSWSYGGWSLDLOMOEADISSYIDNGEMPLMGIPGKRNEKFYECCKEPYE
DYTYTYMRRRFILYYGLHLIPCVLISALALLVFLLEADSGERISLGGITVLLSLTVFM
LLVAEIMPATSDSVPLIAQYFASTMIIVGLSVVTVLVKHHHDPDGKMEKFYECKEPYE
LLVAEIMPATSDSVPLIAQYFASTMIIVGLSVVTVLVLRYHHHDPDGKMEKFRGE
LGMHCAFTPDSGVVCGRLACSFTHDEHLMHGTHPSGGDPDLAKILEDVRYIANRFRCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DESEVICSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFVEAVSKDFA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="neuronal acetylcholine receptor subunit alpha/protein_id="AAC42053.1"
/protein_id="AAC42053.1"
/db_xref="PID:9790854"
/db_xref="GI:790854"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51. .1559
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MCGRRGGIWLALAAALLHVSLQGEFQRRLYKELVKNYNPLERPV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'tissue_type="brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.3%;
88.6%;
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Pred. No. 0.02
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                        mRNA
3' end
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                                                                                                                                                                                        Homo.
                                                                                                                  localization of
                                                                                                      (CHRNA7)
                                                                                                                                                                                                                                                                                                                                                                                                                                     507
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.021;
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Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
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                                                                                                                                             Balzaretti, M. and
                                                                                                             the human alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1848;
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 Cardonille,
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JOURNAL MEDLINE REFERENCE

2 (bases 1 to 1836) Leonard, S., Gault, J.,

TITLE

FEATURES

Center, 4200 E. 9th Location/Qualifiers

JOURNAL TITLE AUTHORS REFERENCE AUTHORS

(bases 1 to 1836)

REYWORDS RGANISM

Homo

sapiens

ERSION ACCESSION

ÃF037646.1 GI:3757808

RESULT AF037646 DEFINITION

v

AF037646 Homo sapiens precursor

1836 bp alpha-7

용 δÃ

Query Match 81.1 Best Local Similarity 100. Matches 30; Conservative

81.18;

<u>,,</u>

VERSION KEYWORDS

neuronal

GI:790853

ACCESSION DEFINITION

alpha 7 mRNA, L37663

cds..

RESULT MUSNARS LOCUS

В Š

294 CAGGCATATTCAAGAGTTCCTGCTACATCG

BASE COUNT ORIGIN

383

misc\_feature

'clone="

Query Match Best Local s Matches 30

Similarity 100. 30; Conservative

81.1%;

FEATURES

Montpellier,

Location/Qualifiers

34094 Cedex,

5, France

/organism="Homo sapiens" /db\_xref="taxon:9606"

source

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BASE COUNT
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TITLE
JOURNAL
REFERENCE
AUTHORS
JOURNAL
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Best Local Similarity
                                                                                                                                                                                               VERSION
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                                                                      REFERENCE
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TITLE
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                                                                                                                                                                                                                                                                                                              CAGGCATATTCAAGAGTTCCTGCTACATCG 37
                                                                                                                                                                                                                                  RATNARAD 2106 bp
Rattus rattus nicotinic
                                                                                                                                                                                                                  mRNA, complete cds.
L31619 M85273
                                                                                                                                   L31619.1 GI:3478618
                                                                                                          Nicotinic acetylcholine receptor subunit gene alpha 7 unpublished (1994)
                       Submitted (06-APR-1994) Department of Psychiatry and Biobehavioral Sciences, University of California, 760 Westwood Plaza, Los Angeles, CA 90055-1759, USA
                                                                                Boulter, J.
Unpublished (1992)
nirect Submission
                                                                                                                                                                                                                                                                                                                                                                                             320
                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                      (bases 1 to 2106)
                                                                                                    (bases 1 to 2106)
               (bases 1 to 2106)
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<1. .1437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide 7"
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/clone_lib="lambda gtll"
                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/product="cholinergic receptor, nicotinic, alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="CHRNA7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="cholinergic receptor, nicotinic, alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="CHRNA7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="PID: 945773"
/db_xref="GI: 457737"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein_id="CAA80672:1"
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                                                                                                                                                                                                                                                                                                                                       score 28.4; DB 10;
pred, No. 0.025;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted (27-AUG-1998) The Salk Institute, Torrey Pines Road, La Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence update by submitter on Aug 27, 1998 this sequence version on Aug 27 Location/Qualifiers
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S53987
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                                                                                                                                                                                                                                                                        GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 124020] from the original journal article. This sequence comes from Fig. 1.
                                                                                                                                                                                                                                                                                                                                                                                            J. Neurosci. 13 (2), 596-604 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.0%;
nilarity 85.7%;
Conservative
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANDSOPLTVYFSLSLLOINDVDEKNOVLTTNIWLOMSWTDHYLOWNNSEYPGVKNVRF
PDGQIWKPDILLYNSADERFDATFHTNVLVNASGHOOYLPFGIFKSSCYIDVRWFPFD
VQQCKLKFGSWSYGGWSLDLONQEADISSYIDNGEWDLMGIPGKRNEKFYECCKEPYP
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DESEVICSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFVEAVSKDFA"
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DVTYTYTMRRRTLYYGLNLLIPCVLSALALLVFLLPADSGEKISLGTTVLLSTTVFM
LLVAEIMPATSDSVPLLAQYFASTMIIVGLSVVTVIVLYYGHHDPDGGKMFKWTRII
LLNWCAWFLRMKRPGEDKVRPACQHRPRRCSLASVELSAGAGPPTSNGNLLYIGFRGL
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/db_xref="pID:93478619"
/db_xref="GI:3478619"
/translation="MCGGRGGIWLALAAALLHVSLQGEFQRRLYKELVKNYNPLERPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="nicotinic acetylcholine receptor alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue_type-"brain"
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                                                                                                                                                    /organism="Rattus sp."
/db_xref="taxon:10118"
/gene="nicotinic receptor alpha 7 subunit"
/note="This sequence comes from Fig. 1. P
                                                                                          /gene nicotinic receptor alpha 7 subunit
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Rattus.
                                             Protein sequence
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464 CCCTCCAGGCATATTCAAGAGCTCCTGCTACATTG 498
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                                                                                                                                                                                                                                                                   Submitted (30-NOV-1995) M. Garcia-Guzman, MAX-PLANCK INSTITUT FUER, FUER EXPERIMENTELLE MEDIZIN (Abt. XI), Hermann-Rein Strasse, 3, D-37075-Goettingen, FRG
                                                                                                                                                                                                                                                                                                                                                                                     alpha-Bungarotoxin-sensitive nicotinic receptors on bovine chromatfin cells: molecular cloning, functional expression and alternative splicing of the alpha 7 subunit Eur. J. Neurosci. 7 (4), 647-655 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Garcia-Guzman, M., Sala, F., S. Gutierrez, L.M. and Criado, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   x93604.1 GI:1181202
alpha7 gene; alpha7 nicotinic receptor; alpha7 subunit; nicotinic
acetylcholine receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Artiodactyla; Ruminantia;
                                                                                                                                                                                                                  by [3]
6, 1996 this sequence version replaced gi:1103382.
Location/Qualifiers
   /organism="Bos taurus"
/db_xref="taxon:9913"
/dev_stage="adult"
                                                                                                                                             /tissue_type="adrenal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="nicotinic receptor alpha 7 subunit"
/protein_id="AAB25224.1"
/db_xref="pID:g264771"
/db_xref="GI:264771"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is in conflict with the conceptual translation; mismatch(469[R->P])"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MCGGRGGIWLALAAALLHVSLQGEFQRRLYKELVKNYNPLERPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Pred. No. 0
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                                                                                                                                             gland medulla"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovinae;
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BASE COUNT
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                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (19-JUN-1997) K. Schiebel, Institute of Human
Im Neuenhelmer Feld 328, D-69120 Heidelberg, FRG
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2251)
Schiebel, K., Winkelmann, M., Mertz, A., Xu, X., Page, D.C., Weil, D., Petit, C. and Rappold, G.A.
Abnormal XY interchange between a novel isolated protein kinase gene, PRKY, and its homologue, PRKX, accounts for one third of a (Y+)XX males and (Y-)XY females
Hum. Mol. Genet. 6 (11), 1985-1989 (1997)
                                                                                                                                                                                                                                                                                                                                                             Schiebel, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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     /!usedin=Y13927:pRKY_CDS
/usedin=Y13927:pRKY_RNA
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426 c 475 g 686
                                                                                                                                                        /clone_lib="PAC"
/clone="152F08"
/map="p11.2"
                                                            'number=5
                                                                                             'gene="PRKY"
                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="Y"
                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                            label=ex5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="GI:1103383"
/db_xref="GI:1103383"
/db_xref="GI:1103383"
/translation="MRGSLCLALAASILIVSLOGEFQRKLYKDLYKNYNPLERPVAND
SLPLTVYESLSLLOLMOVDEKROYLTINIHLOMTWIDHYLOWNASEYPGVKTVRFDYDO
CINKPDILLYNSADERFDATFHTNYLVNSSGHCQYLPFGIFKSSCYIDVRWFPFDYDO
CKLKFGSWSYGGWSLDLOMOEADISGYIPNGEWDLVGYLGKRSEKFYECCKEPYPDV7
FTVSIRRFLYYGLKLLIPCYLISALALLYFLLPADSGEKISGTTVLLSLTVFHLLV
AEIMPATSDSVPLIAQYFASTMIIVGLSVVVTYIVLOYHHHDDDGGKMEKTFRVYLLN
MCAWFLRMKRPGEDKVPPACOHNERRCSLASVEMSAVAGPPATNGNLLYIGFRGLDTM
HCAPTPDSGYVCGRVACSPTHDEHLLHAGQPSEGDPLAKILEDVRYIAHFRCQDES
                                                                                                                          gene-"PRKY"
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FEATURES

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/gene-"alpha7" 'gene="alpha7" sig\_peptide

JOURNAL MEDLINE REFERENCE

AUTHORS TITLE

JOURNAL

Direct Submission García-Guzman, M

(bases 1 to 1551)

SOURCE ORGANISM

caurus.

KEYWORDS H

ERSION

REFERENCE

(bases 1 to 1551)

AUTHORS

TITLE

DEFINITION ACCESSION RESULT BTA7

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Matches )uery Match

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21.772 Million cell updates/sec
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Matches 30
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15-SEP-1994.
08-MAR-1994; U02447.
08-MAR-1993; US-028031.
(SALK ).SALK INST BIOTECHNOLOGY IND AS (SIBI ) SIBIA NEUROSCIENCES INC.
Elliott KJ, Ellis SB, Harpold MM; WPI; 94-303024/37.
P-PSDB; W44153.
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07-JUN-1996; U09775.
07-JUN-1995; US-484722.
(SIBI-) SIBIA NEUROSCIENCES I Elliott KJ, Harpold MM;
WPI; 97-065463/06.
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A DNA sequence (748239) codes for the alpha-7 subunit (W09025) of the human neuronal nicotinic acetylcholine receptor (nAChR). Host cells, esp. mammalian cells or amphibian ocytes, carrying alpha-7 subunit nucleic acids, opt. in combination with other alpha and/or beta recombinant nAChR subunits useful for identifying cpds. that modulate the activity of human nAChRs.

Sequence 1876 BP; 369 A; 553 C; 531 G; 423 T;
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Human neuronal nicotinic acetylcholine receptor alpha-7 subunit cDNA.
Human; neuronal nicotinic acetylcholine receptor; alpha-7 subunit;
brain tissue; screening; NAChR; antibody; ds.
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T48239 V12197

1590 2769 3496 2082 2082 2363 51955 2377 2664 2277 2377 1375

Alpha4 subunit

Neuronal

Human neuronal

Description

Searched: Scoring table:

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311585 seqs, 125096042 residues

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pr activity of the receptor
pr Claim 8; page 78-79; 99pp; English.
CC The present sequence encodes a human neuronal nicotinic acetylcholine
CC The present sequence encodes a human neuronal nicotinic acetylcholine
CC RACHR Subunit The cells expressing the alpha and/or beta
CC RACHR Subunits may be used in a method of screening compounds to
CC Identify any which modulate the activity of human neuronal NACHR.
CC Identify any which modulate the activity of numan neuronal NACHR.
CC Identify any which modulate the activity of numan vs diseased brain
CC and expression density of various subunits in normal vs diseased brain
CC subunit specific antibodies may be used to monitor the distribution
CC subunit specific antibodies may be used to monitor the creeptor
CC subunit combinations with a variety of potential agonists or antagonists
CC individual subunits and should lead to the identification and design of
CC individual subunits and should lead to the identification and design of
CC compounds that are capable of very specific interaction with one or
CC more receptor subtypes. The resulting drugs should exhibit fewer
CC unwanted side effects than drugs identified e.g. screening with cells
CC that express a variety of subtypes.
Sequence 1876 BP; 369 A; 553 C; 530 G; 423 T;
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Presult would encoding variant of human alpha? nicotinic prescribed acid encoding variant of human alpha? nicotinic prescribed acid encoding variant of used to identify modulators of preservity potentially useful for treating neuro-degeneration, preservity edisorders etc.

Prescribed affective disorders etc.

Prescribed acid to express the protein and to identify modulators of the DNA are used to express the protein and to identify modulators of the DNA are used to express the protein and to identify modulators of the DNA are used to express the protein encoders and immune compounds or antagonists that are potentially useful for treating the protein such as cancer, post-herpetic neuralgia, diabetic compounds or antagonists that are potentic neuralgia, diabetic compounds or such as cancer, post-herpetic neuralgia, diabetic compounds of such accaptantials, Alzheimer's or parkinson's diseases, kuru, comparently, osteoarthritis, Alzheimer's or parkinson's diseases, kuru, comparently, osteoarthritis, Alzheimer's or parkinson's diseases, kuru, comparently, while monoclonal the DNA are used to detect the protein for diagnosis (in vitro or by antibodies are used to detect the protein for diagnosis (in vitro or by antibodies are used to detect the protein for diagnosis (in vitro or by antibodies are used to detect the protein for diagnosis (in vitro or by antibodies are used to detect the protein has about 100-fold greater sensitivity to cholinergic receptor agonists (nicotine or acetylcholine) and response to these compared with will be accompanied to these compared with will be accompanied to the protein has about 100-fold greater sensitivity to cholinergic agonists decays more slowly, but the wild-type inward rectification is
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09-0CT-1998 (first entry)
09-0CT-1998 (first entry)
N9-0CT-1998 (first entry)
NACHR variant human alpha? nachR cotylcholine receptor subunit; cancer;
N1pha? naChR; alpha? nicotinic acetylcholine receptor subunit; cancer;
N1pha? naChR; alpha? nicotinication; affective disorder; therapy;
Neurodegeneration; enzyme dysfunction; affective disorder;
neurodegeneration; diabetic neuropathy; Alzheimer's disease;
immune dysfunction; diabetic neuropathy; Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V44687 standard;
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02-JUL-1998.
22-DEC-1997; U23405.
20-DEC-1996; US-771737.
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SQ
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T59196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 30
                                                                                                                                                                                                                                                                New isolated neuronal alpha-bungarotoxin-binding protein DNA - used protein conclinergic agents and other drugs which may affect ligand probability, ion channel or other activities of the protein. Figure 2A-B; 18pp; English.

CC 2cDNA clones (T59196 and T59197) respectively code for the alphal cc subunit (W12368) and alpha2 subunit (W12369) of chick neuronal cc subunit (W12368) and alpha2 subunit (W12369). They were isolated from CC alpha-bungarotoxin binding protein (ABBP). They were isolated from CC alpha-bungarotoxin binding protein (ABBP). They were isolated from CC alpha-bungarotoxin binding protein (ABBP). They were isolated from CC and the N-terminal amino acid sequence of chicken r9198) based on the N-terminal amino acid sequence of chicken cc ancoded the N-terminal portion of alpha1. A subclone, pCh29-3 cc encoded the N-terminal portion of alpha1. A subclone, pCh29-3 cc (ATCC 40641), was used to rescreen the library, yielding clone pCh31-1 (ATCC 40640), which encoded the entire alpha2 sequence. CC clone pCh31-1 (ATCC 40639), encoding the C-terminal portion of clones to ldentify further CC alpha1. The cDNA clones can be used as probes to identify further CC alpha1. The cDNA clones can be used as probes to identify further CC alpha1. The cDNA clones can be used as probes to dentify further CC alpha the C-terminal produm of ABBP.
 RESULT
T48237
ID T4
AC T4
AC T9
DT 05
DE N4
KW N
                                                                                                                                           밁
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Neuronal alpha-bungarotoxin bind
ligand binding; ion channel; ss.
Gallus sp.
                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-FEB-1997.
04-FEB-1997.
28-SEP-1989; 413947.
28-SEP-1989; US-413947.
(SALK ) SALK INST BIOLOGICAL STUDIES.
(SALK ) SALK INST BIOLOGICAL STUDIES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lindstrom JM, Sch
WPI; 97-118297/11.
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                                         T48237 stand
T48237;
09-APR-1997
Neuronal nicotinic acetylcholine receptor alpha-4 subunit DNA. Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmiligand-gated receptor; ds.
                                                                                                                                           498 CAGGCATATTTAAAAGCTCATGCTACATAG 527
                                                                                                                                                                                                              Local
                                                                                                                                                          8 CAGGCATATTCAAGAGTTCCTGCTACATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                      standard; DNA; 3496
                                                                                                                                                                                                    Similarity 83.2
25; Conservative
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milarity 100.0%;
Conservative 0
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137. .1510
/*tag= c
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binding
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                                                                                                                                                                                                         score 22;
pred. No.
0; Mismato
                                                                                ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein alpha1 subunit cDNA.
protein alpha 1; cholinergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C
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0.0015;
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3.1;
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                                                                                                                                                                                                                                            Length 2769;
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                              neurotransmitter;
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affect ligand
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PP Nucleic acids encoding nicotinic accept.

PT Nucleic acids encoding nicotinic accept.

PT used in screening to determine the effect of drugs on the inverse process of the sequence (T48237) codes for the alpha-4 subunit (W09023) of the human neuronal nicotinic acetylcholine receptor (naCha). Host cells, esp. mammalian cells or amphibian occytes, carrying alpha-4 cucleic acids, opt. in combination with other alpha and/or beta combinant nachar subunits useful for identifying cpds. that combinate the activity of human nachas.

CC modulate the activity of human nachas.

CC modulate acids BP; 590 A; 1215 C; 1084 G; 606 T;
                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
T59527
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FH
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PT
                                                                                               AU9656247-A.

09-JAN-1997.

28-JUN-1996; 056247.

28-JUN-1995; AU-003840.

(UYBO-) UNIV BONN.

(UYME-) UNIV MELBOURNE.

(WOME-) WOMEN'S & CHILDREN'S HOSPITAL.

Berkovic SF, Mulley JC, Phillips HA, P
Scheffer IE, Steinleinok, Sutherland GR

WPI; 97-100506/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 27
   Claim 5; Fig 13; 20pp; English.
The DNA sequence of the normal nAChR is given in T59527, the DNA sequence of the ADNFLE-inducing mutant is given in Mutations at codon 248, which have the effect of replacing
                                                                 CHRNA4 gene encodes neuronal fragment - used in diagnosis
                                                                                              P-PSDB; W11824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1996; U09775
07-JUN-1995; US-484722.
(SIBI-) SIBIA NEUROSCIENCES I:
Elliott KJ, Harpold MM;
WPP; 97-065463/06.
                                                                                                                                                                                                                                                                                                                                    nAChR; mutation; autosomal
                                                          obe epilepsy
                                                                                                                                                                                                                                                            mutation
                                                                                                                                                                                                                                                                                            misc_rna
                                                                                                                                                                                                                                                                                                         Key
                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                         ADNFLE; neuronal acetylcholine
                                                                                                                                                                                                                                                                                                                                               05-OCT-1997 (first entry)
Alpha4 subunit of normal nachR.
                                                                                                                                                                                                                                                                                                                                                                             T59527 standard;
T59527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9641876-A1
27-DEC-1996.
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Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTCCCCGGCCATTTACAAGAGCTCCTGCAGCATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . Similarity 73.(
27; Conservative
                                                                                                                                                                                                                    inducing
                                                                                                                                                                                                                             /*tag= b
/note= "TCC 248 TTC
                                                                                                                                                                                                                                                       /note= "ion channel"
1016. .1018
                                                                                                                                                                                                                                                                                       Location/Qualifiers
902. .1168
                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                    DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.8%;
73.0%;
                                                                                                                                                                                                                                                                                                                                                                                   2082
                                                                                                                                                                                                                    mutation
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                                                                                                                                                                                                                                                                                                                                dominant nocturnal
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                                                                nicotinic ace of autosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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Pred.
                                                                                                                                                                                                                                                                                                                         receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
No.
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                                                           acetyl:choline receptor
                                                                                                             GR,
                                                                                                                                                                                                               the ADNFLE-
T59528)"
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                                                                                                          Propping PJ;
3R, Wallace RH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
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                                                                                                                                                                                                                                                                                                                               frontal lobe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3496;
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                in T59528
                                                                                                                                                                                                                                                                                                                            epilepsy;
                                                           frontal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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RESULT
V12196
ID V1
AC V1
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RESULT
TO 528

ID 528

AC 75

DE AL

KW AD

OS HO

                                                                                                                                                                                            T CHRNA4 gene encodes neuronal nicotinic acetyl:choline receptor

fragment used in diagnosis of autosomal dominant nocturnal front

T lobe epilepsy

Claim 6; Fig 13; 20pp; English.

The DNA sequence of the normal nAChR is given in T59527,

the DNA sequence of the ADNFLE-inducing mutant is given in T59528.

Mutations at codon 248, which have the effect of replacing

serine by another amino acid (e.g. phenylalanine) in the sixth

c smino acid of the transmembrane domain 2 (M2) of the alpha4

subunit of nAChR have been found to be associated with ADNFLE.

The primers given in T59529 and T59530 were used in the

sequence 2082 BP; 367 A; 767 C; 592 G; 356 T;
                                                                                                             Matches
                                                                                                                                   Query Match
Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AU9656247-A.
09-JAN-1997.
28-JUN-1996;
28-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; W11825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mutation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alpha4 subunit of mutant nAChR (TCC 248 TTC). nAChR; mutation; autosomal dominant nocturnal ADNFLE; neuronal acetylcholine receptor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T59528;
05-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T59528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    serine by another amino acid (e.g. phenylalanine) in the amino acid of the transmembrane domain 2 (M2) of the all subunit of nAchs have been found to be associated with The primers given in T59529 and T59530 were used in the amplification of part of exon 5.

Sequence 2082 BP; 367 A; 768 C; 592 G; 35
                          1 ACCCACACAGGCATATTCAAGAGTTCCTGCTACATCG
                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                632
ACTCCCCGGCCATTTACAAGAGCTCCTGCAGCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ACCCACACAGGCATATTCAAGAGTTCCTGCTACATCG
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27; Conser
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27; Conserv
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AU-003840.
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illarity 73.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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1016. .1018
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inducing mutation (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                     56.8%;
73.0%;
                                                                                          Score 21; DB
Pred. No. 7.6;
0; Mismatches
                                                                                                 0
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Pred.
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                                                                                                                  DB
7.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Propping PJ;
GR, Wallace RH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the ADNFI
T59527)"
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  899
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                                                                                                                                   Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2082;
                                                                                        Indels
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V12196 standard; V12196;

CDNA;

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The present sequence encodes a human neuronal nicotinic acetylcholine creeptor (NAChR) subunit. The cells expressing the alpha and/or beta creeptor (NAChR) subunit and a method of screening compounds to NAChR subunits may be used in a method of screening compounds to compound the identify any which modulate the activity of human neuronal NAChR. CC subunit specific antibodies may be used to monitor the distribution cc and expression density of various subunits in normal vs diseased brain cc and expression density of various subunits or specific receptor cc tissues. Testing of single receptor subunits or specific receptor subunits or antagonists or subunit combinations with a variety of potential agonists or antagonists cc provides information with respect to the function and activity of the cc provides information with respect to the function and activity of the cc provides information with respect to the interaction with one or cc compounds that are capable of very specific interaction with one or compounds that are capable of very specific interaction with one or compounds that are capable of very specific interaction with one or compounds that are capable of very specific interaction with one or compounds that are capable of very specific interaction with one or compounds that are capable of very specific interaction with one or compounds that are capable of very specific interaction with one or compounds that are capable of very specific interaction with one or compounds that are capable of very specific interaction with one or compounds that are capable of very specific interaction with one or compounds that are capable of very specific interaction with one or compounds that are capable of very specific interaction with one or compounds that are capable of very specific interaction with one or compounds that are capable of very specific interaction with one or compounds that are capable of very specific interaction with one or compounds that are capable of very specific interaction with one or compounds tha
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Human neuronal nicotinic acetylcholine receptor alpha-4 subunit cDNA.
Human, neuronal nicotinic acetylcholine receptor; alpha-4 subunit;
brain tissue; screening; NAChR; antibody; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OB-MAR 1994; U02447.1
OB-MAR 1993; US-028031.
OB-MAR-1993; US-028031.
(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC (SBLF) SIBIA NEGROSCIENCES INC. ELLIOTT KJ, ELLIS SB, Harpold MM; WPI; 94-303024/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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15-SEP-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human neuronal nicotinic acetylcholine receptor subunits and DNA also transformed cells useful for screening cpds. which modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activity of the receptor claim 4: Page 74-75; 99pp; English
                                                                                                                                                                                                                                                                                  07-JUN-1999 (first entry)
07-JUN-1999 (first entry)
Tomato pest resistance Mi gene (copy 1).
Pest resistance; nematode resistance; disease resistance; Mi gene;
Pest resistance; nematode resistance; biological control; ss.
                                                                                                                                                                                                                                                                                                                                                     V26084 standard; cDNA; 51952 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                         626
                                                                                                                                                                                                                                                               tomato; transgenic plant; crop protection;
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 WO9815171-A1
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27; Conserv
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173. .2056
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/product= "neuronal nicotinic acetylcholine receptor
/product= alpha-4 subunit"
                                                                                                                                                                                                                        Cocation/Qualifiers
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/note=
42798.
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73.0%;
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nucleic
                                                       "copy 1
                                                                                                        "Mi gene (copy 2); encodes W55975"
.44461
                      "Mi gene (copy 1); encodes W55974"
                                                                                                                                                             .19932
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                                                                                                                                                                             promoter; specifically claimed c acid construct of Claim 9"
                                                                         gene promoter"
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with nematode resistance, Declared by genetic analysis to a region chromosome (BAC). Mi was localised by genetic analysis to this cof the tomato genome of about 65 kb. DNA corresponding to this cegion was cloned into BAC vectors. Sequence analysis of a 52 kb coresion was cloned into BAC vectors. Sequence analysis of probably a pseudogene. By RNA blot analysis, transcripts of probably a pseudogene. By RNA blot analysis, transcripts of copy contained by 4 kb corresponding to copy 1 and copy 2 were found in the copy and copy 2 were found in copy contained by 4 kb corresponding to copy 1 and copy 2 (see copy full-length transcripts of copy 1 (see v26082) and copy 2 (see copy full-length transcripts of copy 1 (see v26082) and copy 2 (see copy full-length transcripts of copy 1 (see v26082) and copy 2 (see copy 1) identical and contain structural features similar to known copy 1 identical and contain structural features similar to known copy 1 identical and contain structural features similar to known copy 1 identical and contain structural features similar to known copy 1 identical and contain structural features similar to known copy 1 identical and contain structural features similar to known copy 1 identical and contain structural features similar to known copy 1 identical and contain structural features similar to known copy 1 identical and contain structural features similar to known copy 1 identical and contain structural features similar to known copy 1 identical and contain structural features similar to known copy 2 identical structural features similar to known copy 2 identical structural features similar to known copy 2 identical and copy 2 identical structural features similar to known copy 2 identical structural features similar to known copy 2 identical and copy 2 identical structural features similar levels to the similar copy 2 identical structural features identical structural features identical structural features similar levels to the similar copy 2 identical structural features identical structura
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Best Local S
Matches 25
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09-OCT-1997; U18802.
10-OCT-1996; US-028191.
(REGC ) UNIV CALLFORNIA.
Bodeau J, Kaloshian I, Mi
Yaghoobi J,
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P-PSDB; W55974, W55975.

Nucleic acids encoding M1 polypeptide(s) conferring nematode

Nucleic acids encoding M2 polypeptide(s) conferring nematode

Nucleic acids encoding M2 polypeptide(s) conferring nematode

Nucleic acids encoding nematode

Nucleic acids encoding
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                                                                                                                                                                                                                                                                                 18-MAY-1995.

08-NOV-1994; U12859.

08-NOV-1993; US-149503.

(SALK ) SALK INST BIOTECHNOLOGY IN (SALK ) SALK IN (S
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30-NOV-1995
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Claim 2; page 43-46; 54pp; English.
DNA encoding the human nNAChR alpha2 subunit was isolated froma
human thalamus tissue cDNA library using corresp. rat cDNA. The
                                                                                                                                                              modulating activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is the nucleotide sequence of the tomato Mi locus associated
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nilarity 78.1%;
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therapy and for
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RESULT TA 8235 ID AC TA 8235 AC TA 8235 AC TA STANDAR NO STANDAR N
FTH OS
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V12199
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Matches 25
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                                                                       14-MAY-1998 (first entry)
Human neuronal nicotinic acetylcholine receptor alpha-2
                                          Human; neuronal nicotinic acetylcholine receptor; brain tissue; screening; NAChR; antibody; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                  Homo sapiens.
                                                                                                                                                      V12199 standard;
V12199;
                                                                                                                                                                                                                                                                                                           1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding nicotinic acetylcholine receptor sub-units used in screening to determine the effect of drugs on the receptor Disclosure, Page 49-52; 108pp; English.

A DNA sequence (T4823) codes for the alpha-2 subunit (W09021) of the human neuronal nicotinic acetylcholine receptor (nAChR). Host cells, esp. mammalian cells or amphibian cocytes, carrying alpha-2 nucleic acids, opt. in combination with other alpha and/or beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SIBI-) SIBIA NEURO
Elliott KJ, Harpol
WPI; 97-065463/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subunit nucleic acids (see also T48232-34, T48236-41), recombinant nAChR subunits useful for identifying cpds. modulate the activity of human nAChRs. Sequence 2664 BP; 518 A; 815 C; 743 G; 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T48235 s
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07-JUN-1996; U09775.
07-JUN-1995; US-484722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; W09021.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neuronal nicotinic acetylcholine receptor alpha-2 subunit DNA.
Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;
ligand-gated receptor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    insert of one clone obtd. was ligated with the insert of another clone to generate a full-length alpha 2 subunit cDNA. The DNA can be used to identify function nNAChRs. Cells contg. the DNA can be used nNAChRs. The human nNAChR alpha 2 subunit can be used to product the nucleic acids can be used in immunohistochemistry, diagnosis and and creating animal models.

Sequence 2277 BP; 451 A; 696 C; 643 G; 487 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-APR-1997
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25; Conserv
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73.5%;
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Pred. No. 29;
0; Mismatches
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1-2 subunit;
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PT Human aspartic protease and related DNA - which may be involved in PT processing of endothelin and pro-opiomelanocortin pro-hormone(s)  
CC Interest Sequence represents a partial cDNA sequence from a human  
CC espartic protease, isolated from a cDNA library of human origin. The  
CC espartic protease. Isolated from a cDNA library of human origin. The  
CC from human cDNA libraries having partial DNA sequences and also ESTs  
CC espartic protease. Compounds which inhibit aspartic proteases an  
CC espartic protease. Compounds which inhibit aspartic protease, especially  
CC used in therapy where needed. Important functions of aspartic proteases  
CC are the processing of endothelin and pro-opiomelanocortin prohormones.  
CC They may also be involved in the processing of serum amyloid A protein.  
SQ Sequence 377 BP; 62 A; 97 C; 121 G; 89 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT :
V28636/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC The present sequence encodes a human neuronal nicotinic acetylcholine CC receptor (NAChR) subunit. The cells expressing the alpha and/or beta CC NAChR subunits may be used in a method of screening compounds to CC identify any which modulate the activity of human neuronal NAChR. CC and expression density of various subunits in normal vs diseased brain CC subunit specific antibodies may be used to monitor the distribution CC subunit combinations with a variety of potential specific receptor CC provides information with respect to the function and activity of the CC individual subunits and should lead to the identification and design of CC compounds that are capable of very specific interaction with one or more receptor subtypes. The resulting drugs should exhibit fewer CC unwanted side effects than drugs identified e.g. screening with cells SQ Sequence 2277 Bp; 451 A; 695 C; 643 G; 486 T;
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Best Local
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                                                                                                                                                                                                                                                                                      (SMIK) SMITHKLINE BEECHAM
(UYWA-) UNIV WALES.
Hill J, Kay J, Powell D;
WPI; 98-207396/18.
                                                                                                                                                                                                                                                                                                                                                                      09-SEP-1997; G02426.
11-SEP-1996; GB-018966.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pro-opiomelanocortin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, aspartic protease partial cDNA EST 857644 SEQ ID Human, aspartic protease; EST; endothelin; serum amyloi
                                                                                                                                                                                                                                                                                                                                                                                                                  19-MAR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human aspartic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human neuronal nicotinic acetylcholine receptor subunits also transformed cells useful for screening cpds. which mactivity of the receptor pisclosure; Page 67-68; 99pp; English.
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15-SEP-1994: 08-MAR-1994; 08-MAR-1993; 0
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08-MAR-1993; US-028031.
(SAIK ) SAIK INST BIOTECHNOLOGY IND ASSOC.
(SIBI-) SIBIA NEUROSCIENCES INC.
Elliott KJ, Ellis SB, Harpold MM;
PERIS 94-303024/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; W44155.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prohormone;
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Pred. No. 29;
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Query Match Best Local S

Similarity

51.98; 75.08;

Score 19.2; pred. No. 31;

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RESULT 1
V28626/c
ID V286
AC V286
DT 29-J
DE Huma
KW Huma
KW PIO-
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Best Local S
Matches 24
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homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human aspartic protease encoding cDNA SEQ ID NO:2. Human aspartic protease; EST; endothelin; serum a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-MAR-1998:
09-SEP-1997; G02426.
11-SEP-1996; GB-018966.
11-SEP-1996; GB-018966.
(SMIK ) SMITHKLINE BEECHAM P
(SMIK ) UNIV WALES.
(UYWA-) UNIV WALES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V28623
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                                                                                                                                                                                                                                                                                                                                                            processing of endothelin and pro-optomelanocortin pro-hormone(5)

The present sequence encodes a human aspartic proteases and also ESTs from invention describes novel human aspartic proteases which encodes an invention contains a having partial DNA sequences which encodes an also be aspartic protease. Compounds which inhibit aspartic protease, especially human cDNA libraries having partial therapy where needed. The protease can also be antibodies can be used in therapy where needed. The protease can also be antibodies can be used in therapy where needed. The protease can be used in therapy where needed. The protease can be used in therapy where needed. The protease can be used in the processing of aspartic proteases are the processing of endothelin and pro-optomelanocortin prohomones.

They may also be involved in the processing of serum amyloid A protein. They may also be involved in the processing of serum amyloid A protein.

Sequence 1375 BP; 255 A; 419 C; 396 G; 305 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human aspartic protease and related DNA - which may be
                          Human aspartic protease partial cDNA EST 424772 SEQ ID NO:4.
Human; aspartic protease; EST; endothelin; serum amyloid A protein;
                                                                                                                                                                                                V28626;
                                                                                                     v28626 standard; cDNA; 452
               pro-opiomelanocortin
                                                                                                                                                                                                                                  ACACAGGCATATTCAAGAGTTCCTGCTACATC 36
                                                                                                                                                                                                                                                                             24;
                                                                                                                                                                                                                                                                         h 51.9%;
Similarity 75.0%;
24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Powell D;
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transl_except= (pos:1331..1333,aa:Ala)
/transl_except= (pos:1334..1336,aa:Thr)
/transl_except= (pos:1334..1339,aa:Gln)
/transl_except= (pos:1337..1339,aa:Gln)
/transl_except= (pos:1337..1339,aa:Gln)
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                         prohormone; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    could decode
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Pred. No. 38;
0; Mismatches
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(SMIK ) SMITHKLINE BEECHAM PLC.
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AA050499 mj20f02.r A1683454 tw51f01.x 224849 HSB58E072 S AA826609 of34d07.s A1557790 P15.2test AA537135 vk45c09.r AA8962246 vy11h04.r AA929019 co04d04.s AA929246 ct52b11.s AA929246 ct52b11.s AA9392246 ct52b17.s AA139821 mf27604 r AA139821 mf27604 r AA139821 mf27674 r AA139821 mg37f04.s

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H01869 yj32a12.r1
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W03952 za62c08.r1
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Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 261)

1 (bases 1 to 261)

Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,

Auffray,C., Deprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,

Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,

Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,

Sebastiani-Kabaktchis,C. and Tessier,A.

Sebastiani-Kabaktchis,C. and Tessier,A.

Sebastiani-Kabaktchis,C. and Tessier,A.
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1, rue de 1'Internationale, BP60 91002 EVRY
Tel: 33169472800
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Single read.
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Homo sapiens Chordata; Craniata; Verte Eukaryota; Metazoa; Chordata; Craniata; Verte Eukheria; Primates; Catarrhini; Hominidae; Ho Eutheria; Primates; Catarrhini; Hominidae; Ho Lasses 1 to 502)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                         Contact: Robert Strausberg,
                                                                                                                                                  On Aug 21,
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Email: Robert_Strausberg@nih.gov
CDNA Library_Preparation: M. Bento Soares,
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On Jan 9, 1998 this sequence version replaced gi:936210.
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Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 235.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                         gh69d08.xl Soares_fetal_liver_spleen_lnFLS_S1 Homo sapiens cDNA clone IMAGE:1849935 3' similar to gb:x70297 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-7 CHAIN (HUMAN); mRNA sequence.
                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.
1 (bases 1 to 497)
1 (Clases 1 to 497)
1 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGA)
Tumor Gene Index
Unpublished (1997)
On Aug 21, 1998 th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "98 c 122 g 154 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note "Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDi was prepared from mRNA obtained from Clontech was prepared from mRNA obtained with a Not I - oligo(dT) independently. Inc., and primed with a Not I.
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                               GI:3836895
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this sequence version replaced
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Pred. No. 1 3e-05;
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                                                                                       Project (CGAP),
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TITLE
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 476)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro
                                                                                                                                                                                                                                                                                                                                                                                                             AI368029 476 bp mRNA EST 13-FEB-199: qq45a03.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA cli IMAGE:1935436 3' similar to qb:x70297 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-7 CHAIN (HUMAN); mRNA sequence. AI368029 q4137774
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B
                                                                                                                                                                                                                                      Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                              AI368029.1
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                                                                                                                                                                                                                                                                                                                                                                 numan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMAGE Consortium (info@image.llnl.gov) for further : Seq primer: -40UP from Gibco
High quality segmence ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: (301) 496-1550
                                                                                                                                                                                                              Nov 29, 1993 this sequence version replaced g1:635922
                                                          126
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Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1935436"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; This is a subtracted version of the original Soares fetal liver spleen luft. library. Ist strand cDNA was primed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B (ampicillin resistant)"
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/clone="IMAGE:1849935"
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/db_xref="taxon:9606"
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Pred. No.
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1.3e-05;
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Best Local
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                                                                                                                                                                                                                                                                             Seq primer: m13 -40 forward
High quality sequence stop: 327.
                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Sep 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The WashU-Merck EST Project Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g1228346
N71634.1
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                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wilson, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
lst strand cDNA was primed with a Pac I - oligo(dT) primer
                                                                                                                                                    /organism="Homo sapiens"
/db_xref="GDB:1240037"
/db_xref="taxon:9606"
/clone="IMAGE:295116"
                                                                                                                  /sex="male"
                                                                                                                               clone_lib="Soares fetal liver spleen lNFLS"
                                                                                                                                                                                                                                                          ocation/Qualifiers
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94 c 109 g 151 t 1 others
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/lab_host="DH10B"
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/dev_stage="8-9 weeks"
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Pred. No.
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1.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         replaced
                                                                                                                                                                                                                                                                                                                                                                                                                           Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 476;
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(bases 1 to 405)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g1422491
                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seg primer: mob.REGA+ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The WashU-Merck EST Project
Unpublished (1995)
On Sep 21, 1992 this sequence version replaced gi:279006
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                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110
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/map="19p12-p13.1"
                                                                                                                                                                                                                                         /db_xref="GDB:1323554"
                                                                                                                                                                                                                                                       organism="Homo sapiens"
                                                                                                                                                 /dev_stage="20 week-post conception fetus"
                                                                                                                                                                               /clone_lib="Soares_fetal_liver_spleen_lNFLS.
                                                                                                                                                                                                                                                                                     ocation/Qualifiers
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100.0%;
                                                                                                                                                                                                IMAGE: 415084"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hillier L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Mohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W86805 106 bp mRNA.

Zh64g04.s1 Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA clone IMAGE:416886 3' similar to gb:X70297 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-7 CHAIN (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 106)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         namur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
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/dev_stage="20 week-post conception fetus"
/lab_bost="bH10B (ampicillin resistant)"
/lab_bost="bH10B (ampicillin resistant)
/lab_bost="bH10B (ampicillin resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         went through one round of normalization. Library constructed by Bento Soares and M.Fatina Bonaldo.
78 c 93 g 124 t 4 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism-"Homo sapiens"
/db_xref="GDB:1325356"
/db_xref="taxon:9606"
/clone="IMAGE:41886"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1995 this sequence version replaced gi:802594.
                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Soares_fetal_liver_spleen_1NFLS
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                                                                                                                                                                                                                                                                                                                                                                                           The WashU-Merck EST Project
Unpublished (1995)
On Jan 24, 1995 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 560)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
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          went through one rounceonstructed by Bento
                                                                                                                                                          /note="Organ: parathyroid gland; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: No Site_2: Eco RI; 1st strand cDNA was primed with a
                                                                                                                                                                                                                                                                                            /db_xref="GDB:1258900"
/db_xref="taxon:9606"
                                                                                                                                                                                                                             /clone_lib="Soares_parathyroid_tumor_NbHPA"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
                                                                                                                                                                                                                                                                             /clone="IMAGE: 321242"
                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                                                                                                            lab_host="DH10B (ampicillin resistant)"
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96.4%;
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Pred. No.
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provided by Dr. Stephen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: estewatson.wustl.edu
Insert Size: 2357
High quality sequence stops: 241 Source: IMAGE Consortium, LLNI
High quality sequence stops: 241 Source: IMAGE Consortium, LLNI
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2357
Insert Length: 2357
Std Error: 0.00
Seq primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R88973 293 bp
ym97b10.r1 Soares adult
IMAGE:166843 5', mRNA se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
On Jan 24, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 293)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-Merck EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                quality sequence stop: 241.
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double-stranded CDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M.Fatima Bonaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a
                                                                                                                                                       /organism="Homo sapiens"
/db_xref="GDB:587538"
/db_xref="taxon:9606"
/clone="IMAGE:166843"
                                                                                                                                                                                                                                                                                  'sex="Male"
                                                                                                                                                                                                                                                                                                       /clone_lib="Soares adult brain N2b4HB55Y"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Institute
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brain N2b4HB55Y Homo sapiens cDNA clone
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No. 0.
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
Eukaryota; Me
Eutheria; Rod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI509992 511 bp mRNA EST 12-MAR-1999 mj19h09.yl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:476609 5' similar to gb:U15647_cds1 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R. Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R. Jackson,Y., Cardenas,M., McCann,R., The WashU-MCI Mouse EST Project 1999
Unpublished (1999)
On Jun 5, 1998 this sequence version replaced gi:3188684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
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Putative full length read
                                                                                                                                                                                                                                                                                                                                                                                                                                                        This read is a RESEQUENCE of a previous read has been verified (found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    house mouse.
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theria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
(bases 1 to 511)
                                                                                                                                                                                                                                                                                                                      primer: -40RP from Gibco
h quality sequence stop: 447
Location/Qualifiers
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80 g 69 t 5 others
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="Ib="Soares mouse embryo
                                                                                    /lab_host-"DH10B"
                                                                                                            /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
                                                                                                                                                            /sex="unknown
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77.1%;
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Pred. No. 8.
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Best Local Similarity
Matches 26; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H01869 426 bp mRNA
yj32a12.rl Soares placenta Nb2HP Homo
IMAGE:150430 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                            High qality sequence stops: 322 Source: IMAGE Consorthum, LLNL free through LLNL; contact the This clone is available royalty-free through LLNL; contact the IMAGE Consorthum (info@image.llnl.gov) for further information. Insert Length: 1235 Std Error: 0.00 Seq primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1995)
On May 9, 1995 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 426)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
Insert Size: 1235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human.
                                                                                                                                                                                                                                                                                        quality sequence stop:
Location/Qualifiers
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I 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2 ]; double-stranded cDNA was ligated t Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo. "
                                                                                                                                                                                          /db_xref="taxon:9606"
/clone="IMAGE:150430"
                                                                                                                                                 /sex="Female"
                                                                                                                                                                  /clone_lib="Soares placenta Nb2HP"
                                                                                                                                                                                                                                  organism="Homo sapiens"
/db_xref="GDB:562415"
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Pred. No. 12;
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몂 22; 8

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Best Local S
Matches 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 CCCACACAGGCATATTCAAGAGTTCCTGCTACATC 36
                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
Insert Size: 1281
High quality sequence stops: 244
Source: IMAGE Consortium, LINL
This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1281 Std Error: 0.00
Seq primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hillier, L., Clark, N., Dubuque, T., ELLISCOU, N., CONTO, MARTA, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R32633 411 bp mRNA EST 28-APR yh73h02.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135411 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                         quality sequence stop: 244.
Location/Qualifiers
        74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69
(Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pY773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo. " a 136 c 122 g 95 t 4 others
                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="GDB:541344"
/db_xref="taxon:9606"
/clone="IMAGE:135411"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primates;
                                                                                                                                                                                                                          'dev_stage="placenta obtained at birth (full term)"
                                                                                                                                                                                                                                                   'sex≖"Female"
                                                                                                                                                                                                                                                                lone_lib="Soares placenta Nb2HP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 22.2;
Pred. No. 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Box 8501, St. Louis, MO 63108
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1995)
On May 18, 1995 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R71355 393 bp mRNA EST 01-JUN y154f12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:143087 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 347
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hillier,L., Clark,N., Dubuque,T., Elliston,K., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennor Parsons,J., Rikin,L., Rohlfing,T., Soares,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 393)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through IMAGE Consortium (info@image.llnl.gov) for funsert Length: 1209 Std Error: 0:00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stops: 347 Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
Insert Size: 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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                                                    double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pTTT3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo. " 129 c 113 g 79 t 4 others
                                                                                                                                                                            /clone_lib="Soares placenta Nb2HP"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                   /db_xref-"taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="GDB:552210"
                                                                                                                                                                                                                                                         'dev_stage="placenta obtained at birth (full term)"
'lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:143087"
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Pred. No. 15;
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Louis,

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Lennon,G., Ma es,M., Tan,F.,

Hawkins, M., Marra, M.,

Mammalia;

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SOURCE VERSION 밁 Š

Query Match

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                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tocal
2 CCCACACAGGCATATTCAAGAGTTCCTGCTACATC 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trace considered overall poor quality Insert Length: 1697 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA621981 418 bp mRNA EST 31-OCT-1997 ng24c12.s1 NCI_CGAP_Col0 Homo sapiens cDNA clone IMAGE:1144822 3' similar to TR:G1339923 G1339923 PHENOL SULFOTRANSFERASE SUBUNIT;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: Robert_Strausberg@nih.gov
Tissue_Procurement: Ilan Kirsch, M.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 418)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
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                                                                                                                                Similarity
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                                                                                                                                                                                                                                                /note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from RER+ colon tumor, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Patima Bonaldo (N-Soares4). "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Index:114822"
/clone_lib="NCI_GGAP_Co10"
/tissue_type="colon tumor RER+"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'lab_host="DH10B"
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                                                                                                                                59.5%;
83.3%;
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                                                                                                                                                      Score 22;
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AA964815/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence tag present in the cDNA between the Notl site and the oligo-dT track served to identify it as a clone from the normalized adult Kidney library. cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics The following repetitive elements were found in this cDNA sequence: 1-54, >AT_rich#Low_complexity 57-143,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eutheria; Rodentia;
1 (bases 1 to 395)
Bonaldo, M.F., Lenno
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UI-R-CO-gx-a-10-0-UI.sl UI-R-CO Rattus norvegicus cDNA clone
UI-R-CO-gx-a-10-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    >(CATA)n#Simple_repeat
Seq primer: M13 Forward.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Normalization and subtraction:
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                                                                                                          /lab_host="bH108 (Life Technologies)"
/lab_host="bH108 (Life Technologies)"
/note="vector: p773D-Pac (Pharmacia) with a modified
/note="vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CO
library is a subtracted library derived from the UI-R-Al
and UI-R-El libraries. The UI-R-Al library consisted of a
mixture of individually tagged normalized libraries
constructed from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, and muscle. The UI-R-El
library consisted of a mixture of individually tagged
normalized libraries constructed from 8, 12 and 18-day
embryo. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dT track which
allows identification of the library of origin of a clone
within the mixture. The subtracted library (UI-R-CO) was
constructed as follows: PCR amplified CDNA inserts from a
pool of UI-R-Al and UI-R-El clones from which 3' ESTS had
been derived was used as a driver in a hybridization with
the pooled UI-R-Al and UI-R-El library in the form of
single-stranded circles. The remaining single-stranded
circles (subtracted library) was purified by
hydroxyapatite column chromatography, converted in the number
of the pooled of column chromatography.
                double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-CO library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /map="6p21.3; 5q33"
/clone="UI-R-CO-gx-a-10-0-UI"
/clone_lib="UI-R-CO"
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/db_xref="taxon:10116"
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Search completed: September 17, 1999, 21:28:29 Job time: 14293 sec	Qy 4 CACI 	Query Match Best Local Similarity Matches 26; Conserv	BASE COUNT ORIGIN
ed: Septeml	CACACAGGCATATTCAAGAGTTCCTGCTACAT 		71 a
per 17, 1	DAAGAGTTO         DAAGAGATO	58.9%; 78.8%; ative	76 c
1999, 21:28:29	4 CACACAGGCATATTCAAGAGTTCCTGCTACATC 36 	Query Match 58.9%; Score 21.8; DB 46; Length 395; Best Local Similarity 78.8%; Pred. No. 21; Matches 26; Conservative 0; Mismatches 7; Indels 0	108 g · 140 t
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                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                     Score
             392
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                                         Gault,J., Robinson,M., Berger,R., Drebing,C., Logel,J., Hopkins,J., Moore,T., Jacobs,S., Meriwether,J., Choi,M.J., Kim,E.J., Walton,K., Buiting,K., Davis,A., Breese,C., Freedman,R. and Leonard,S. Genomic organization and partial duplication of the human alpha7 neuronal nicotinic acetylcholine receptor gene Genomics 52 (2), 173-185 (1998)
Leonard,S., Gault,J., Logel,J., Drebing,C., Robinson,M., Berger,R.,
Breese,C., Davis,A., Hopkins,J. and Freedman,R.
                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 392)
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Homo sapiens
           2 (bases 1 to 392)
Leonard, S., Gault, J.,
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G40486 Z6971 Zebra
AC005443 Homo sapi
AC003066 Mus muscu
AL022327 Homo sapi
AC007294 Homo sapi
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Z86099 Herpes simp
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31 Human high

Result No.

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                                                                                                                                                                                                                                                                                                         HSU52436 1876 bp mRNA PRI 11-JAN-1997
Human nicotinic acetylcholine receptor alpha7 subunit precursor,
mRNA, complete cds.
                                                                                                                                                                                                                                                                   g1458119
U62436.1
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2 (bases 1 to 1876) Elliott, K.J.
Direct Submission
                                                                                         1 (bases 1 to 1876)
Elliott, K.J., Ellis, S.B., Berckhan, K.J., Urrutia, A.,
Elliott, K.J., Ellis, S.B., Dohnson, E.C., Velicelebi, G. and Harpold, M.M.
Chavez Noriega, L.E., Johnson, E.C., Velicelebi, G. and Harpold, M.M.
Comparative structure of human neuronal alpha 2-alpha 7 and beta
2-beta 4 nicotinic acetylcholine receptor subunits and functional
expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                            beta 4 subunits
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                                                            Neurosci. 7 (3),
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pred. No. 2.6e-46;
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                                                                217-228 (1996)
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                               Rowen, L., Madan, A., Qin, S., Abbasi, N., Dors, M., Dickhoff, R., James, R., Loretz, C., Lasky, S., Madan, A., Prescott, S., Ratcliffe, A., Shaffer, T. and Hood, L.
                                                                                                                                                 Rowen, L., Madan, A., Qin, S., Abbasi, N., Dors, M., Dickhoff, R., James, R., Loretz, C., Lasky, S., Madan, A., Prescott, S., Ratcliffe, A., Shaffer, T. and Hood, L.
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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                                                                                                                               sequencing of human chromosome 14q24.3 region
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Direct Submission Submitted (30-MAY-1999)
                                                                                                             Unpublished
                                                                                             (bases 1 to 168919)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.4%; Score 72; DB 10; 100.0%; Pred. No. 0.021; Eive 0; Mismatches
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14 clone BAC 2289B16 map 14q24.3, LOW-PASS
   Multimegabase
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     Sequencing Center, University
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42461 GGCGCGGGTGCGGGGGTTGCGGCGCGAGCCGGGTGGCCTGGGCGGGTGGGCGGTTCGN 42520
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ULISYBÉ 342379 bp DNA HTG
CAENOThabditis elegans chromosome V clone Y3:
SEQUENCE, in unordered pieces.
N 795399
95042206
295399.5 GI.EA.A.
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Caenorhabditis elegans.
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This record will be updated with the finished sequence as soon as it is available and the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peng,X., Katz,M., Gerzanich,V., Anand,R. and Lindstrom,J. Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from the SH-SY5Y cell line and determination of pharmacological properties of native receptors and functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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PDGQIWKPDILLYNSADERFDATFHTNVLVNSSGHCQYLPPGIFKSSCYIDVRWFPFD
VQHCKLKFGSWSYGGWSLDLQMQEADISGYIPNGEWDLVGIPGKRSERFYECCKBPYP
DVTFTVTMRRRTLYYGLNLLIPCVLISALALLVFLLPADSGEKISLGITVLLSLTVFM
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alpha-7 subunit"
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               GI:330283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLVAEIMPATSDSVPLIAQYFASTMIIVGLSVVVTVIVLQYHHHDPDGGKMPKWTRVI
LLNWCAWFLRMKRPGEDKVRPACQHKQRRCSLASVEMSAVGPPPASNGNLLYIGFRGL
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db_xref="PID:g496607"
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/cell_line="SHSY-5Y"
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'translation="MRCSPGGVWLGLAASLLHVSLQGEFQRKLYKELVKNYNPLERPV
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95.9%;
                                                                                    type 2
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Pred. No. 0.041;
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                                                                                  VRL immediate-early (IE5)
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                                                                                                 Herpes simplex virus end.
                                                       9330281
M29384.1
Herpes simplex virus type 2 (strain HGS Timbury, 1971) DNA, passed in baby hamster kidney clone 21 (C13) cells. human herpesvirus 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           whitton, J.L. and Cle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The junctions between the repetitive and the short unique sequences of the herpes simplex virus genome are determined by the polypeptide-coding regions of two spliced immediate-early mRNAs J. Gen. Virol. 65, 451-466 (1984)
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/db_xref="taxon:10310"
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/protein_id="AAA45849.1"
/db_xref="PID:9330284"
/db_xref="GI:330284"
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                                                                                                           DNA VRL type 2 immediate-early
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Pred. No. 0.091;
D; Mismatches 160;
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Alphaherpesvirinae; Simplexvirus.
1 (bases 1 to 1560)
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                                                                                                            HSGG1 43058 bp DNA PRI 19-MAR-1997 HSGG1 DNA sequence from cosmid GG1 from a contig from the tip the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contai alpha and zeta globin genes and ESTs.
                Omo
Eukaryota; Metazoa;
                                               16p13.3; alpha-globin;
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/db_xref="taxon:10310"
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/db_xref="PID:g555152"
/db_xref="GI:555152"
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   Chordata;
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Pred. No. 0.16;
0; Mismatches 167;
                                             globin;
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   .Vertebrata;
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        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (28-JAN-1997) Sanger Centre, Hinxton, Cambridgeshire, CB10 1RQ, UK. E-mail enquires; humpub@sanger.ac.uk. IMPORTANT: This sequence is the entire insert of clone GG1. This clone was sequenced at the Institute of Molecular Medicine. The true left end of clone GG1 is at 1 in this sequence. The true rig end of clone GG1 is at 1 in this sequence. The true rig end of clone GG1 is at 43058.

GG1 is from a 280xb clone contig extending from the telomere of 16p. Higgs D.R., Fiint J. unpublished. MRC Molecular Haematology Unit, Institute of Molecular Medicine, Oxford.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primates; Catarrhini; Hominidae; 1 (bases 1 to 43058) Flint, J. and Higgs, D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       came from the Los Alamos,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4231. .4328
/note="MIR r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /map="16p13.3"
/clone="GG1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="FRAM repeat: matches 98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'chromosome="16"
                                                                                                                                                                                                                                                                                                                                                                                /note="AluSg repeat; matches 130.
incomplete repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note-"Alux repeat: matches incomplete repeat"
                                                                                                                    /note="LIME3 repeat: matches 229.
7979. .8281
/note="AluSx repeat: matches 1. .:
                                                                                                                                                                                                                    7045. .7351
/note="AluY repeat:
                                                                                                                                                                                                                                                                                     6531. .6825
/note="Alusg
                                                                                                                                                                                                                                                                                                                   'note-"L1MB7
                                                                                                                                                                                                                                                                                                                                                 700te-"L1MB5 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"AluSg
                                                                                                                                                                                                                                                                                                                                                                                                                                                               note-"AluJb repeat: matches 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="AluY repeat: matches"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="AluY repeat: matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="LIMB8 repeat: matches 134. .862 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="L1ME3A repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note-
     9928. .8997
/note="LLME3 repeat: matches 631.
)052. .9327
                                                       8635. .8924
/note="AluJb
                                                                                    note-"AluY repeat:
                                                                                                                                                                                      note="MSTD repeat: matches 294.
                                                                                                                                                                                                                                                      note="MSTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alusc repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AluSg repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L1 repeat: matches 5163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat: matches 182.
                                                                                                                                                                                                                                                    repeat: matches 1. .136 of
                                                                                                                                                                                                                                                                                   repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                   repeat: matches
                                                       repeat: matches 12.
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matches 2.

.146 of consensus"

.5328 of

consensus"

.300 of

consensus" consensus"

.294 of consensus"

.166 of

human Chromosome 16

right

297.

.1 of consensus"

.85 of consensus"

.300 of .301

consensus" consensus"

O.ff

.296 of consensus;

297.

.133

of consensus;

2. .297 of consensus"

matches 1. .301 of consensus"

.299 of consensus"

. 700

of.

.302

of.

consensus"

matches 1. .301 of consensus"

.394 of consensus"

.569 of consensus

matches

295. .1 of consensus"

consensus"

matches

922.

.459

of consensus'

<u>ب</u>

.208 of

consensus"

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repeat\_region

repeat\_region

/note-"AluY repeat: 10382. .10428

repeat\_region

note="AluSx repeat:

note="AluSp repeat: ncomplete repeat"

note="L1MB8 repeat:

.10966

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'note-"AluSx repeat: matches 1.
                                                                                                                                                                                                                                                 'note="AluJo repeat: matches 1.
8715. .18833
                                                                                                                                                                                                                                                                                        /note="AluJo repeat: matches 153.
Incomplete repeat"
18106. 18426
                                                                                                                                                                                                                                                                                                                                                                        note="AluJo repeat: matches ncomplete repeat"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="AluY repeat: matches 301.
6892 .17027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="MIR2 repeat: matches 145.
.6241. .16541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="3 copies of 36 mer 83 % conserved'
15747..15875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="Putative CpG island"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="Alusg repeat: matches oin(13773. .13867,14755. .1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="AluSx/g repeat: matches 245. .291 of consensus;
incomplete_repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'db_xref="SWISS-PROT:P02008"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product="zeta-globin 1"
protein_id="CAB06552.1"
db_xref="PID:e300370"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation-"MSLTKTERTIIVSMWAKISTQADTIGTETLERLFLSHPQTKTYF
HFDLHPGSAQLRAHGSKVVAAVGDAVKSIDDIGGALSKLSELHAYILRVDPVNFKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       b_xref="PID:g1817576"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23. .14090
e="12_copies of 14 mer 89 % conserved"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           matches 13. .294 of consensus"
          matches
                                                                     matches
                                                                                                                                                                                                                                matches 744. .865 of
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.14959,
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    .255 of consensus;

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                                                                                                                                                                                      .296 of consensus"
                                                                                                                                                                                                                                                                      .301 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .136 of consensus;
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),15135.
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                                                                   . 63
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Best Local Similarity
Matches 137; Conserv
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                                                                                                                         GGGGTCGCGGGGCCGGGCCC 25848
                                                                                                                                                               GGGGGCGCGCCCGGCTCC 283
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21546. 21617
/note="2 cor"
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/note="AluSx repeat: matches
/ncomplete repeat"
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20709. .20856
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1398. .21469
'note="2 copies of
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note="4 copies of 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="3 copies of 37
20996. .21067
'note="2 copies of 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20709. .20856
'note="4 copies of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note-"AluSx repeat: matches 1. .302 of consensus" oin(23985. .24079,25345. .25549,25891. .26019)
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note="2 copies of 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     roduct="zeta-globin
b_xref="PID:e300371"
135. .24680
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'note="L1MB7 repeat:

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/note="AluSg repeat:
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note="AluSg repeat:

.12761 .12616

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'note="AluSp repeat: .1466. .11635

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VERSION
KEYWORDS
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                                                                    BASE COUNT
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene sequence shown below is considered a pseudogene because of the terminating codon at base 429. There are only two additional single-base differences between the coding sequences of the zeta and pseudogeta genes, although there are conspicuous differences in the 5' and 3' flanking regions. Moreover the first intron of this locus demonstrates length variation, apparently stemming from the repeat sequence 'acaytygyagygy' which is also found in the zeta gene and, in a similar form,in the 5' flank of the human insulin gene. The repeat sequence 'cgggg' is characteristic of the second introns of the zeta genes [1].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proudfoot, N.J., Gil, A. and Maniatis, T. The structure of the human zeta-globin nearly identical pseudogene Cell 31 (3 Pt 2), 553-563 (1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pseudogene
700184
                                                                      454
About 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         zeta - pseudozeta - pseudoalpha-1 - alpha-2 - alpha-1 -3'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human alpha globin gene cluster, located on the short arm of mosome 16, spans about 30 kb and includes the following five
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         duplication; pseudogene; repeat region; zeta-globin
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/note="t in p
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2521. .2526
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.k sfter segment 2.
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join(411..505
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/note="repeat sequence,
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/gene="phbz"
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ne="phbz"
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       DB 10;
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RESULT 1
HSV2HG52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             major capsid protein; membrane-associated phosphoprotein; minor capsid protein; membrane-associated phosphoprotein; minor capsid protein; neurovirulence factor; protease; protein kinase; ribonucleotide reductase large subunit; ribonucleotide reductase small subunit; RL1 gene; RL2 gene; RS1 gene; tegument protein; thymidine kinase; Uf1 gene; Uf10 gene; Uf17 gene; Uf12 gene; Uf13 gene; Uf18 gene; Uf19 gene
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                                                             Everett, R.D. and Fenwick M.L.
Comparative DNA sequence analysis of the host shutoff genes of different strains of herpes simplex virus: type 2 strain HG52 encodes a truncated UL41 product
J. Gen. Virol. 71 (Pt 6), 1387-1390 (1990)
                                                                                                                                                                                                                                                                                                                                                         McGeoch,D.J., Moss,H.W., McNab,D. and Frame,M.C. DNA sequence and genetic content of the HindIII l region in the short unique component of the herpes simplex virus type 2 genome identification of the gene encoding glycoprotein G, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human herpesvirus 2
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                  evolutionary comparisons
J. Gen. Virol. 68 (Pt 1), 19-38 (1987)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alphaherpesvirinae; Simplexvirus.
                                     90278430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lycoprotein D; glycoprotein E; glycoprotein G; glycoprotein H; lycoprotein I; glycoprotein L; glycoprotein L; lycoprotein M; host shut off factor; integral membrane protein;
                                                                                                                                                                                                                          (bases 1 to 154746)
   (bases 1 to 154746)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 154746)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     herpesvirus 2. herpesvirus 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US9 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          simplex virus type 2 (strain HG52), complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154746 bp
                                                                                                                                                                                                  and Fenwick, M.L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barnett, B.C., Dolan, A., Telford, E.A., Davison, A.J. and McGeoch, D.J. A novel herpes simplex virus gene (UL49A) encodes a putative membrane protein with counterparts in other herpesviruses J. Gen. Virol. 73 (Pt 8), 2167-2171 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McGeoch, D.J., Cunningham, C., McIntyre, G. and Dolan, A.
Comparative sequence analysis of the long repeat regions and
adjoining parts of the long unique regions in the genomes of herpes
simplex viruses types 1 and 2
J. Gen. Virol. 72 (Pt 12), 3057-3075 (1991)
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                                                                                                                                                                                                                                                                                                                                                                                                                   /product="neurovirulence factor" 1738. .1743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="6"
943. .1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MSRRRGPRRRGPRRRFRPGAPAVPRPGAPAVPRPGALPTADSQM
VPAYDSGTAVESAPASSLLRRWLLVPQADDSDDAVXGNDDAEMANSPPSEGGGRAP
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APRGKVCFSPRVQVRHLVAWETAARLARRGSWARERADRDRFRRRVAAAEAVIGPCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEARARARARAHEDGGPAEEEEAAAAARGSSAAJ
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/gene="RL1"
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255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="5"
1089. .1379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAB06759.1"
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                                                                                                                                                                                                                                 )oin(2303. .2377,2785. .3462,3644. .5368)
'gene="RL2"
                                                                                                                                                                                                                                                                                                      'gene="RL2"
                                                                                                                                                                                                                                                                                                                                                                                            gene="RL1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'rpt_family="7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note-"start of TRL (terminal copy of Long Repeat region)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref-"taxon:10310"
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repeat_region
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                                                                                                                                               10211...10978
/gene-"UL2"
10211...10978
/gene-"UL2"
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SQPAATRPAPPGAPRSSSGGAPLRAGVGSGSGGGPAVAAVVPRVASLPPAAGGGRAQ
ARRVGEDAAAAEGRPGRAGPAAGVPTVISDSPPSSPRPAGGGLLSYSSSSAQV
SSGPGGGLPQSSGRAPARPRAAVAPRVRSPPRAAAAPWFASASADAAGPAPPAYPDAH
RAPRSRMTQAGTDTQAQSLGRAGATDARGSGCPGAEGGPGVPRGTNTPGAAPHAAEGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(7732)
/gene="RL2"
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/gene="RL2"
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                                                                                                                                                                                                                                                                                                                                                                                                     /product="virion glycoprotein
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/db_xref="PID:e304262"
/db_xref="PID:g1869823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="start of UL (Long Unique region)"
9427. 10101
'gene="UL1"
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AAAPAWSRRTLLPEHARNCVRPPDYPTPPASEWNSLWMTPVGNMLFDQGTLVGALDFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rpt_family="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="primary transcription initiation site for latency issociated transcripts (LAT's)" 047. 9193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ′gene="RL2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="proposed LAT splice donor site (5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene-"RL2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="proposed LAT splice acceptor site"
'618. .5623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="RL2"
                                                                                                                                                                                                                                                                                                                                                                                    db_xref-"GI:1869823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              427. .10101
gene="UL1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="RL2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rpt_family="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        codon_start=1
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HSV2HG52/c
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     AUTHORS
TITLE
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Best Local Similarity
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                                                                                                                                                                   genome; deoxyribonuclease; deoxyuridine triphosphatase; DNA
polymerase; envelope protein; glycoprotein B; glycoprotein C;
glycoprotein D; glycoprotein E; glycoprotein B;
glycoprotein I; glycoprotein J; glycoprotein K; glycoprotein L;
glycoprotein N; host shut-off factor; integral membrane protein;
major capsid protein; membrane-associated phosphoprotein kinase;
ribonucleotide reductase large subunit; ribonucleotide reductase;
small subunit; RL1 gene; RL2 gene; RS1 gene; tegument protein;
major capsid protein; membrane-associated phosphoprotein kinase;
ribonucleotide reductase large subunit; ribonucleotide reductase
small subunit; RL1 gene; UL10 gene; UL11 gene; UL12 gene; UL13
gene; UL14 gene; UL15 gene; UL16 gene; UL17 gene; UL18 gene; UL19
gene; UL14 gene; UL20 gene; UL16 gene; UL17 gene; UL18 gene; UL19
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Z86099
                                                human herpesvirus 2.
human herpesvirus 2.
Viruses; dsDNA viruses, no RNA stage;
Alphaherpesvirinae; Simplexvirus.
1 (bases 1 to 154746)
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MCGeoch, D.J., Moss, H.W., McNab, D. and Frame, M.C.

DNA sequence and genetic content of the HindIII 1 region in
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simplex virus
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/gene="UL3"
11033. .11734
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11033. .1173
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48.7%;
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type 2 (strain HG52),
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Pred. No. 0.083;
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                                                                                                     Herpesviridae;
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2 (bases 1 to 154746)
Everett,R.D. and Fenwick,M.L.
Comparative DNA sequence analysis of the host shutoff genes of different strains of herpes simplex virus; type 2 strain HG52 encodes a truncated UL41 product
J. Gen. Virol. 71 (Pt 6), 1387-1390 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (25-FEB-1997) A. Dolan,
Street, Glasgow, Gll 5JR, UK
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 (bases 1 to 154746)
Barnett, B.C., Dolan, A., Telford, E.A., Davison, A.J. and McGeoch, D.J. A novel herpes simplex virus gene (UL49A) encodes a putative membrane protein with counterparts in other herpesviruses J. Gen. Virol. 73 (Pt 8), 2167-2171 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 (bases 1 to 154746).
3 (bases 1 to 154746).
McGeoch,D.J., Cunningham,C., McIntyre,G. and Dolan,A.
Comparative sequence analysis of the long repeat regial adjoining parts of the long unique regions in the gen simplex viruses types 1 and 2
3. Gen., Virol. 72 (Pt 12), 3057-3075 (1991)
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                                                                /gene="RL1"
2303,
                        2303. .124947
/gene="RL2"
2303. .2377
                                                                                                                             /product="neurovirulence factor" 1738. .1743
                                                                                                                                                                                                                                                                                                                                                                                                                                      /trānslation="msrrrgprrrgprrrpprapapavprpgapavprpgalptadsqm
vpatdsgtavesapaassllerwllvvqaddsddadyagndsglabepsegggrap
eaphaapaapacpppprkegropprplallertttetylatislrrrppaspapa
aprgkvcfsprvqvrhlvawetaarlarrgswareradrdrfrrvaaaeavigpcle
                                                                                                                                                                                                                                                                                                                                                                                                              PEARARARARAHEDGGPAEEEEAAAAARGSSAAAGPGRRAV'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="CAB06759.1"
/db_xref="PID:e308397"
/db_xref="PID:g1869821"
/db_xref="GI:1869821"
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                                                                                                                                                                                                                                                                                                        rpt_family-"6"
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/gene="RL1"
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'gene="RL1"
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/gene="RL2"
                                                                        /db_xref="SWISS-PROT:P28278"
/taanslation="McFVCLF61LYVMCAMGAMGGSQATEYVLRSVIAKEVGDILRVPC/Translation="McFVCLF61LYVMCAMGAMGGSQATEYVLRSVIAKEVGDILRVPCMRPLPAAGMRPADDVSMRYEABSVUVNEPTLFAAGFLDCFGLDTFLMDRHAQRAYLVNEPTLFAAGFLDLSHSVFPADTGETTTRRALYKEIRDALGSRKQAVSHAPVRAGCVNFDYSRTRRC
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/gene="RL2"
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/gene="RL2"
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APRSLISLIGHTVRALSPTPPRGTDDEDDDLADVDYVPPAPRRABPRRGGGAGATTGT
SOPAATRXAP PGAPRASSGGAPLRAGVGSGSGGPAVAAVVPRVASLIPPAAGGRAG
SOPAATRXAP GAPRASSGGAPLRAGVGSGSGGPAVAAVPRVASLIPPAAGGRAQV
ARRVGEDAAAAEGRTPPARQPRAAQEPPIVISDSPPPSPRRPAGPGPLSFVSSSSAQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MEPRPGTSSRADPGPERPPRQTPGTQPAAPHAWGMLNDMQWLAS
SDSEEETEVGISDDDLHRDSTSEAGSTDTEMFEAGLMDAATPPARPPAERQGSPTPAD
AQGSCGGGPVGEEEAEAGGGGDVCAVCTDEIAPPLRCQSFPCLHPFCIPCMKTWIPLR
                                                           VGRRDLRPANTTSTWEPPVSSDDEASSQSKPLATQPPVLALSNAPPRRVSPTRGRRRH
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LAT species)"
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/gene="RL2"
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RAPRSRMTQAQTDTQAQSLGRAGATDARGSGGPGAEGGPGVPRGTNTPGAAPHAAEGA
AARPRKRRGSDSGPAASSSAASSSAAPRSPLAPQGVGAKRAAPRRAPDSDSGDRGHGPL
                                                                                                                                                                                         'product="virion glycoprotein
'protein_id="CAB06761.1"
'db_xref="PID:e304262"
                                                                                                                                                                                                                                                                    9427. .10101
'gene="UL1"
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1618. .5623
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                                                                                                                                                                                                                                                                                                                                                                    'gene="RL2"
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'db_xref="PID:e304156"
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                       .10978
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                                                                                                                                                                                       REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
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Best Local Similarity
Matches 171; Conserv
                                                                                                                            JOURNAL
                                                                                                                                                     TITLE
                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
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                                                                                                                                                                                                                                                                                                                                             genomic sequence.
AD000684
                                                                            GSDB:S:1010600
                                                                                                                                                                                                                                                                               AD000684.1 GI:1905917 chromosome 19; transcription factor
                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                    numan.
                                                       Human Genome Center
Biology and Biotechnology Research Program
Lawrence Livermore National Laboratory
7000 East Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11033. .11734
/gene="UL3"
11033. .11734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="CAB06762.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'db_xref="SWISS-PROT:P28275"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="PID:g1869824"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="GI:1869824"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start-1
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48.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.083;
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Db 148292 GGGGGACGGGGGACGGGGGGACGGGGGGGACGGGGGGGACGGGGGACGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 148352 GCCGGGGGGCCGGGGGCCCGGGGGGACGGGGGACGGGGGACGGGGGACGGGGGACG 148293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 148412 GACGGGCCGGGGGACGGCCCGGGGGGACGGGCCGGGGGGCCGGGGGCCCGGGGG 148353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 148472 GCCGGGGGGACGGGCCGGGGGACGGGCCGGGGGGACGGGCCCGGGGGACGGGCCCGGGGG 148413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              337 CCGGGCGACAGCCGAGACGTGGAGCGCGCCGGCTCGCTGCAGCTCCGGGAC 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCCCTGGCCTGGCCAGAGGCGCGAGAGCCCGCTCGGTGGAGACTGGGGGTGGA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTGGGTGGCCGCGAGACGCTGGCCCGGGCTGGAGGGATGGCGGGGGCGGGGACGGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTGCCCGGAGCGTACCCAGCGCGCGGGAGTACCTCCCGCTCACACCTCGGGCTGCAGTTC 156
Direct Submission
Submitted (10-DEC-1996) J.E. Lamerdin, Human Genome Center, Submitted (10-DEC-1996) J.E. Lamerdin, Human Genome Center, Lawrence Livermore National Laboratory, 7000 East Ave, Live CA, USA, 94551 jane@acgt.llnl.gov ow@tornak.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CH19x30879 41936 bp DNA PRI 01-APR-1997 Homo sapiens DNA from chromosome 19-cosmid R30879 containing USF2,
                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 41936)
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PLLEPELANPITARLLAEYDTREQTEEVIEPREDVESWTRYTEDVRVVIIGQDPYH
HPGQAHGLAFSVRADVPVPPSIRNVLAAVKNCYPDARMSGRGCLEKWARDVLLLNT
LTVKRGAAASHSKLGWDRFVGGVVQRLAARRPGIVFMLWGAHAQNAIRPDPRQHYVLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FSHPSPLSKVPFGTCQHFLAANRYLETRDIMPIDWSV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="uracil-DNA glycosylase"
/protein_id="CAB06762.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 17; Length 154746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180;
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	/ CLASSIC LATION = ROLLTFDCTAWGDSGYYYCSYVSAQDLQGNNEAYAELIYLGRTSG / TRANSLAFILON = ROLLTFDCTAWGDSGYYYCSYVSAQDLQGNNEAYAELIYLGRTSG / TRANSLAF LON = ROLLTFDCTAWGDSGYYCFCCYPCPDKC VAELLPGFQAGF IEGWLFVVVVCLAAFLIFLLGICWCQCCPHTCCCYYRCPCCPDKC CCPEARYAAGKAATSGYPSIYAPSTYAHLSPAKTPPPPAMIPMGPAYNGYPGGYPGDV DRSSGYRSGYRIQASQQDDSMRVLYYMEKELANFDPSRPGPPSGRVERGMSEVTSLH	
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repeat_regi	0 ·   1 · 1 4 · 1	repeat_region
repeat_regi	/:ptemilty Ard 40314288 /note="repeat match = HSAL01019; putative" /rpt_family="Alu"	repeat_region
repeat_reg	1030. 4168 4030. 4168 /note="repeat match = HSALO3448; putative"	repeat_region
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repeat_regi		repeat region
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repeat_regi	/organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="19"	
repeat_regi	Location/Qualifiers 141936	FEATURES
	Livermore, CA 94550 USA constructed at LLNL from flow-sorted chromosomes from hybrid 5HL2-B, which carries chromosome 19 as its only human broncome.	Livermore constructed from hybrid

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/note="repeat match - H

/rpt_family="Alu"

10359. 10498

/note="repeat match - H

/rpt_family="Alu"

11510. .11657
/note="similarity: gb|H06137|H06137; y177c10.s1 Homo sapiens cDNA clone 44249 3'. . . ; putative"
16785, .16867
/note="similarity: gb|H06137|H06137; y177c10.s1 Homo sapiens cDNA clone 442249 3'. . ; similarity: gb|R39945; yf52e09.s1 Homo sapiens cDNA clone 25701 3' similar to . . ; similarity: gb|R36881|R36881; yf52e08.s1 Homo sapiens cDNA clone 25701 3' similar to . . ; similarity: gb|R36881|R36881;
                                                                                                                                                                         /note-"similarity: gb|H06137|H06137; yl77c10.s1 Homo sapiens cDNA clone 44249 3'. . . .; putative" 16646 . .16699 /gene-"LISCH7"
                                                                                                                                                                                                                                                                              /note="similarity: gb|R39945|R39945; yf52e09.s1 Homo
sapiens cDNA clone 25701 3' similar to . . .; putative"
16594 . .16650
                                                                                                                                                                                                                                                                                                                                                            /note="similarity: gb|R36881|R36881; yf52a08.s1 Homo sapiens cDNA clone 25687 3'. . . .; putative" 16577. .16699
                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similarity: gb|R39945|R39945; yf52e09.sl Homo sapiens cDNA clone 25701 3' similar to . . .; putative" 16573 . .16699 /gene="LISCH7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similarity: gb|H42128|H42128; yo61b12.rl Homo sapiens cDNA clone 182399 5'.; putative" 11957. .12072 /note="repeat match = HSAL10157; putative" /rpt_family="Alu" 11981. .12253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8303. .8386

/note="repeat match = HSAL05819; putative"
/rpt_family="Alu"
/rpt_family="Alu"
/rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(12645. .13088)
/note="repeat match = HSAL02504; putative"
/rpt_family="Alu"
16521. .16586
/gene="LISCH7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(9257 .9546)
/note="repeat match = H
/rpt_family="Alu"
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LDDLTPPSTAESGSRSPTSNGGRSRAYMPPRSRSRDDLYDQDDSRDFPRSRDPHYDDF
RSRERPPADDRSHHHRTRDPRDNGSRSGDLPYDGRLLEEAVRKKGSEERRRPHKEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(12391. .12982)
/note="repeat match = HSAL02441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="repeat match = ALU; putative"
/rpt_family="Alu"
12168. .12279
12168. .12279
/note="repeat match = HSAL03934; putative"
/rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (12334.
                                                                                                                                                                                                                                                          /gene="LISCH7"
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/gene="LISCH7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="Alu"
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                      RESULT 1
HSUSF2/c
                                          REFERENCE
                                                                                                                                                            VERSION
                                                                                                                                          KEYWORDS
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                                                                                                                                                                                                                    DEFINITION
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Best Local
                          AUTHORS
                                                                                                                                                                                                                                                                                                                                17949 GCAGGAGGGGACGGAGAGATACGGGAGCCGCTCGCGCTGATCACGGGGACA 17898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18069 CATGGGGGGGGGGGGGGGGGGGGGGGGCCCCGGGGGGGGAGGGGAAGGGGAAG 18010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115
                                                                                                                                                                                                                                                                                                                                                                      295 CGAGCCGAGCGGCGAGGTGCCTCTGTGGCCGCAGGCGCAGGCCCGGGCGACA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                235 GTGGAGAGGCGCGGGGGGGGGGGGGGGGGGGGGGGGCGCCCGGCTCCTTAAAGGCGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCGCGAGGCCGAGAGCCCCGCTCGGTGGAGACTGGGGGGTGGAGGTGCCCGGAGCGTACCC 114
                                                                                                                                                                                                                                                                                                                                                                                                            GGAGGGAGGGGGGGGGGGGGGGGGGGGGCCCCGAGCCCGGCGCTCACGCCGCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCGGCGGCAGCAGCGGTGGCCGAGGCAGCGGGATCCAGACCC---GGGTCCAGCATGTC 18070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCGCCGGGAGTACCTCCCGCTCACACCTCGGGCTGCAGTTCCCTGGGTGGCCGCCGAGA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155;
                                                                                                                                      g1806093
Y07661.1
USF2 gene.
                                  Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 14440)
    Groenen, P.M., Garcia, E., Debeer, P., Devriendt, K.,
Van de Ven, W.J.
                                                                                                                                                                                                                                      HSUSF2
                                                                                                Homo sapiens
                                                                                                                                                                                                                  .sapiens
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19412...19562,19683...19770,20048...20106,27663...27757,
27911...28039,28132...28221)
/gene="USF2"
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16852...16907
//note="similarity: gb|H06137|H06137; y177c10.s1 Homo sapiens cDNA clone 44249 3'...; putative"
16852...16877
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/translation="MIMIDPGLDPAASATAAAAASHDKGPEAEEGVELQEGGDTAGAVSVV
EQTAVAITSVQQAAFGDHNIQYQFRTETNGGQVTYRVVQVTDGQLDGQGDTAGAVSVV
STAAFAGGQQAVTQVGVDGAAQRPGPAAASVPPGPAAPFPLAVIQNPFSNGGSPAAEA
VSGEARFAXFPASSVGDTTAVSVQTTDQSLQAGGQFYVMMTPQDVLQTGTQRTIAPRT
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                                                                                                                                                                                                                    USF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="upstream stimulatory
/protein_id="AAB51179.1"
/db_xref="pID:g1905919"
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/note="putative"
                                                                                                                                                            GI:1806093
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Pred. No. 0.2;
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Direct Submission
Submitted (27-AUG-1996) P. Groenen,
Laboratory for Molecular Oncology, 1
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5183. .5302
/gene="USF2"
/number=5
                                                                          5032. .5182
/gene="USF2"
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/gene="USF2"
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/gene="USF2"
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GGILSKACDVIRELRQTNQRMQETFKEAERLQMDNELLRQQIEELKNENALLRAQLQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MDMLDPGLDPAASATAAAAASHKGPEAREGVELQEGGDGPGAE
EQTAVAITSVQQAAFGDHNIOYQFRTETNGGVTYRVVQVTDGQLDGQGDTAGAVSV
STAAFAGGQQAVTQVGVDGAAQRPGFAAASVPFGPAAFFLAVIQNFESNGGSPAAFA
VSGEARFAYFPASSVGDTTAVSVQTTDQSLQAGGQFYVMMTPQDVLQTGTQRTIAPRT
                                                                                                                                  4589. .5031
/gene="USF2"
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/gene="USF2"
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5032. .5182,5303. .5390,5668. .5726,13284. .13
13532. .13660,13753. .13842)
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/db_xref="taxon:9606"
/chromosome="19"
                                                                                                                                                                                            388. .4588
'gene="USF2"
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'gene="USF2"
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'gene="USF2"
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/gene="USF2"
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'db_xref="GI:1806094"
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db_xref="PID:e291919"
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'gene="USF2"
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1032. .5182,5303. .5390,5668. .5726,13284. .13378,
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        Streptomyces coelicolor.
Streptomyces coelicolor
Streptomyces coelicolor
Bacteria; Firmicutes; Actinobacteridae;
                                                                                                                      acetyltransferase; ATP-binding; Clp-family ATP-binding cseB; cseC; DNA repair; DNA-binding; ECF sigma factor; L-aspartate oxidase; lrpA; Lsr2; mutY; nadB; nadC; nicotinate-nucleotide pyrophophorylase; pantoate-amino
                                                                                                                                                                                                           AL049628.1 GI:4585581
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                                                                                kinase; sigE.
                                                                                                    putative adenine glycosylase;
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/gene="USF2"
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'gene="USF2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAI
                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         upstream initiation codon.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for small overlap between neighbouring submissions.

Cosmid E94 lies between E7 and E126 on the AseI-E genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22/22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (12-APR-1999) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mall: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Redenbach, M., Kieser, H.M., Denapaite, D., Kinashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coelicolor),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 by the BBSRC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces coelicolor sequencing at The Sanger Centre is funded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Details of S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 38532)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 38532)
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                                                                                                                                                                                                                                                                                   /organism="Streptomyces c
/strain="A3(2)"
/db_xref="taxon:1902"
/clone="cosmid E94"
complement(1..1512)
/gene="SCE94.01c"
                                                                                                                                                                                   /note="Nominal overlap
complement(<1. .1512)
/gene="SCE94.01c"</pre>
                 /product="alanine-rich
/protein_id="CAB40850.1
/db_xref="PID:e1424928"
                                                                                /label=SCE94.01c
                                                                                                                                                               note="SCE94.01c, partial"
                                                                                                                                                                                                                                                /gene="SCE94.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Harris, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 to 38532)
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                                                                                                    _table=11
                                                                                                                                              len: >503aa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Denapaite, D.,
                                                hypothetical
                                                                                                                                                                                                                             with
                                                                                                                                                                                                                                                                                                                                                                                            coelicolor"
                                                                                                                                                                 CDS
                                                                                                                                                                                                                             Streptomyces
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                                                           protein'
                                                                                                                                                                                                                               coelicolor E7."
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/db_xref="FID:9458583"
/db_xref="FID:94588383"
/db_xref="FID:
                                                                                                                                                                                                                                                                                                                           RGNTGGLIVLGSDKTVESMCTGGFVLDVEFTATRLRELCKLDGGIVLSSDLSKILRAG VQLLPDPTIPTEETGTRHRTAARVSKQVGFPVVSVSQSMRLIALYVDGQRRVLEDSAA ILSRANQALATLERYKLDEVAGTLSALEIDLVTVRDVSAVAQRLEMVRRIATEIA ELVVELGTGGRRULALLDELJAGVEPERELLVRDYVPEPTAKRSRTVDEALAELDKLS HAELLELSTVARALGYTGSPETLDSAVSPRGFELLAKVPRLPGAIIDRLVEHFGGLQK LLAASVDDLQTVDGVGEARARSVREGLSRLAESSILERYV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="putative DNA-binding protein"
/protein_id="CAB40852.1"
/db_xref="PID:e1424930"
/db_xref="PID:94585584"
/db_xref="GI:4585584"
/translation="MAANDRAAAPGKSGGSAGADGLMRASLSAVAPGTSLRDGLERVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fasta scores; opt: 1338, z-score: 1480.9, E(): 0, (59.9% identity in 347 ma overlap). Contains Pfam match to entry pr00633 HHH, Helix-hairpin-helix motif."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="SCE94.02, possible DNA repair protein, len: 469a similar to many eg. SW:RADA_ECCLI RadA, DNA repair protein (mechanism unknown) from Escherichia coli (460 aa) fast scores; opt: 1218, z-score: 1309.3, E(): 0, (41.4% identity in 452 aa overlap). Contains Prosite match to PS000017 ATP/GTP-binding site motif A (P-loop)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SCE94.02"
2126. .3535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ETGTCAGVARLTGDNRYVLSTALRRELVRHVDDCPRCRRTAERAIPGRWPGTSVTPAE
LPVLEAPRTALHVALAHTSRARSAAPREDRRGFPMDFKDRAARRDRLRARAVTTTVVA
TVVAAPVLALWAAYRGTPVVEGEEGRSASASEAQDPDATDGESAGGAYGYENAGNAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="GI:4585582"
/translation="MRSSPETRTTGAHRAHREARDRTAARALAQPPAQRPPARYAA
YDAYLDGLETYCLSVLCDHDAATAALGDVLAIAERRGHRGPAPAADRRSWLYALARWA
CLRKLAEAKQKRSPSTHAAGRPAPVTRQTAQTTPTAPTTPTNDETHQRHRSELALLAWP
EAAGTTPEQREALELAVRHHLAPHEVAAVLGTDLAATRELLASAACEVERTRAALAVV
                                                                                 complement(4778. .5158)
/gene="SCE94.04c"
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VAIGEVGLAGEVRRVTGVQRRLSEAHRLGFTHALVPADPGRVPDGMKVLEVADMGDAL
                                                                                                                                                             Helix-hairpin-helix
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complement(4778. .5158)
/gene="SCE94.04c"
                                                                                                                                                         /gene="פנטיא.ייי
/note="Pfam match to entry PF00633 HHH,
מאריי-האיייליי-האווא motif., score 26.50,
                                                                                                                                                                                                                                      /gene="SCE94.03"
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/note="PS00017 A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similar to hypothetical proteins eg. TR:053571 (EMBL:AL022075) from Mycobacterium tuberculosis (358 aa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note-"SCE94.03, possible DNA-binding protein, len: 374aa; imilar to hypothetical proteins eg. TR:053571
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                                                                                                                                                                  E-value 0.00061."
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CFGTPBPAM/c
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DEFINITION
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Best Local
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CFGTPRPAM 1927
C.familiaris mRNA
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gene

CDS

gene

CDS

for

stimulatory GTP binding protein alpha

22-MAY-1993

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33360 GAGCGCGGAGACGTAGTCCATGGGACCAGGGTAGCCAGGCGCCGTCAGCCGGCGGCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 GGCCTTGGGCAGCCCCTGGCCAGAGGCGCGAGGCCCGAGAGCCCGCTCGGTGGAGA 85
                                            CAGGCGCAGGCCGGGCGACAGCCGAGACGTGGAGCGCGCCGG
                                                                                                                                                                                                          CTGGGGGTGGAGGTGCCCGGAGCGTACCCAGCGCCGGGAGTACCTCCCCGCTCACACCTCG 145
TGGTGCCGGGAGTCCGGGGCGGGGGGGGCGGGCCGGGCTTGCGGGGCGGGAAGACC 33479
                                                                                                                                                                                                                                                                                                                  GGCTGCAGTTCCCTGGGTGGCCGCCGAGACGCTGGCCCGGGCTGGAGGGATGGCGGGGCG 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTCTTCACGATCACCCGGATCAAGCCGATGAAGAAGACGGCCATGACGGCCGGGGGCAG 33359
                                                                                                                                 GGGCGCGCGCGCGCTCCTTAAAGGCGCGCGAGCCGAGCGGCGAGGTGCCTCTGTGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adenine glycosylase from Streptomyces coelicolor (183 aa) fasta scores; opt: 1220, z-core: 1357.4, E(): 0, (100.0%) identity in 183 aa,overlap). Also similar to many others eg. SW:MUTY_SALTY muty, adenine glycosylase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product* hypothetical proline-rich protein*
/protein_id="CAB40854,1"
/db_xref="FDI:e1424932"
/db_xref="FDI:e1424932"
/db_xref="FDI:9458586"
/db_xref="GI:458586"
/db_xref="GI:458586"
/db_xref="GI:458586"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="SCE94.06, mutr, putative adenine glycosylase, len: 308aa; previously partially sequenced therefore partially identical to TR:E1358524 (EMBL:AJ131213) mutr, putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5816. .6742
/gene="SCE94.06"
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/gene="SCE94.05"
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|TPASGDDAYWASDDCVEGAGSLRYRVTAGSGITYTVKWDRKPSAPECGTPPAGSAKA
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/protein_id="CAB40853...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              label=SCE94.05
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Best Local Similarity 52.1%;
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cecce 15
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1 (bases 1 to 1927)
Ishikawa, Y. and Homcy, C.J.
cDNA sequence for alpha subunit of stimulatory guanine nucleotide binding protein from canine heart
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g311336
Z12168.1 GI:311336
GTP binding protein; GTP binding protein alpha subunit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ishikawa,Y.
Direct Submission
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WNNRWLRTISVILFLNKQDLLAEKVLAGKSKIEDYFPEFARYTTPEDATPEPGEDPRV
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LLGAGESGKSTIVKOMRILHYNGFNGGGEEDDQAARSNSDGEATKVQDIKNNILKEA
IETIVAAMSULVPPVELANDENQFKVDYILSVMVVDPDFDFPEFYEHAKALWEDEGVF
ACYERSNEYQLIDCAQYFLDKIDVIKQADYVPSDQDLLRCRVLTSGIFETKFQVDKVN
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/protein_id="CAA78161.1"
/protein_id="CAA78161.37"
/db_xref="FID:9311337"
/db_xref="SWISS-PROT:P04895"
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/clone="clone 7M"
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'db_xref="taxon:9615"
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R P-PSDB; W09025.

T Nucleic acids encoding nicotinic acetylcholine receptor sub-units - 2T Nucleic acids encoding nicotinic acetylcholine receptor sub-units - 2T Nucleic acids encoding nicotinic acetylcholine receptor (most of 2D Na Sequence (T48239) codes for the alpha-7 subunit (W09025) of CC the human neuronal nicotinic acetylcholine receptor (mAChR). Host CC cells, esp. mammalian cells or amphibian occytes, carrying alpha-7 CC nucleic acids, opt. in combination with other alpha and/or beta crecombinant nacids (see also T48232-38, T48240-41), express CC subunit nucleic acids (see also T48232-38, T48240-41), express CC modulate the activity of human nAChRs.

Sequence 1876 BP; 369 A; 553 C; 531 G; 423 T;
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Best Local S
Matches 72
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W09420617-A2.
15-SEP-1994.
08-MAR-1994; U02447.
08-MAR-1993; US-028031.
(SALK ) SALK INST BIOTECHNOLOGY IND (SIBI-) SIBIA NEUROSCIENCES INC.
                                                                                                                                                                                                                                                                                                               Human neuronal nicotinic acetylcholine receptor alpha-7 subunit cDNA Human; neuronal nicotinic acetylcholine receptor; alpha-7 subunit; brain tissue; screening; NAChR; antibody; ds.
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27-DEC-1996.
07-JUN-1996; U09775.
07-JUN-1995; US-484722.
                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                               V12197 standard; cDNA; 1876 BP. V12197;
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Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;
ligand-gated receptor; ds.
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100.0%; Pred. No.
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M. tuberculosis in
HSV L/ST ORF1. Her
PACE composite seq
Human PACE coding
Wild type SNF 5' u
Human T-cell leuka
Human L-myc oncoge
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Infected cell prot Paired basic amino Paired basic amino

HSV-1 (F) ICP34.5 HSV-1 (CVG-2) ICP3 Mycobacterium tube

Human adenosine Al HSV L/ST region. H cDNA sequence of f HSV L/ST region. H

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Scoring table: Perfect score: Sequence:

IDENTITY\_NUC

311585 seqs, 125096042

residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Title:

US-08-956-518A-101 392 1 AGAACGCAAGGGAGAG

AGAACGCAAGGGAGGTAG.....CTGCAGCTCCGGGACTCAAC

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nucleic search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 1998 Comp

Compugen Ltd

September 18, 1999, 00:34:37;

7; Search time 425.19 Seconds (without alignments) 230.662 Million cell updates/sec

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RESULT
Q51543/c
ID Q515
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DT 24-M
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   Provides information with a variety of potential agonists or subunit combinations with a variety of the function and should status for compounds that are capable of very specific interaction with one or mover receptor subunits and should lead to the function and design of the unital agonists of the compounds to the subunit specific antibodies may be used to monitor the distribution and expression density of various subunits in normal vs diseased brain tissues. Testing of single receptor subunits on specific receptor subunit combinations with a variety of potential agonists or antagonists provides information with respect to the function and activity of the individual subunits and should lead to the identification and design of compounds that are capable of very specific interaction with one or more receptor subtypes. The resulting drugs should exhibit fewer unwanted side effects than drugs identified e.g. screening with cells that express a variety of subtypes.

Sequence 1876 BP; 369 A; 553 C; 530 G; 423 T;
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Best I
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W09322437-A.
11-NOV-1993.
28-APR-1993; E01022.
30-APR-1992; EP-401231.
(INNO-) INNOGENETICS NV
Devos K, Fransen L, Va
                                                                                                                                                                                                                                                                                                                                                                                         Lipopolysaccharide induced protein gene.
Macrophage; induced; lipo-polysasccharide; antitumour;
antiinflammatory; trypanocidal agent; antibody; cell practivation; cytotoxicity; ds.
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WPI; 94-303024/37
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(represented by (N)40 in t
estimated length ca. 1000
3841. .3846
                                                                                                                                                                                                                                                            /note= "Intron 1 is only partially sequenced
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estimated length ca. 5400 bp"
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     Query Match
Best Local Similarity
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The polypeptide induced in macrophages by lipopolysaccharide stimulates cell prolification (esp. when costimulated with IL-4) promote activation, cytotoxicity, and mobilisation of LAK cells; promote recruitment of suppressive peritoneal exudate cells; promote generation of immunocompetent lymph node cells (LMC) and have trypanocidal and trypanolytic activity. The human and murine sequences are given in (Q51543-45), peptide fragments able to generate antibodies are given in (R51951-61) sequence 3861 BP; 542 A; 1241 C; 1292 G; 658 T;
New isolated nucleic acid encoding the new human cytokine Tango-77 used to inhibit inflammation and to screen for specific modulators Example 5; Figure 3; 226pp; English.

X03956-X03048 and X2301-X2304 are overlapping BAC genomic sequences containing alternatively spliced forms of human II-Ira. Such fragments are used in the method of the invention which describes the isolation a novel human TANGO-77 encoding nucleic acid and protein. Tango-77 is inflammation by binding to the interleukin-1 receptor (II-IR). It may also bind to a new receptor so could regulate other cellular processes associated with acute or chronic inflammation, e.g. asthma, chronic
                                                                                                                                                                             Pan Y;
WPI; 99-15369
New isolated
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03-AUG-1998; U
02-JUL-1998; U
04-AUG-1997;
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22-JUN-1999 (first entry)
22-JUN-1999 (first entry)
Human IL-1ra BAC contiguous DNA sequence 19.
Human IL-1ra BAC contiguous DNA sequence 19.
Tango-77; human; IL-1ra; cytokine superfamily; inflammation; inhibitic interleukin-1 receptor; IL-1R; regulation; asthma; rheumatoid arthrit; interleukin-1 receptor; psoriasis; inflammatory bowel disease; chronic myelogenous leukaemia; psoriasis; inflammatory bowel disease; chronic myelogenous leukaemia; psoriasis; inflammatory BAC; ss.
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P-PSDB; R43682.
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1998; US-091650.
1997; US-054646.
MILLENNIUM BIOTHERAPEUTICS
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Pred. No. 0.00
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25-MAR-1999; U19419
17-SEP-1998; US-093972.
09-JUN-1998; US-093972.
17-SEP-1997; US-059160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
          Disclosure; Page 37; 120pp; English.

The specification describes antisense oligonucleotides (X52869-X55271) directed against at least 2 mRNAs selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides
                                                                                                                                                                                                                                                                                                                                                 acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasoconstriction; emphysem chronic obstructive pulmonary disease; leukemia; lymphoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepaticellular carcinoma; kidney cancer; melanoma; hepatic m
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human adenosine Al receptor antisense oligonucleotide fragme Antisense oligonucleotide; multiple target; antisense treatminpaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis;
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X53491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     myelogenous leukaemia, rheumatoid arthritis, psoriasis and inflammatory bowel disease. It may also induce or suppress interleukins, cytokines are growth factors. Modulators of this protein are used to treat or prevent conditions associated with abnormal levels of inflammation, or activity of IL-1 or its receptor complex.

Sequence 3198 BP; 807 A; 847 C; 681 G; 846 T;
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                                                                                                                                               New antisense oligonucleotides used in treatment of, e.g. pulmonary
                                                                                                                                                                                  WPI; 99-229400/19.
                                                                                                                                                                                                                                                                                                                                      prostate cancer;
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X55272-74.
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Best Local
                                                                                                                                                                                                                                                                                                                                                           HSV-1 (MGH-10) ICP34.5 gene.
Herpes simplex virus; avirulent; vaccine;
Herpes simplex virus.
Key
Location /~~~
New recombinant Herpes Simplex Virus vaccines - rendered avirulent by deletion of ICP 34.5 gene encoding active gene prod. Disclosure; Fig 1; 78pp; English.

Herpes simplex virus-1 (MGH-10) was isolated from a recurrent facial vesicle and passaged a maximum of four times in cells in culture. Viral DNA was prepd. from virons that accumulated in the cytoplasm of infected VERO cells (Kieff et al., J. Virol., 8, 125-132 (1971)). The BamHI SP junction fragments contg. the domain of the gene that specified ICP34.5 were cloned into a pUC18 plasmid using HSV-1(F) sequences as probes in colony blot hybridisation. Further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oligonucleotides (specifically X55180-271) can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastasses, as well as all types of cancers which may metastasize or have metastasized to the lungs, including breast and prostate cancer.

Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T;
                                                                                                                                                                      P-PSDB; R21707.
New recombinant Herpes
                                                                                                                                                                                                             Roizman B;
WPI; 92-114074/14.
                                                                                                                                                                                                                                                                  W09204050-A.
19-MAR-1992.
10-SEP-1991; U06532.
10-SEP-1990; US-579834.
                                                                                                                                                                                                                                                   (ROIZ/) ROIZMAN
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Pred. No. 0
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 TAKE BAKE
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Best Local Similarity 40...
165; Conservative
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                                                                                                                                                                                                                                                                                                                               04-SEP-1998 (first entry)
Human chromosome 19 derived USF2 gene sequence.
Hydronephrosis gene; HNG gene; USF2 gene; renal disease; renal
vesical-ureteral reflux; pelvi-ureteral junction obstruction;
multicystic renal dysplasia; renal agenesis; hydronephrosis;
von Mayer-Rokitansky-Kuester disorder; bifid ureter; ss.
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                                       /number= 2
1572. .1690
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1. .1088
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/*tag= f
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                         Py disorders, e.g. vesical-ureteral reflux, pelvi-ureteral junction problems of the state of diagnose renal diseases and problems of the state of th
                                                                                                                                                                                                                                                                           16-ARR-1998.
09-OCT-1997; E05583.
09-OCT-1996; EP-202820.
(VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG FIYNS JPGJ, Groenen PMA, Van De Ven WJM; WPI; 98-240833/21.
P-PSDB; W60569.
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2797. .3074
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밁
        ps Disclosure; Page 37; 120pp; English.

Control of the specification describes antisense oligonucleotides (x52869-x55271)

Control of the specification describes antisense oligonucleotides (y52869-x55271)

Control of the specification describes antisense oligonucleotides (your genes, gene coding regions of RNAs corresponding to target genes, gene coding regions, genomic flanking regions, intron-exon borders, the complete control of the specification between coding and non-coding control of the second the second of the second of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human adenosine Al receptor antisense oligonucleotide fragment. Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nyce JW;
WPI; 99-229400/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-1999.
17-SEP-1998; U19419.
09-JUN-1998; US-093972.
17-SEP-1997; US-059160.
(UYEC-) UNIV EAST CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X53491 standard; DNA; 114955
X53491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antisense oligonucleotides used in treatment of, e.g. pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hepatocellular carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity hes 183; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGCCGAGGCAGCGGATCCAGACCC - - - GGGTCCAGCATGTCCATGGGGGGGGGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGCTCGGTGGAGACTGGGGGTGGAGGTGCCCGGAGCGTACCCCAGCGCCGGGAGTACCTC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCGCTCACACCTCGGGCTGCAGTTCCCTGGGTGGCCGGAGACGCTGGCCCGGGCTGGA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGATACGGGAGCCGCTCGCGCTGATCACGGGGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCCTCTGTGGCCGCAGGCGCAGGCCCGGGCGACA
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Pred. No. 0.017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
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                                                                                                             08-DEC-1994.
20-MAY-1994; UO5770.
20-MAY-1993; US-065146.
20-MAY-1993; US-065146.
(DAND ) DANA FARBER CANCER I
(DAND ) DANA FARBER CANCER I
SCHaffer PA, Yeh L;
WPI; 95-022825/03.
Herpes Simplex Virus (HSV) s;
- for inhibiting HSV L/ST sy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104635 NNHNNNSGCGGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as well as all types of cancers which may metastasize or metastasized to the lungs, including breast and prostate cancer. Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T;
Disclosure; Page 38-44; 64pp; English. An HSV-specific junction-spanning transcript (L/ST) maps at the end to the b repeat sequences of HSV DNA at approx. 3 and 125 kb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_rna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_rna
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSV L/ST region.
HSV; junction-spanning transcript;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 GCCTGGCCTTGGGCAGCCCCTGGCCTGGCCAGAGGCGGAGGCCGAGAGCCCGCTCGGTG
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370. .372
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199. .204
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229
                                                                                                                                                                                                                                                                                                                                                                                         /note- "first codon of ORF-1"
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                                                                                                                      specific junction synthesis, in the 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           end of the L/STs'
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25-FEB-1998; U03689.
26-FEB-1997; US-807014.
(CIBL-) CIBLEX CORP.
Baird A, Florkiewicz RZ;
WPI; 98-495377/42.
Inhibiting export of leaderless protein with agent that inhibits binding to transporter protein - especially for treating binding to transporter protein - especially for treating anglogenesis and restenosis by preventing export of fibroblast anglogenesis and restenosis by preventing export of restenosis by preventing export of specials anglogenesis and restenosis by preventing export of specials anglogenesis and restenosis by preventing export of specials with a special proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-DEC-1998 (first entry)
04-DEC-1998 (first entry)
cDNA sequence of fibroblast growth factor-2 (FGF-2).
Fibroblast growth factor-2; FGF-2; leaderless protein; export; angiogenesis; restenosis; treatment; tumour; ir cell proliferation; diabetes; retinopathy; infection;
cell proliferation; diabetes; atherosclerosis; ss.
                               Claim 2: Pages 53-54; 116pp; English.

The present sequence encodes fibroblast growth factor-2 (FGF-2), a leaderless protein. A leaderless protein refers to a protein that is found in an extracellular environment, but lacks a canonical leader sequence. The specification describes a method for inhibiting export of a leaderless protein from a cell. The method for inhibiting export can leaderless protein from a cell. The method for inhibiting export the cell with an agent that inhibits binding between the leaderless protein and a transport molecule. Treatment with the inhibiting agent is specifically used to treat angiogenesis and restenosis, i.e. where expression of FGF-2 is inhibited, and the agent is applied to endothel or smooth muscle cells. Other applications are treatment of tumours (melanoma, teratocarcinoma, ovarian carcinoma, bladder cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and extends into the c repeat sequences of HSV DNA. Compounds that inhibit HSV L/ST synthesis may be used as anti-HSV virucides. The HSV-1 DNA sequence in the region of the L/STs is given in Q76213.

Sequence 12001 BP; 1568 A; 4557 C; 4315 G; 1561
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cell proliferation, compi:
viral, bacterial or fungal
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Best Loc
Matches
                                                                                                                                                WO9428156-A.
08-DEC-1994.
20-MAY-1994;
20-MAY-1993;
Disclosure; Page 38-44; 64pp; English.
An HSV-specific junction-spanning transcript (L/ST) maps at the end to the b repeat sequences of HSV DNA at approx. 3 and 125 and extends into the c repeat sequences of HSV DNA. Compounds that inhibit HSV L/ST synthesis may be used as anti-HSV virucides. The HSV-1 DNA sequence in the region of the L/STs is given in Q76213.

Sequence 12001 BP; 1568 A; 4557 C; 4315 G; 1561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polycystic
Sequence
                                                                                           WPI; 95-022825/03.
Herpes Simplex Virus
- for inhibiting HSV
                                                                                                                                                                                                              misc_rna
                                                                                                                                                                                                                                           misc_rna
                                                                                                                                                                                                                                                                          misc_binding
                                                                                                                                                                                                                                                                                                                             HSV L/ST region.
HSV; junction-spanning transcript;
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                                                                                                                                                                                                                                                                                                                   Herpes
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                                                                                  infection
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                                                                                                                            (DAND ) DANA FARBER CANCER Schaffer PA, Yeh L;
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                                                                                                                                                                                                                                                                                                                   simplex
                                                                                                                                                                                                                                                                                                                                                                       standard;
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US-065146.
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/note= "5'
370. .372
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                                                                                             (HSV)
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"first codon
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                                                                                             ) specific junction spanning synthesis, in the treatment
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293 C; 342
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                                                                                                                                                                                                                       the L/STs"
                                                                                                                                                                                                                                                                                                                             L/ST; therapy; virucide;
                                                                                                                                                                                          of ORF-1'
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of HSV
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                                                                                                                                                                   New polynucleotide encoding PACE endo-peptidase - used for e.g.
reducing blood pressure
Sclaim 1; Figure 1; 81pp; English.
The mammalian endopeptidases PACE 4 and PACE 4.1 (an alternative form of PACE 4) are involved in the production of mature polypeptides from precursor polypeptides by cleavage at pairs of Dasic amino acids e.g Lys-Ray, Lys-Lys and Arg-Arg. The enzymes are stimulated by the presence of calcium ions and inhibited by phenylmethyl sulphonyl fluoride. PACE 4 and 4.1 convert prorenin to renin in the human kidney, causing elevation of blood pressure. They can therefore be used to identify other inhibitors of their action and may also be used to inhibit blood coagulation.
Sequence 4403 BP; 1016 A; 1253 C; 1214 G; 920 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                        Matches
                                                                                                                  Query Match
Best Local
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247927 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paired basic amino acid converting enzyme (PACE) Paired basic amino acid converting enzyme; PACE; hypertension; blood; coagulation; ss.
                                                                                                                                                                                                                                                                                                                                                            Barr PJ, Klefer MC;
WPI; 93-303473/38.
                                                                                                                                                                                                                                                                                                                                                                                                                 16-SEP-1993.
09-MAR-1993;
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                                                                                                                                                                                                                                                                                                                                                  P-PSDB; R41662.
                                                                                                                                                                                                                                                                                                                                                                                     09-MAR-1992; US-848629
(CHIR ) CHIRON CORP.
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313
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                       CCAGCGCCGGGAGTACCTCCCGCTCACACCTCGGGCTGCAGTTCCCTGGGTGGCCGCCGA 172
                                                                            GAGGCGCGAGGCCGAGAGCCCGCTCGGTGGAGACTGGGGGGTGGAGGTGCCCGGAGCGTAC 112
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137;
                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 170. .3079
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/product= PACE 4
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49
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                                                                                                      Score 51.8; I
Pred. No. 0.19
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 52.4; DB Pred. No. 0.12;
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                                                                                                                  DB 1;
.19;
                                                                                                      167;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 gene.
prorenin; renin;
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                                                                                                                                Length 4403;
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PH NESULT PRESULT 10 Q479 DT Q479 DT Q479 DT PAIR KW hype OS Homo FF Cds FT Cds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotide encoding PACE endo-peptidase - used for e.g. reducing blood pressure

Example 2; Figures 1 and 3; 8lpp; English.

The mammalian endopeptidases PACE 4 and PACE 4.1 (an alternative form of PACE 4) are involved in the production of mature polypeptides from precursor polypeptides by cleavage at pairs of polypeptides from precursor polypeptides by cleavage at pairs of pasic amino acids e.g Lys-Arg, Lys-Lys and Arg-Arg. The enzymes are stimulated by the presence of calcium ions and inhibited by phenylmethyl sulphonyl fluoride. PACE 4 and 4.1 convert prorenin to renin in the human kidney, causing elevation of blood pressure. They can therefore be used to identify other inhibitors of their action and may also be used to inhibit blood coagulation.

Sequence 2218 BP; 534 A; 623 C; 623 G; 438 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 49.7
Matches 164; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-MAR-1993; U02147.
09-MAR-1993; U02147.
...--1992; US-848629.
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Paired basic amino acid converting enzyme;
Paired basic amino acid converting enzyme;
hypertension; blood; coagulation; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q47929;
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WPI; 93-303473/38.
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                                                                                                                                                ACGTGGAGCGCCGGCTCGCTGCAGCTCCGGG
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                                                       CCAGCGCCGGAGTACCTCCCGCTCACACCTCGGGCTGCAGTTCCCTGGGTGGCCGCCGA
                                                                                                                                                                                                                                                                                                                                          GAGGCGCGAGGCCCGAGAGCCCCGCTCGGTGGAGACTGGGGGGTGGAGGTGCCCCGGAGCGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 51.8; DB Pred. No. 0.21; 0; Mismatches :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         167;
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                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 167
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23-JUL-1997; U12904.
26-JUL-1996; US-690473.
(ARCH-) ARCH DEV CORP.
                                                                                                                                                                                                                                                                                                                                                                                            Use of herpes simplex virus ICP4 polypeptide - useful for, e.g. blocking apoptosis in cells, production of proteins and gene therapy blsclosure; Fig 2; 63pp; English.

The herpes simplex virus (HSV) alpha-4 gene encodes infected cell protein number 4 (ICP4). Both the alpha-4 gene and ICP4 can be used to block cell apoptosis. Similarly the administration of an agent that inhibits ICP4 or the alpha-4 gene can induce apoptosis in HSV infected cells. This can be used for the immortalisation of cells, production of proteins, gene therapy, or inhibition of cells death induced in vivo. They can also be used for production of therapeutics comprising inhibitors of HSV ICP4 function, useful for treating HSV function.

Sequence 4257 BP; 412 A; 1768 C; 1663 G; 414 T;
                                                     2566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Infected cell protein number 4 alpha-4 Infected cell protein number 4; ICP4; attherapeutics; ss.
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 2506
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                                                                                                                                                                                                                   GCGGGCCGGCCGCGCGGCGGCCGGGCGCGCGGCTGGGCGGGGCGGGCCTCGG
                                                                                                                                                                                                                                                                        GCCGCCAGCCGAGGGGGTCGGGGGCCCTCGGCGGGCGGCGACACGGCCACGGGGC
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CCGCCAGCGCGTCGGCGTCCGGTGCGCTGGCCGCCGCCAGCAGGGGGGGCGCAGG
                                                                                                                                                              TGGGGGTGGAGGTGCCCGGAGCGTACCCAGCGCGCGGAGTACCTCCCGCTCACACCTCGG 146
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                                                                                                        AGGCGCAGGCCCGGCCGACAGCCGAGACGTGGAGCGCGCCGCCTCGCTGCAGCTCCGGG 385
                                                   al Similarity 46.5
167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    simplex virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers 361. .4257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*rag= a
/product= "Infected cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA; 4257
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                                                                                                                                                                                                                                                                                                                                          Score 51.8; DB 1; Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 gene.
alpha-4; cell apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein'
                                                                                                                                                                                                                                                                                                                               192;
                                                                                                                                                                                                                                                                                                                                                       Length 4257;
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Best Local Similarity 46.5
                                                                                                                                                                                                                                                                                                                                                                                           Use of herpes simplex virus U(s)3 polypeptide - for developing products for modulating apoptosis in cells and for identifying compounds which act as stimulators or inhibitors of apoptosis Example 2; pages 60-63; 85pp; English.

Example 2; pages 60-63; 85pp; English.

This is the nucleotide sequence of Herpes simplex virus ICP4 used in the method of the invention as modulators of apoptosis. The methods and products can be used to identify compounds which modulate (stimulate or inhibit) apoptosis in cells. They can be used to immortalise cells for the study of these cells or for growing cells in large numbers for the productions of proteins. They can also be used for stimulating apoptosis in cells, e.g. for treating a subject with a HSV infection.
                                                                                                                                                                                                             2746
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Key
CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The nucleotide sequence of the Herpes simplex virus ICP4; HSV stimulation; inhibition; HSV in
 2506
                                                    2566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-APR-1997; US-843659.
(ARCH-) ARCH DEV CORP.
Leopardi R, Roizman B;
WPI; 98-594559/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V68520
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16-APR-1998; U07573
16-APR-1997; US-8436
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                                                                                                                                                                                   147
                                                                            267
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GGCGCGCGCCCGGCTAAAAGGCGCGAGCCGAGCGGCGAGGTGCCTCTGTGGCCGC
                                                                                                                               GCTGCAGTTCCCTGGGTGGCCGGCCGAGACGCTGGCCCGGGCTGGAGGGATGGCGGGGCGG
                                                                                                                                                                                                             TGGGGGTGGAGGTGCCCGGAGCGTACCCAGCGCGGGAGTACCTCCCGCTCACACCTCGG
                                                                                                                                                                                                                                                                GCCGCCAGCCGAGGGGGTCGGGGGCCCTCGGCGGCGGCGGCGACACGGCCACGGGG
                                                                                                                                                                                                                                                                              GCCTTGGGCAGCCCCTGGCCAGAGGCGCGAGAGCCCGAGAGCCCGCTCGGTGGAGAC
                           AGGCGCAGGCCCGGGCGACAGCCGAGACGTGGAGCGCCGGCTCGCTGCAGCTCCGGG
                                                    GGGCCGGGCCGGACTCTTGCGCTTGCGCCCCCCCCGCGGCGCGCGGAGGCCGGCGGCGG
                                                                                                      standard; DNA; 4257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    simplex virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                   BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 361. .4257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*cag- a
/product- "HSV ICP4
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                                                                                                                                                                                                                                                                                                                               13.2%;
                                                                                                                                                                                                                                                                                                                                                                                   412 A;
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                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                   Score 51.8; DB Pred. No. 0.19; 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herpes simplex virus ICP4; modulator; apop
                                                                                                                                                                                                                                                                                                                                                                                   1768 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                   192;
                                                                                                                                                                                                                                                                                                                                                                                  1663 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              apoptosis;
                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                                                                                                   Gaps
 2448
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2 (bases 1 to 689)
Leonard,S., Gault,J., Logel,J., Drebing,C., Robinson,M.,
Breese,C., Davis,A., Hopkins,J. and Freedman,R.
Direct Submission
                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 689)
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AC007562 Homo sapi
260646 H.sapiens C
AF036903 Homo sapi
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Result No.

Score 689

Berger, R.,

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/clone="CHRNA7-DR1"
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/db_xref="taxon:9606"
/chromosome="15"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 503; DB 11;
Pred. No. 1.2e-111;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Denver, CO 80262, USA
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Best Local Similarity
Matches 345; Conserv
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                                                                                                         CACATAGCT-CCCGCCAAGTCCTCGGTGCCCCTTGCCATTTTCCAGCCGCGCTCCCACGA 179
                                                                                                                                                                     GTACCTGCCTCCAGGCATATTCAAGAGTTCCTGCTACATCG
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                                                                                                                                                      ACAGGAGCAGCGCCTCCTGTCGGTGGAGTCTGTTACAAGGGGAGCAGCCGCCCAGGCCGC
GAGTTGAGGCATCAGGGAGAGGCGGAGCTGGGAGAGCGCCGCGAGAGGTCCCGCGGGTG
                                                          GGGTCACGGCGGGGAGAGGTGGAGCCGCGAGAGCTCGGCCGGGGGCCCCGCCTGGTG 239
                                                                                        CACACAGCTCCCGGAGGCCTCGGTGCCCCTTGCCATTTTCCAGCCCTACTCCGACTA 47525
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Submitted (08-SEP-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
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Homo sapiens clone DJ1129D05,
AC005630
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Submitted (15-JAN-1999) Genome Sequencing Cente
University School of Medicine, 4444 Forest Park
MO 63108, USA
On Jan 15, 1999 this sequence version replaced
Location/Qualifiers
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Waterston, R.H.
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Waterston, R.H.
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1 (bases 1 to 137699)
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/db_xref="taxon:9606"
/clone="DJ1129D05"
30670 c 32412 g 3770
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Pred. No. 6.5e-61
D; Mismatches 6
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t Park Parkway, St.
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Best Local Sim
Matches 284;
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181
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                                                                              CGCGCTCCCACGAGGGTCACGGCGGGGGAGAGGTGGAGCCGCGAGAGCTCGGCCGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNCCCGCCTGGTGGTCGCGGNCATGACAGCGGCTCGGGACAGGCTCCTTTTCCGCGCCCC
                              GCCCCGCCTGGTGGCCGCCGCCCATGACAGCGGCTCGGGACTGGCTCCTTTTCCGCGCCCCC 286
                                                                                                                             GNCCCGCAGGCCGCCACATAGCTCCCGCCAAGTCCTCGGTGCCCCTTGCCATTTTCCAGC
                                                                                                                                                                                          TAAACTGCGGCTTGACGGGAGCCGCGCCTCCTGTCGGTGGAGTCGGTTATAAAGGGAGCA
                                                              CGCGCTCCCACGAGGGTCACGGCGGCGGGGGAGAGGTGGAGCCGCGAGAGCTCGGCCGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 291)

MacDonald, M., Huckle, E., Wilkinson, P. and Micklem, G.

Direct Submission

Submitted (16-OCT-1995) The Sanger Centre, Hinxton, Cambridgeshire,

CB10 IRQ, England. E-mail contact: humquery@sanger.ac.uk

2 (bases 1 to 291)

Cross, S. H., Charlton, J. A., Nan, X. and Bird, A. P.

Purification of CpG islands using a methylated DNA binding column

Nat. Genet. 6 (3), 236-244 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HS2E10F 291 bp
H.sapiens CpG island
read cpg2e10.ft11d.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clones are available from the UK MRC Human Resource Centre, Hinxton, Cambridgeshire CE http://www.hgmp.mrc.ac.uk/ for details or contact: biohelp@hgmp.mrc.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          z58126.1 GI:1029357
CpG island; genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vector: pGEM-52f(-)
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                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                        /dev_stage="adult"
/tissue_type="blood"
/clone_lib="CGI-1"
/clone="2e10"
a 95 c 103 g
                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
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97.6%;
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                                                                                                                                                                                                                                                         Score 282.2; DB 9
Pred. No. 1.7e-58;
0; Mismatches 7
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Best Local
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                                                                                                                                                                     AGCCCTTTCCCAGGCGGTAGCGGGGGCAGTGGTGCTGTTGCCCCTTTTAAACTGCGGCTTG 60
                           GGTCACGGCGGCGGGAGAGGTGGAGGCCGCGAGAGCTCGGCCGGGGGGCCCCGCCTGGTG 239
                                                                                                                                                                                                                            AGCCCTTTCCCAGGCGGTAGCGGGGGCTGTGGTGGCTGTTGCCCCTTTTAAGCTGCGGCTTG 30232
   GAGTTGAGGCAGCAGGAGAGGCGGAGCTGGGAGAGCACCGCCGAGAGGTCCCCGCGGGTG 30412
                                                                          CACACAGCTCCCCGCAGAGGCCTTGGTGCCCCTTGCCATTTTCCAGCCCTACTGTGACTA 30352
                                                                                                               CACATAGCT-CCCGCCAAGTCCTCGGTGCCCCTTGCCATTTTCCAGCCGCGCTCCCACGA 179
                                                                                                                                                  ACAGGAGCAGCGCCTCCTGTCGGTGGAGTCTGTTAGAAGGGGAGCAGCCGCCCAGGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (14-MAY 1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Jun 5, 1999 this sequence version replaced gi:4827309.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 192439)
Waterston, R.H.
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Waterston, R.H.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens clone NH0497C14, WORKING DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                  55693
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/db_xref="taxon:9606"
/clone="NH0497C14"
40710 c 39187 g 5679:
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5353: gap of unknown length
20005: contig of 14652 bp in length
20023: gap of unknown length
98080: contig of 78057 bp in length
98098: gap of unknown length
192439: contig of 94341 bp in length.
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Pred. No. 2.5e-55;
0; Mismatches 76;
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CACATAGCT-CCCGCCAAGTCCTCGGTGCCCCTTGCCATTTTCCAGCCGCGCTCCCACGA 179
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332; Conserv
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Submitted (09-JAN-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
Mo 63108, USA
On Mar 13, 1999 this sequence version replaced gi:4138780.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 178307)
Waterston,R.H.
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/db_xref="taxon:9606"
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38822 c 39355 g 5010
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11181: gap of unknown length
57066: contig of 45885 bp in length
57084: gap of unknown length
178307: contig of 121223 bp in length.
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Pred. No. 2.7e-53;
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                                                  CCCCGCAGGCCGCCACATAGCTCCCGCCAAGTCCTCGGTGCCCCTTGCCATTTTTCCAGCC
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                                                                                                             AAACTGCGGCTTGACGGGAGCCGCGCCTCCTGTCGGTGGAGTCGGTTATATAAAGGGAGCAG 107
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   GCGCTCCCACGAGGGTCACGGCGGCGGGGAGAGGTGGAGCCCGCGAGAGCTCGGCCGGGGG
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                                                                                            AAACTGCGGCTTGACGGGAGCCG - NCCTCCTGTCGGTGGAGTCGGTTATAAAGGGAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (16-OCT-1995) The Sanger Centre, Hinxton, Cambridgeshire, CB10 1RQ, England. E-mail contact: humquery@sanger.ac.uk 2 (bases 1 to 298)
Cross,S.H., Charlton,J.A., Nan,X. and Bird,A.P.
Purification of CpG islands using a methylated DNA binding column Nat. Genet. 6 (3), 236-244 (1994)
                                                                                                                                                                                                                                                                                                                                                                                   Clones are available from the UK MRC Human Genome Resource Centre, Hinxton, Cambridgeshire CB10 IRQ, http://www.hgmp.mrc.ac.uk/ for details or contact: biohelp@hgmp.mrc.ac.uk.

Location/Qualifiers
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MacDonald,M., Huckle,E., Wilkinson,P. and
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                                                                                                                                                                                                                                               /tissue_type="blood"
/clone_lib="CGI-1"
/clone="2g7"
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/db_xref="taxon:9606"
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CTGCCTCCAGGCATATTCAAGAGTTCCTGCTACATCG
                                                            CGCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTCTTCTGGGCATTGCCAGTAC 652
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Homo sapiens alpha-7 neuronal nicotinic acetylcholine
mRNA, alternatively spliced, partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (03-DEC-1997) Psychiatry, Sciences Center, 4200 E. 9th Ave., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leonard, S., Gault, J., Logel, J., Breese, C., Davis, A., Hopkins, J. Direct Submission
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                                                                                                                                                                                                                                                                                                                        /Clone_lib="Soares papathyroid tumor NbHPA library, 
/Clone_lib="Soares papathyroid tumor NbHPA library, 
Reseach Genetics/IMAGE Consortium, LINL"
                                                                                                                                                                                                                                                                                                                                                                         /db_xref="dbEST:W52861"
/db_xref="dbEST:AA037389"
/chromosome="15"
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/db_xref="taxon:9606"
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                                                                                                                                                                          22.6%;
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                                                                                                                                                             Score 155.4; DB 1
Pred. No. 6.3e-28;
0; Mismatches 1
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80262, USA
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                                                                                                                                                                                                                                                     534 AATTCCAATTGCTAATCCAGCATTTGTGGATAGCTGCAAACTGCGATATTGCTGATGAGC 593
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          H.sapiens CpG forward read cp
254415
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Homo sapiens alpha-7
                                                  HS115G2F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (03-DEC-1997) Psychiatry, University of Colorado Health Sciences Center, 4200 E. 9th Ave., Denver, CO 80262, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leonard, S., Gault, J., Logel, J., Drebing, C., Robinson, M., Breese, C., Davis, A., Hopkins, J. and Freedman, R. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gault,J., Robinson,M., Berger,R., Drebing,C., Logel,J., Hopkins,J., Moore,T., Jacobs,S., Meriwether,J., Choi.M.J., Kim,E.J., Walton,K.,
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                                                                                                                                                                                                                                                                                                                                                                      383
                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="dbEST:W03952"
/db_xref="dbEST:N73891"
/chromosome="15"
                                                                                                                                                                                                                                                                                                                                                               /note="alpha-7 neuronal nicotinic acetylcholine precursor; intron included in 5' region" sold c 469 g 481 t
                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Soares fetal liver spleen library, Genetics/IMAGE Consortium, LLNL"
                                                                                                                                                                                                                                                                                                                                                                                                                        note="unprocessed mRNA with intron"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'clone"
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                      Island DNA genomic Msel fragment, clone 115g2, cpg115g2.ftla.
                                   180 bp
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Pred. No. 1.1e-27;
0; Mismatches 1;
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Best Local Similarity
Matches 140; Conserv
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47 TAAACTGCGGCTTGACGGGAGCCGCGCCTCCTGTCGGTGGAGTCGGTTATAAAGGGAGCA 106
Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 171)

5 Dodsworth, S.J., Huckle, E., Wilkinson, P. and Mickle Direct Submission

Submitted (16-OCT-1995) The Sanger Centre, Hinxton CB10 IRO, England. E-mail contact: humquery@sanges

CB10 IRO, England. E-mail contact: humquery@sanges

CB10 IRO, England. B-mail contact: humqu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAAGCTGCGGNTTGACAGGGGCCGCCCCCCCTCTTGTCGGTGGAGTCGGTTACAAAGGGAGCA
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H.sapiens CpG island :
forward read cpg165h1
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Submitted (16-OCT-1995) The Sanger Centre, Hinxton, Cambridgeshire,
CB10 IRQ, England. E-mail contact: humquery@sanger.ac.uk
(bases 1 to 180)
Cross 1. Charlton, J.A., Nan, X. and Bird, A.P.
Purification of CpG islands using a methylated DNA binding column
Nat. Genet. 6 (3), 236-244 (1994)
94282070
                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
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1 (bases 1 to 180)
MacDonald, M., Huckle, E., Wilkinson, P. and
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/tissue_type="blood"
/clone_lib="cGI-1"
/clone="115g2"
a 57 c 58 g
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d; genomic Msel fragment.
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/db_xref="taxon:9606"
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l.ftla.
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Pred. No. 3.8e-19;
0; Mismatches 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Msel fragment,
                                                                                                                                                                             Centre, Hinxton, Cambridgeshire, humquery@sanger.ac.uk
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                                                     DNA binding column
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone
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Matches 138;
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Human a7 nicotinic acetylcholine receptor mRNA.
L25827
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                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nicotinic acetylcholine receptor alpha 7 subunit;
                                                                                                                                                                                                                                                                                                          Cloning and sequence of the human a7
                                                                                                                                                                                                                                                                                                                       Doveette-Stamm,L., Monteggia,L.M., Donnelly-Roberts,D., Wang,M.T.,
Lee,J., Tian,J. and Giordano,T.
                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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Location/Qualifiers
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/tissue_type="blood"
/clone_lib="CGI-1"
/clone="165h1"
/clone="165h1"
a 56 c 57 g
                                                                                                                                           /tissue_type="brain"
/tissue_lib="clontech HL1065b; ATCC 37433"
463 c 440 g 342 t
                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/dev_stage="fetus"
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/db_xref="taxon:9606"
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Pred. No. 1.6e-16;
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Pred. No. 1.6e-18;
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574 CTGCGATATTGCTGATGAGCGCCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTC 633

Query Match Best Local S Matches 111

Local Similarity les 111; Conserv

15.7%;

Score 108; DB 10; Pred. No. 1.6e-16; ); Mismatches 5;

Length 2087;

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peng, X., Katz,M., Gerzanich,V., Anand,R. and Lindstrom,J.
Human alpha 7 acetylcholine receptor: cloning of the alpha 7
subunit from the SH-SYSY cell line and determination of
pharmacological properties of native receptors and functional alpha
7 homomers expressed in Xenopus occytes
Mol. Pharmacol. 45 (3), 546-554 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSARA7A 2087 bp mRNA PRI 01-JUN-1994
H.sapiens mRNA for neuronal nicotinic acetylcholine receptor alpha-7 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (04-FEB-1993) M. Katz, Univ of Pennsylvania School Medicine, Dept of Neuroscience, 36th & Hamilton Walk, Rm 235 Stemmler Hall, Philadelphia, PA 19104, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2087)
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                                                                              LLNWCAWFLRMKRPGEDKVRPACQHKQRRCSLASVEMSAVGPPPASNGNLLYIGFRGL
DGVHCVPTPDSGVVCGRMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRCQ
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1. .2087
                                                                                                                                                                                                                                          'db_xref-"GI:496607"
                                                                                                                                                                                                                                                                            protein_id="CAA49778.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="brain"
/cell_type="neuroblastoma"
/cell_line="SHSY-5Y"
                                                                                                                                                                                                                                                             'db_xref="PID:g496607"
                                                                                                                                                                                                                                                                                                                                      codon_start=1
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'lpha-7 subunit"
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db_xref="taxon:9606"
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1 (bases 1 to 1509)

Groot Kormelink, P.J. and Luyten, W.H.

Cloning and sequence of full-length cDNAs encoding the human neuronal nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and expression of seven nAChR subunits in the human neuroblastoma cell line SH-SY5Y and/or IMR-32

FEBS Lett. 400 (3), 309-314 (1997)
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Submitted (27-SEP-1996) P.J. Groot Kormelink, Janssen Research
Foundation, Exp. Mol. Biol. Dept., Turnhoutseweg 30, B-2340 Beerse,
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Y08420.1 GI:2808623
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Jan 25, 1998 this sequence version
Location/Qualifiers
                                  297
                                                                                                       /gene-"nAChRA7"
67. .1506
                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAA69697.1"
//db_xref="pid:e1246208"
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/translation="MRCSPGGWILALAASILHVSLOGEFQRKLYKELYKNYNPLERPV_NTSPALITION FOR THE CONTROLLY NAD CONTROLLY 
                                                                                                                                                                                                                                                                                DVTFTVTMRRRTLYYGLNLLIPCVLISALALLVFLLPADSGEKISLGITVLLSLTVFM
LLVAEIMPATSDSVPLIAQYFASTMIIVGLSVVVTVIVLQYHHHDPDGGKMPKWTRVI
LLNWCAWFLRMKRPGEDKVRPACQHKQRRCSLASVEMSAVAPPPASNGNLLYIGFRGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   precursor"
                                                             /gene="naChRA7"
                                                                                                                                                                                                                                                 DGVHCVPTPDSGVVCGRMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRCQ
                                                                                                                                                                                                               DESEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFVEAVSKDFA"
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Query Match

15.7%;

Score 108;

DB 10;

Length 1509;

Query Match

15.7%;

Score

108;

DB 10;

Length 1876;

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U62436.1
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Human nicotinic acetylcholine receptor alpha7 subunit precursor, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (28-JUN-1996) Kathryn Inc., 505 Coast Blvd. So., La Jo
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chavez-Noriega,L.E., Johnson,E.C., Velicelebi,G. and Harpold,M.M. Comparative structure of human neuronal alpha 2 alpha 7 and beta 2-beta 4 ntcotintc acetylcholine receptor subunits and functional expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1876)

Elliott, K. J., Ellis, S.B., Berckhan, K. J., Urrutia, A.,
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LLVAEIMPATSDSVPLLAQYFASTMIVGLSVVYJVQYHHIDPDGGXMFKWTRVI
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                                            /product="nicotinic acetylcholine receptor alpha7 subunit"
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                      423
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Human cardiac hype
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BamHI J-I fragment
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Neuronal nicotinic
Alpha4 subunit of
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YT Nucleic acids encoding nicotinic acetylcholine receptor sub-units -
YT Nucleic acids encoding nicotinic acetylcholine receptor sub-units -
YT used in screening to determine the effect of drugs on the receptor
YT Screening to determine the effect of drugs on the receptor
YT Screening to determine the effect of drugs on the receptor
YT Screening to determine the alpha-7 subunit (W09025) of
YT Screening Page 71-73; 108pp; English.
YT AND Sequence (T48239) codes for the alpha-7 subunit ecceptor (nAChR). Host
YT Screening Page 71-73; 108pp; English.
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Matches 111;
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27-DEC-1996.
07-JUN-1996; U99775.
07-JUN-1995; US-484722.
(SIBI-) SIBIA NEUROSCIENCES I:
Elllott KJ, Harpold MM;
WPI, 97-065463/06.
W09420617-A2.
15-SEP-1994.
08-MAR-1994; U02447.
08-MAR-1993; US-028031.
(SALK ) SALK INST BIOTECHNOLOGY IND
(SIBI-) SIBIA NEUROSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-1998 (first entry)
Human neuronal nicotinic acetylcholine receptor alpha-7 subunit cDNA.
Human; neuronal nicotinic acetylcholine receptor; alpha-7 subunit;
brain tissue; screening; NAChR; antibody; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V12197 standard; cDNA; 1876
V12197;
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Neuronal nicotinic acetylcholine receptor alpha-7 subunit DNA.
Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;
11gand-gated receptor; ds.
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T48239;
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11; Conservative
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73. .1581
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aipha-7 subunit"
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Pred. No. 4.8e-21;
0; Mismatches 5
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SUMMARIES

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US-08-956-518A-102

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GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd

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CThe present sequence encodes a human neuronal nicotinic acetylcholine receptor (NAChR) subunit. The cells expressing the alpha and/or beta NAChR subunits may be used in a method of screening compounds to identify any which modulate the activity of human neuronal NAChR. Subunit specific antibodies may be used to monitor the distribution and expression density of various subunits in normal vs diseased brain tissues. Testing of single receptor subunits or specific receptor subunit combinations with a variety of potential agonists or antagonists provides information with respect to the function and activity of the individual subunits and should lead to the identification and design of compounds that are capable of very specific interaction with one or more receptor subtypes. The resulting drugs should exhibit fewer unwanted side effects than drugs identified e.g. screening with cells that express a variety of subtypes.

Sequence 1876 BP; 369 A; 553 C; 530 G; 423 T;
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                                                      P-PSDB; W69216.

Nucleic acid encoding variant of human alpha7 nicotinic acetyl-choline receptor sub-unit - used to identify modulators of the receptor, potentially useful for treating neuro-degeneration, cancer, affective disorders etc.

Claim 14; Fig 2: 44pp; English.

This sequence encodes the v2477 variant of human alpha7 nicotinic acetylcholine receptor (nAChR) subunit of the invention. Cells containing the DNA are used to express the protein and to identify modulators of alpha7 nAChR activity or cytoprotective agents, e.g. antisense compounds or antagonists that are potentially useful for treating annumentation answer dvsfunction, affective disorders and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-OCT-1998 (first entry)
V274T variant human alpha7 nAChR coding sequence.
Alpha7 nAChR; alpha7 nicotinic acetylcholine receptor subunit; cancer; neurodegeneration; enzyme dysfunction; affective disorder; therapy;
neurodegeneration, enzyme dysfunction, affective disorders and immune dysfunction, such as cancer, post-herpetic neuralgia, diabetic neuropathy, osteoarthritis, Alzheimer's or Parkinson's diseases, kuru
                                                                                                                                                                                                                                                                                                                                                                                   (ABBO ) ABBOTT LAB.
Briggs CA, Goplakrishnan M, McKenna DG, Monteggia
Roch J, Sullivan JP, Touma E;
WPI; 98-377593/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immune dysfunction;
schizophrenia; ss.
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V44687;
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activity of the receptor
Claim 8; Page 78-79; 99p;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human neuronal nicotinic acetylcholine receptor subunits and also transformed cells useful for screening cpds. which modul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Elliott KJ, Ellis
WPI; 94-303024/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-DEC-1996; US-771737.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
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9. .1517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diabetic neuropathy; Alzheimer's disease;
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95.7%;
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Pred. No. 4.8e-21;
0; Mismatches 5
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밁 Q

OKKWKEDIC

Query Match Best Local S Matches 90

Similarity

10.8%;

Conservative

0

Score 74.4; DB 1; Pred. No. 1.5e-11; 0; Mismatches 26;

26;

0

Gaps

0

Length

574 CTGCGATATTGCTGATGAGCGCCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTC 633

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                          New isolated neuronal alpha-bungarotoxin-binding protein DNA - used to screen cholinergic agents and other drugs which may affect ligand protein pinding; ion channel or other activities of the protein.

Claim 1; Fig 2A-B; 18pp; English.

C aDNA clones (T59196 and T59197) respectively code for the alphal subunit (W12369) of chick neuronal cubin (W12368) and alpha2 subunit (W12369) of chick neuronal subunit (W12369) of chick neuronal cubina-bungarotoxin binding protein (ABBP). They were isolated from an 18-day embryo chick brain cDNA library using a probe (see also T59198) based on the N-terminal amino acid sequence of chicken cubrain ABBP. The probe isolated partial clone pCh29-1, which encoded the N-terminal portion of alpha1. A subclone, pCh29-3 (ATCC 40641), was used to rescreen the library, yielding clone pCh31-1 (ATCC 40640), which encoded the entire alpha2 sequence. A probe based on the C-terminal region of pCh31-1 was used obtain clone pCh34-1 (ATCC 40649), encoding the C-terminal portion of alpha1. The cDNA clones can be used as probes to identify further capha1. The cDNA clones can be used as probes to identify further capha1. The cDNA clones can be used as probes to identify further capha2 since the combinant production of ABBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 15.7
Best Local Similarity 95.7
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                               WPI; 97-118297/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T59196 standard; cDNA; 276
T59196;
17-JUN-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       psychosis and schizophrenia. Probes based on the DNA are used to detect the DNA in usual hybridisation or amplification tests; while monoclonal antibodies are used to detect the protein for diagnosis (in vitro or by in situ immuno-fluorescent assay). Compared with wild-type alpha7 nAChR, the protein has about 100-fold greater sensitivity to cholinergic receptor agonists (nicotine or acetylcholine) and response to these agonists decays more slowly, but the wild-type inward rectification is
  Sequence
                                                                                                                                                                                                                                                                                                                                                             P-PSDB; W12368
                                                                                                                                                                                                                                                                                                                                                                                                                  28-SEP-1989; US-413947.
(SALK ) SALK INST BIOLOGICAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             signal_peptide
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LBBP subunits, and in the recombinant production of Algequence 2769 BP; 790 A; 604 C; 571 G;
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71. 136
/*tag= b
137. 1510
/*tag= c
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Pred. No. 4.5e-21;
0; Mismatches 5
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                      of ABBP.
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RESULT
V68408,
ID V6
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KW T1
KW at
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DR P-PSDB; W12369.

PT New isolated neuronal alpha-bungarotoxin-binding protein DNA - used PT to screen cholinergic agents and other drugs which may affect ligand binding, ion channel or other activities of the protein.

PT binding, ion channel or other activities of the protein.

CC claim 1; Fig 3A-B; 18pp; English.

CC an 18p-day embryo chick brain claim (ABBP). They were isolated from CC an 18p-day embryo chick brain cNA library using a probe (see also CC an 18p-day embryo chick brain cNA library using a probe (see also CC an 18p-day embryo chick brain cNA library using a probe (see also CC an 18p-day embryo chick brain con althal. A subclone, pch39-3 (ATCC 40641), was used to rescreen the library, yielding clone CC (ATCC 40641), which encoded the entire alpha2 sequence clone pch34-1 (ATCC 40639), encoding the C-terminal portion of alpha1. The cDNA clones can be used as probes to identify further Sc Sequence 2101 BP; 582 A; 406 C; 454 G; 659 T;
                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                   Matches
Human BAZ1-beta cDNA #1. Transcription; BAZ1-alpha; bromodomáin; BAZ; atypical zinc finger; testis; human; tumour; BAZ1-beta; BAZ2-alpha; dru
                                                     05-MAY-1999
                                                                      V68408;
                                                                               V68408 standard;
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28-SEP-1989; 413947.
28-SEP-1989; US-413947.
(SALK ) SALK INST BIOLOGICAL
(SALK ) SALK INST BIOLOGICAL
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T59197;
17-JUN-1997
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Neuronal alpha-bungarotoxin
ligand binding; ion channel;
Gallus sp.
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                                                                                                                                                                                                                                                                             Similarity
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                                                    (first entry)
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                                                                               cDNA to
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146. .1498
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56. .145
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                                                                               mRNA;
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Pred. No. 5.1e
0; Mismatches
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Best Local S
Matches 111
        WO9847920-A1.
29-OCT-1998.
17-APR-1998; J01783.
24-OCT-1997; JP-310027.
18-APR-1997; JP-116570.
(CHUG-) CHUGAI RES INST M
Jones
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MOLECULAR MEDICINE INC

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DR PPSDB; W81172.

PT Transcriptional regulator gene family containing bromodomain - way properly be expressed in testis tissue and is useful for treatment of cancer proliferative disorders

PT and other proliferative disorders

CC This sequence encodes the human BAZ1-beta protein, a member of a CC family of transcriptional regulator genes containing a bromodomain (BAZ, in testis tissue and also in certain tumour lines. Transgenic cells may CC be used for the preparation of the BAZ1-alpha, BAZ1-beta proteins. These proteins can be used in the treatment of cancer their binding ability to the expression products (e.g. for use as drugs sequence 5561 BP; 1665 A; 1261 C; 1471 G; 1164 T;
                                                                                          Transcriptional regulator; transcription; BAZ1-alpha; bromodomain; atypical zinc finger; testis; human; tumour; BAZ1-beta; BAZ2-alpha; BAZ2-beta; treatment; cancer; proliferative disorder; screening; ds
                                                                                                                                                                     05-MAY-1999 (first entry)
Human BAZ1-beta cDNA #2.
                                                                                                                                                                                                                   V68409 standard; cDNA
V68409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 TCCCTCACCGCCGGCGGCGGCGCGACAGTCATGGAGCGGAACGCCACGGCGCAGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-APR-1998; J01783.
24-OCT-1997; JP-310027.
18-APR-1997; JP-116570.
(CHUG-) CHUGAI RES INST
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29-OCT-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 CCAGGCGGTAGCGGGGGCAGTGGTGCTGTTGCCCCTTTTAAACTGCGGCTTGACGGGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 50.9 ses 111; Conservative
                                                                                                                                                                                                                                                                                                                                 GGCCGGCAGTCACGACTCCTCCTCAGCAGCACCGGAGG
                                                                                                                                                                                                                                                                                                                                                             GGCGGGGAGAGGTGGAGCCCGCGAGAGCTCGGCCGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                            CCCGCGCACACCGCGCGCCTCCCAGCAGCCCCCGCCGACCTCCGGCTTCGGGTCCCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCGCCTCCTGTCGGTGGAGTCGGTTATAAAGGGAGCAGCCCCCGCAGGCCGCCACATAGCT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCGCCAAGTCCTCGGTGCCCTTGCCATTTTCCAGCCGCGCTCCCACGAGGGTCACGGC
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                       346. .4941
/*tag= a
                                                                Location/Qualifiers
  /product-
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/product= "BAZ1-beta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.98;
                                                                                                                                                                                                                                to mRNA;
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"BA21-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 46.8; D
Pred. No. 0.00
0; Mismatches
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          CCCCCCSTTRAPPDONKEW
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Claim 2: Page 145-157; 187pp; Japanese.

This sequence encodes the human BAZ1-beta protein, a member of a family of transcriptional regulator genes containing a bromodomain (BAZ, Bromodomain with Atypical Zinc finger) which are expressed specifically in testis tissue and also in certain tumour lines. Transgenic cells may be used for the preparation of the BAZ1-alpha, BAZ1-beta, BAZ2-alpha and BAZ2-beta proteins. These proteins can be used in the treatment of cancer and other proliferative disorders, and in screening of compounds for their binding ability to the expression products (e.g. for use as drugs by modulation of transcriptional regulation).

Sequence 5573 BP; 1668 A; 1267 C; 1472 G; 1166 T;
vasoconstriction
Disclosure; Page 37; 120pp; English.
Disclosure; Page 37; 120pp; English.
The specification describes antisense oligonucleotides (X52869-X55271)
directed against at least 2 mRNAs selected from target genes, coding armon-coding regions of RNAs corresponding to target genes, gene initiation codons, genemic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .ches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transcriptional regulator gene family containing be expressed in testis tissue and is useful for t
                                                                                                                                                                                   Nyce JW;
WPI; 99-229400/19
                                                                                                                                                                                                                                            25-MAR-1999.
17-SEP-1998; U19419.
09-JUN-1998; US-093972.
17-SEP-1997; US-059160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human adenosine Al receptor antisense oligonucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                             colon cancer; breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                   pulmonary
                                                                                                                                                                 New antisense oligonucleotides used in treatment of, e.g.
                                                                                                                                                                                                                                                                                                                                                                       prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                          hepatocellular carcinoma; kidney cancer; melanoma;
                                                                                                                                                                                                                                                                                                                                                                                                                              chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (53491 standard; DNA; 114955 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCGGGGAGAGGTGGAGCCCGCGAGAGCTCGGCCGGGGG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCGCGCACACCGCCGCCCCCAGCAGCCCCCCCGCCGACCTCCGCTTCGGGTCCCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCCGCCAAGTCCTCGGTGCCCCTTGCCATTTTCCAGCCGCGCTCCCACGAGGGTCACGGC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCCTCACCGCCGCGCGCCGCCGCACAGTCATGGAGCGGAACGCCACGGCGCAGAGCT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCGCCTCCTGTCGGTGGAGTCGGTTATAAAGGGAGCAGCCCCGCAGGCCGCCACATAGCT 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98-583603/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypertension; pulmonary vasoconstriction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                       SS.
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                                                                                                                                                                                                                                                                                                                                                                                                           Lung
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                                                                                                                                                                                                                                                                                                                                                                                                           cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                           pancreatic cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fibrosis;
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treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 5573;
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                                                                                                                                                                                                                                                                                                                                                                                          hepatic metastasis;
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                                                                                 coding and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or more diseases, conditions or mixtures. The antisense oligonucleotides can be derived from sequences x55272-74. These multiple target coligonucleotides (specifically x55180-271) can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, concluding lung diseases, pulmonary vasoconstriction, inflammation, concluding lung diseases yndrome, pain, cystic fibrosis, pulmonary concludinary vasoconstriction, emphysema, chronic obstructive culmonary disease (COPP), and cancers such as luekemias, lumphomas, cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as well as all types of cancers which may metastasize or have metastasize to the lungs, including breast and prostate cancer.

Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                         Plasmid pZPC13
                                               Q06086 standard; cDNA; 2460
Q06086;
                           24-JAN-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGCGCCTCCTGTCGGTGGAGTCGGTTATAAAGGGAGCAGCCCCGCAGGCC--GCCACATA 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114;
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                        (first entry)
  encoding
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  neuronal nicotinic acetylcholine
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Pred. No. 0.0054;
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                                                                                                                      signal_peptide
                                                                                                                                                  Rattus rattus
                                                                                                                                                        beta 4 subunit.
Rat; nAChR; ss.
repeat_unit
                    repeat_unit
                                         repeat_unit
                                                                                                     /*tag= b
121. .1545
        /number= 1
1625. .1668
/*tag= g
/number= 2
                                                                                                                                    Location/Qualifiers
61. .1548
                                                                                                  /*tag= c
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       'number-
                                                                                          'product=nAChR beta 4 subunit
                                   .569. .1612
*tag= f
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                                                                     'label-splice site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ុ និនិនិនិនិនិនិនិនិនិនិនិនិនិ
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                               DE19619918-A1.
20-NOV-1997.
17-MAY-1996; 019918.
17-MAY-1996; DE-0199
                   DNA encoding maize starch synthase type transgenic plants
                                                                               P-PSDB; W38218
                                                                                                17-MAY-1996; DE-01998
(PLAN-) PLANTIEC BIOTECHNOLOGIE GMBH
Frohberg C, Kossmann J;
WPI; 98-000821/01.
                                                                                                                                                                                                                                                                                                                                                                                                  Zea
                                                                                                                                                                                                                                                                                                                                                                                                                        Maize starch synthase type I cDNA Maize; starch synthase type I cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T95785 standard; cDNA to mRNA; T95785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            469 AACGGCAGCATCCAGTGGCTGCCCCCTGCTATCTACAAGAGTGCCTGCAAGATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    635 TOTGGGCATTGCCAGTACCTGCCTCCAGGCATATTCAAGAGTTCCTGCTACATCG 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               409 TACAACAATÓCCGATGGCACCTATGAGGTGTCTGTCTACACCAACGTGATTGTGCGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             575 TGCGATATTGCTGATGAGCGCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTCT 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New neuronal nicotinic acetyl:choline receptor -beta 4 sub-unit and DNA sequences encoding them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; R07143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heinemann SF; Deneris ES; Duvoisin RM; Patrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SALK ) SALK INST FOR BIOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polya_signal
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                                                                                                                                                                                                                                                                                                                                                                                                  mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 sub-unit and DNA sequences n 11; F1g 3; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity 61.77; Conservative
Pages 16-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2460 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U01403.
US-321384.
US-492555.
                                                                                                                                                                                                                                                                                                                                                                                                           synthase type I; starch;
                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
2. .1951
                                                                                                                                                                                                                                                                                     /rtag= a
                                                                                                                                                                                                                                                                                                             /*tag=
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2436 .2441
/*tag= i
conflict
/*tag= j
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="conflict between genomic and cDNA sequences"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      519 A;
                                                                                                                                                                                                                                                                            starch_synthase_type_I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STUD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44.6; DB 1; Length 2460;
Pred. No. 0.0031;
0; Mismatches 44; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      767 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               replace(268. .270, gac)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
                                         I protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      587
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PT New transcription factor designated FREAC11 which regulates
PT adipose tissue expressed genes involved in lipid metabolism and
PT adipose tissue expressed genes involved in lipid metabolism and
PS Claim 1; Fig 1; 23pp; English;
CC This sequence represents the Freac11 gene of the invention. The encoded
CC This sequence represents the protein is involved in lipid metabolism
CC This sequence represents the Freac11 gene of the invention. The encoded
CC tissue expressed genes. The protein is involved in lipid metabolism
CC and/or adipocyte differentiation. FREAC11 is selectively expressed in
CC expressed genes. The DNA or protein can be used as drugs for treating
CC adipose tissue, and is used for transcriptional regulation of adipocyte
CC expressed genes. The DNA or protein can be used as drugs for treating
CC adipocyte expressed genes, e.g. FREAC11 can be used as a drug that blocks
CC antisense constructs of Freac11 can be used as a drug that blocks
CC antisense constructs of Freac11 can be used to down regulate expression;
CC the cis elements of adipose expressed genes to inhibit gene expression;
CC antisense that affect the activity of FREAC11, such as inhibitors,
CC antagonists, or agonists. Conditions which can be treated include
CC diseases, catabolic conditions, anorexia, bulimia.

SC Sequence 2106 BP; 419 A; 757 C; 602 G; 328 T;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lipid metabolism; adipocyte differentiat non-insulin dependent diabetes mellitus; catabolic condition; anorexia; bulimia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Freacll gene.
Freacll; transcription factor; adipose tissue expressed gene; obesity; incld metabolism; adipocyte differentiation; obesity related condition;
                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; Y01097
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carlsson P, Enerbaeck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAY-1997; SE-001963.
(PHAA ) PHARMACIA & UPJOHN AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-DEC-1998;
26-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes maize starch synthase type I, useful in the production of starch. Starch can be used in various conventional starch applications, e.g. starch hydrolysate products, foods, papermaking, adhesives, textiles, building materials, soil stabilisation, agrochemicals, pharmaceuticals, cosmetics, coal briquettes, ore and coal slurries, foundry casting, rubber, leather and synthetic polymers. The enzyme produces a starch stated to have deliferent physicochemical properties, especially viscosity and sequence 2383 Bp; 582 A; 546 C; 633 G; 622 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X28103 standard; DNA; 2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 GCGCCCGATGCCACCCGCGCTGCTGGCGCCCCGGCTCGTGCCCGGCCTTCCTCGCGCCCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCCGAGCCCACGGGTGAGCCGGCATTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGCCGGAGGTGAGGGGAAGATGTCCATGTC 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCGCCTGGTGGCCGGCCATGACAGCGGCTCGGGACTGGCTCCTTTTCCGCGCCCCCTCC 289
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Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .0099;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Query Match 6.0%; Best Local Similarity 49.1%; Matches 109; Conservative

Score 41.2; DB 1; Pred. No. 0.026; 0; Mismatches 113;

Length 2106;

0;

Gaps

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RESULT 13
V66832
ID V66832
AC V66832
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                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CINA encoding soluble starch synthase - used to produce transgenic plants with increased capacity for producing and storing starch producing all storing starch producing and storing starch producing and storing starch producing all storing starch producing and scape (17-20; 44pp; English.

CLAIM 5; Page 17-20; 45pp; English.

CLAIM 5; Page 17-20; 44pp; 44p
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 72
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V66832 standard; DNA; 2990 BP V66832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ZENE ) ZENECA LTD.
Keeling PL, Knight ME;
WPI; 97-319782/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-DEC-1996; G02990.
06-DEC-1995; GB-024938.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soluble starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Soluble starch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zea mays inbred line W64A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167285 standard; cDNA; 2992
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                                                                                                                                                                                                                                                                                                                                                      694
                                                                                                                                                                                          290 cecce
                                                                                                                                                                                                                                                                                                 230
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                                                                                                                                                                                                                                                                                               CCGCCTGGTGGCCGGCCATGACAGCGGCTCGGGACTGGCTCCTTTTCCGCGCCCCCTCC 289
                                                                                                                                                                                                                                                                                                                                                   GCTCCCACGAGGGTCACGGCGGGGGGGGAGAGGTGGAAGAGCTCGGCCGGGGGCC 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGGGCGGGCGGACGCACATGTGCGCCGGCCGCTCGGCCCC 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGGAGAACCAGGAGCCACAGCCGCGCGCGCTCACGGCCCCACCGC 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGGTTGAGAGCGCTCAGGGGCGACGTGGGGCCGCTCGGGTGGTCCGAGAGGGCCTCGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Conservative
                                                                                                                                                818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40.2; DB 1; Length 2992; 
Pred. No. 0.058; 
0; Mismatches 53; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSS10.52.
transgenic plant; cereal; maize;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                  813
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T35520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 72
Altering expression of genes encoding thrombopoletin, DNase I or beta-interferon - using DNA constructs useful in gene therapy to treat, e.g. cystic fibrosis and multiple sclerosis.

Claim 7; Fig 4A-D; 115pp; English.

A genomic DNA fragment (T35520) corresponds to nucleotides -6373 to -1886 upstream of the initiation codon of the human thrombopoletin (TPD) gene. It forms part of a DNA clone isolated from a human leukocyte genomic DNA library; another portion of the clone, comprising part of the 5' untranslated region and coding sequences of the TPO gene, is given in T35521. Non-coding genomic sequences, e.g. exon 1, within and upstream of the transcribed regions of the TPO gene may be used as targeting sequences in DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents an isolated nucleic acid molecule which has been isolated and comprises a nucleotide sequence encoding a polypeptide having soluble starch synthase (SSS) activity, where the polypeptide is encoded by a maize gene. The isolated nucleic acid molecule can be used to produce transgenic plants with altered starch production. The transgenic plants produced using the nucleic acid molecule have an enhanced ability to produce structurally-altered starch. Sequence 2990 Bp; 758 A; 655 C; 801 G; 776 T;
                                                                                                                                                                                                                   WPI; 96-443186/44.
                                                                                                                                                                                                                                    Hauge BM,
                                                                                                                                                                                                                                                    26-SEP-1996. U03377.
12-MAR-1996; U03377.
17-MAR-1995; US-406030.
(TRAN-) TRANSKARYOTIC T
                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                          14-JAN-1997 (first entry)
Human thrombopoietin gene 5' flanking sequence.
Gene targeting; gene activation; homologous recombination;
thrombopoietin; thrombocytopenia; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acid molecule, used to produce transgenic plants comprises nucleotide sequence encoding polypeptide having soluble starch synthase activity, where polypeptide is encoded by maize goliaim 1; Column 25-28; 29pp; English.
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29-NOV-1994;
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Zea mays soluble starch synthase gene SSS1052 and SSS64.

Zea mays; US yellow-dent corn line; maize; soluble starch synthase; SSS; glycogen biosynthetic pathway; branching enzyme; ss.

Zea mays.

Zea mays.
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15-DEC-1995;
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Best Local Similarity
nucleic acid substitution, deletion, insertion or inversion or a combination of these. The preferred substitutions are a combination of substitutions are a combination of substitutions selected from those where the nucleic acid is modified so that the codon encoding His at position 37 is replaced on the encoding Ary, the codon encoding Glu at position 355 is changed to one encoding Asp, and the codon encoding Val at position 375 is changed to a codon encoding Ala. A mutation in the control elements of the ORF localised in an intergenic sequence may also result in a failure of expression of the polypeptide.
                                                                                                                                                      reading frame, used partic. In vaccines for immunising pigs.
Claim 1; Page 23-24; 33pp; English.
A pseudorables virus with a mutation in this open reading frame can be used in the production of vaccines for combatting infectious diseases in pigs. The pseudorables virus mutant produced fails to produce the antigenic or functional polypeptide described in R51272 and expresses a polypeptide with altered antigenic or functional properties or one that is non-funtional. The mutation is either a
                                                                                                                                                                                                                                                                               New pseudo:rables virus mutants - having a mutation in an opreading frame, used partic. in vaccines for immunising plgs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Open reading frame of pseudorables virus. Pseudorables virus; antigen; polypeptide; vaccine; pig; swine; disease; mutant; mutation; ds.
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06-OCT-1992; EP-2030
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SUMMARIES

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## ALIGNMENTS

RESULT

NID		DEFINITION		W52861
#32861 g1350351	IMAGE:321242 5' similar to gb:x70297 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-7 CHAIN (HUMAN);, mRNA sequence.	zc03e02.rl Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone	W52861 560 bp mRNA EST 10-OCT-1996	

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TITLE
JOURNAL
COMMENT
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
11 (bases 1 to 560)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           T-3'], double-stranded cDNA was size selected, ligated to ECO RI adapters (Pharmacia), digested with Not I and cloned into the Not I and ECO RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a COt = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: parathyroid gland; Vector: pT7T3D
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Soares_parathyroid_tumor_NbHPA"
/tissue_type="parathyroid tumor"
/dev_stage="adult"
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/clone="IMAGE:321242"
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/db_xref="GDB:1258900"
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Pred. No. 5.1e-29;
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                                         541 TGAGCGCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTCTTCTGGGCATTGCCA 600
                                                                                                                                                                                  482 TTTCAGTTCCAATTGCTAATCCA-GCATTTGTGGATAGCTGCAAACTGCGATATTGCTGA 540
                                                                                                                                         153 TTCTAGTTCCAATTGCTAATCCACGCATTTNINGATAGCTGCAAACTGCGATATTGCTGA 212
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1 (bases 1 to 409)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W03952 409 bp mRNA EST 19-APR-1996 Za62c08:11 Soares fetal liver spleen 1NFLS Homo sapiens CDNA IMAGE:297134 5' similar to 9b:X70297 NEURONAL ACETYLCHCLINE RECEPTOR PROTEIN, ALPHA-7 CHAIN (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The WashU-Merck EST Project Unpublished (1995)
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Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMAGE Consortium (info@image.linl.gov)
Seq primer: mob.REGA+ET
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/clone="IMAGE:297134"
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Location/Qualifiers
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Pred. No. 1.1e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1996)
On Apr 14, 1993 this sequence version replaced
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Eutheria; Primates;
1 (bases 1 to 170)
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K4329F Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 4169785650
Email: liewcc@ut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Liew CC
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primer: GAAATTAACCCTCACTAAAGGG.
                                                          standard;
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1 47 c 46 g 34 t
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/db_xref="taxon:9606"
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Pred. No. 1.7e-17;
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DKFZp586B2218)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Please contact the RZPD: Ressourcenzentrum, Heubnerweg
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available at the RZPD in Berlin
Plasse contact the RZPD: Ressourcenzentrum, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No s1 sequence available
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12-MAR-1999
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                                                                                                                                                                                                                                               79 GCGGGGAGAGGTGGAGCCGCGAGAGCTCGGCC---GGGGGCCCCGCCTGGTGGCCGCGGC 135
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                                                                                                 CCTCTATCTTCCAGGAGAACCAGGAGCCA 265
                                                                                                                                 CCGCCGGAGATGAGGGGAAGATGTCCGTGTCAGGGCTCAAGGCCGAGCTGAAGTTCCTGG
                                                                                                                                                       CCGCCGGAGGTGAGGGGAAGATGTCCATGTCAGGGTTCAAGGCCAAACCGAAGTTACTGG
                                                                                                                                                                               CGTGACGGCGGCTCCGGGCTCCCCTTCCGCGCCCGCCTCCCCTTCCGCGCCCCCTC
                                                                                                                                                                                                   GCTCGACGAGCCGCGAGAGCCGCCCAGGCCGAGCCCCCCGCGGCTCGCCGC
                                                                                      CGTCCATCTTCGACAAGAACCACGAGCGA
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3', mRNA
AA861176
                  AA861176 487 bp mRNA ak36d09.s1 Soares_testis_NHT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence
         sequence
                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/clone="DKRZp586B2218"
/clone_lib="586 (synonym: hutel).
/clone_sites NotI + Sall/MluI"
/dev_stage="adult"
/tissue_type="uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                              118 A; 154 C; 150 G;
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Last updated,
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8a D-82152 Martinsried, GERMANY
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Pred. No. 8.2e-14;
0; Mismatches 33;
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Genome Project
                     Homo
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                                                                                                                                                                                                                                                                                                                              88 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vertebrata; Mammalia; Eutheria;
                     sapiens
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                   ST 04-JAN-1999
CDNA clone IMAGE:1408049
                                                                                                                                                                                                                                                                                                                                                                                     Vector pSport1; host
                                                                                                                                                                                                                                                                                            Length 510;
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                                                                                                                                  182
                                                                                                                                                       236
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KEYWORDS SOURCE

AA861176.1 EST. human.

GI:2953316

VERSION

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JOURNAL COMMENT
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AUTHORS
TITLE
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AA333244
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                                                                                                                                                                                                                                                                                     427
                                                                                                                                                                                                                                                                                                                                                       487
                                                                                                                                                                                                                                                                                                                                                                        457 GCAAAAATATTGCATCTACCAGCATTTTCAGTTCCAATTGCTAATCCAGCATTTGTGGAT 516
                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                       GCAAAAATATTGCATCTACCAGCATTTTCAGTTCCAATTGCTAATCCAGCATTTGTGGAT 428
                                                                                                                                                     AA333244 335 bp mRNA EST EST37317 Embryo, 8 week I Homo sapiens cDNA similar to interleukin-2 receptor, alpha cha
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                         protein,
AA333244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLML at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert Length: 758 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 458.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
On Jan 9, 1998 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index
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                                                                                      AA333244.1 GI:1985508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 œ
                                                                                                                                      mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: P77T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cD was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the No and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "95 c 102 g 159 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1408049"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                                                                                                                                                                                                        11.9%; 98.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 76.4; DB 39;
Pred. No. 8.7e-10;
0; Mismatches 1;
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ain, kappa B binding
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Best Local
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77; Conserv
            fruit fly.
Drosophila melanogaster
                                                                                                     melanogaster
AI292581
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Fax: 3018699423
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175 TCCCGCCGGAGGTGAGGGGAAGATGTCCATGTCAGGGTTCAAGGCCCAAACCGAAGTTACT 234
                                                                                                                                                                                                                                                                                                                 235 GGCCTCTATCTTCCAGGAGAACCAGGAGCCA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RS Adams, M.D., Kellavage, A.R., Fleischmann, R.D., Fuldner, R:A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Mai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, I.M., Fitzhugh, W.M., Fritchnan, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Pillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
                                                                                                                                                                                                                                             GGCGTCCATCTTCGACAAGAACCACGAGCGA 91
AI292581 607 bp mRNA ESGH15518.5prime GH Drosophila melanogaster melanogaster cDNA clone GH15518 5prime, mF
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on May 18, 1995 this sequence version replaced gi:811121.
Other_ESTs: THC185696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="ATCC (inhost):134920"
/db_xref="taxon:9606"
/clone_lib="Embryo, 8 week I"
/dev_stage="embryo, 8 wks"
/note="Organ: Embryo, 8 weeks; Vector: pBluescript SK-;
Site_1: ECORI; Site_2: xhoI"
site_1: ECORI; Site_2: 69 t
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Pred. No. 7.5e~08;
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       mRNA sequence
                            head pOT2 Drosophila
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1 (bases 1 to 607)

DRS Harvey,D., Hong,L., Evans-Holm,M., Pendleton,J., Su,C., Brokstein,P., Lewis,S. and Rubin,G.M.

BDGP/HHMI Drosophila EST Project

Unpublished (1997)
On Jun 18, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        587 TCTGGGCATTGCCAGTACCTGCCTCCAGGCATATTCAAGAGTTCCTGCTACATCG 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       398 TACAACAGCGCGGATGAGGGATTCGATGGCACGTATCACACCAGCGTTGTGGTCAAACAT 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCGGCAGTTGTCTGTACGTGCCCCCCTGGTATCTTCAAGAGCACATGCAAGATGG 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCGATATTGCTGATGAGCGCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTCT 586
                                                                                                  Tumor Gene Index
Unpublished (1997)
On Jun 5, 1998 this sequence version
                                                                                                                                                                                                                                                                                                                                                              AI655990 501 bp
tt42c03.x1 NCI_CGAP_GC6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: http://www.fruitfly.org/EST,
hit genomic sequence AC005890
Plate: 155 row: B column: 6
High quality sequence stop: 465.
                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 501) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGA
                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            University of California Berkeley 539 LSA, Berkeley, CA 94720-3200, USA
                                                                                                                                                                                                                                                                                                                                                                                  AI655990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Harvey, D.
                                                                  Contact: Robert Strausberg,
                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                               A1655990.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
mail: Robert_Strausberg@nih.gov
'issue Procurement: Christopher A.
'. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M. Rubin-Molecular and Cell Biology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                    (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="DH5 - alpha"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2. Plasmid cDNA library."
pOT2 151 c 162 g 137 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="GH Drosophila melanogaster head pOT2'
/sex="male and female"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                mRNA
Homo
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                                                                    Ph.D.
                                                                                                                                                                                                                                                                                                                                                                sapiens
                 Moskaluk,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            est@fruitfly.berkeley.edu
                                                                                                                                                                                                                                                                                                                                                                  CDNA
                                                                                                      replaced gi:3188057
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clone IMAGE:2243428
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Best Local S
Matches 52
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499 ATAATGAAACAGCCACCAGTTAAATTTGATGCAAAAATATTGCATCTACCAACATATTCA
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                                                                                                                                                                                                                   1 (bases 1 to 274)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. washU-Merck EST Project 1997
Unpublished (1997)
                                           4444 Forest Park Parkway,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                      Washington University
                                                                                                                                                   Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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zx49h09.sl Soares_testis_NHT
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Location/Qualifiers
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-GGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                    Sep 12, 1996
est@watson.wustl.edu
lone is available roya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:2243428"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
ob_xref="taxon:9606"
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                                                                                                                                                                                              this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Mammalia; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 46; DB 49;
Pred. No. 0.051;
0; Mismatches 10
                                                                                                                      School
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ox 8501, St. L
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AA844642/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3', mRNA sequence
AA844642
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On Jan 17, 1998 th
                                                                                                                                                                                                                                                                                                                                                                                                                   Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 436)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                 Insert Length: 497 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 415.
                                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ĀA844642.1 GI:2931093
                                                                                                                                      DNA Sequencing by: Washington University Genome Clone distribution: NCI-GAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                            Email: Robert_Strausberg@nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
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Seg primer: -41m13 fwd. ET from Amersham.
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                                                                                                                                                                                                        Library Arrayed by: Greg Lennon, Ph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker: Site_1: Not I; Site_2: ECO RI; 1st strand cD
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                 Location/Qualifiers
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/db_xref="GDB:6038961"
/db_xref="taxon:9606"
/clone="IMAGE:795617"
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 0.17;
0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                replaced gi:1900948.
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                                                                                                                                                                       Sequencing Center information can be
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                                                                                                                                                                                                                                              M. Fatima
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AI367541/c
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l Similarity 92.0%;
46; Conservative
                                                                                                                                                                                                                                             Seq F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor Gene Index Unpublished (1997)
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AI367541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                           Insert Length: 1828
                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome S Clone distribution: NCI-CGAP clone distribution i found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                    primer: -40UP from Gibco
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                                                                                                                                                                                                                   quality sequence stop: 370.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Double-Stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. "96 c 103 g 122 t
                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IndgE:1989142"
/clone_1lb="NCI_CGAP_Ut2"
/tissue_type="moderately-differentiated endometrial adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand was prepared from mRNA obtained from Clontech
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'note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
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                        526 CTGCGATATTGCTGATGAGCGCCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTC 585
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CTTCAATAATGCCGATGGCAACTACGAGGTGCGCTACAAGTCCAACGTGCTGATTTATCC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 494)
Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C.,
Brokstein, P., Lewis, S. and Rubin, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster head BlueScript Drosophila melanogaster cDNA clone HL02253 5prime similar to M20316: D.melanogaster acetylcholine receptor-related protein mRNA, complete cds, mRNA sequence.

AA697326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Harvey, D.
G. M. Rubin Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BDGP/HHMI Drosophila EST Project
Unpublished (1997)
On Nov 20, 1997 this sequence version replaced gi:1172316.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu plate: 22 row: E column: 5
High quality sequence stop: 416.
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Average insert size 1.85 kb. Life Technologies catalog
11539-012"
a 86 c 97 g 115 t
                                                                                                                                                                                                                               /note-"Organ: head--brain & sensory organ; Vector: BlueScript SK; Site_I: EcoRI; Site_Z: XhOI; Constructed using Stratagene ZAP-cDNA Synthesis kit. Oligo dT-primed and directionally cloned at EcoRI and XhoI in BlueScript
                                                                                                                                                                                                                                                                                                             /clone_lib="HL Drosophila melanogaster head BlueScript"
/sex="male and female"
/dev_stage="adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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46
                                          26 GTCCTCGGTGCCCCTTGCCATTTTCCAGCCGCGCTCCCACGAGGGTCACGGCGGGGGGA
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GGCCGCGCTGCCCCGGTTCGCGCCCCTGCTCGGCGCTCTCTTGAGGCGCCGCGTCCGGGG 105
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On May 18, 1998 this sequence version replaced gi:3136536.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: "+vvr __.... 65. High quality sequence stop: 65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
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AI492967.1 GI:4393970
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                                                                                                       Similarity
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                                                                                                                                                                                                                                     /note-"Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI CGAP Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 132376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:2030018"
/clone_lib="NCI_CGAP_Kid11"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCGCGACCGGAGCCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Travaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         www.uryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 354)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 zh60e03.rl Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA clone IMAGE:416476 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 584 Std Error: 0.00 Seq primer: mob.REGA+ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On Apr 14, 1993 this sequence version replaced gi:315330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                         quality sequence stop: 217.
Location/Qualifiers
                   8
         D
                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="GDB:1324946"
                                                                                                                                                                                                                                                                               /clone_lib="Soares_fetal_liver_spleen_1NFLS
/sex="male"
                                                                                                                                                                                                                                                                                                                   clone="IMAGE:416476"
                                                                                                                                                                                                                                                                                                                                    db_xref="taxon:9606"
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REFERENCE
AUTHORS
BASE COUNT
ORIGIN
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Best Local S
Matches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                           source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                      Email: Robert_Strausberg@nih.gov
This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 862 Std Error: 0.00
Seq primer: -40Up from Gibco
Seq primer: -40Up from Gibco
High quality sequence stop: 118.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 557)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
AI192683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Al192683 557 bp mRNA EST 29-OCT-1998 qe62d07.x1 Soares_fetal_lung_NbHL19W Homo Sapiens CDNA clone IMAGE:1743565 3' similar to SW:CDNC_HUMAN P49918 CYCLIN-DEPENDENT KINASE INHIBITOR 1C ;contains MER22.b3 TAR1 repetitive element ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On Jan 14, 1998 this sequence version replaced gi:1797633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                  62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
           /clone_lib="Soares_fetal_lung_NbHL19w"
/dev_stage="19 weeks"
                                                                                                                                                                                                                                                                                                      /clone-"IMAGE:1743565"
                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                              'lab_host="DH10B (ampicillin resistant)"
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Pred. No. 2
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2.5;
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Query Match Best Local Matches

104;

Conservative

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Score 39; DB 43; Pred. No. 3.2; 0; Mismatches 90

90;

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Gaps

Length 557; Indels

Similarity

6.1%; 53.3%;

Search completed: September 17, 1999, 21:28:34 Job time: 14298 sec

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Mutant EPM1 gene Chimeric rhPDGF-B

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Best Local Similarity

Matches 111; Conserv
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07-JUN-1995; US-484722.
07-JUN-1995; US-484722.
(SIBI-) SIBIA NEUROSCIENC
Elliott KJ, Harpold MM;
WPI, 97-065463/06.
P-PSDB; W09025.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding nicotinic acetylcholine receptor sub-units used in screening to determine the effect of drugs on the receptor pisclosure; Page 71-73; 108pp; English.

A DNA sequence (T48239) codes for the alpha-7 subunit (W09025) of the human neuronal nicotinic acetylcholine receptor (nAChR). Host cells, esp. mammalian cells or amphibian occytes, carrying alpha-7 nucleic acids, opt. in combination with other alpha and/or beta subunit nucleic acids (see also T48232-38, T48240-41), express recombinant nAChR subunits useful for identifying cpds. that modulate the activity of human nAChRs.

Sequence 1876 BP; 369 A; 553 C; 531 G; 423 T;
W09420617-A2.
15-SEP-1994.
08-MAR-1994; U02447.
08-MAR-1993; US-028031.
(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC (SIBI-) SIBIA NEUROSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                    14-MAY-1998 (first entry)
Human neuronal nicotinic acetylcholine receptor alpha-7 subunit cDNA.
Human, neuronal nicotinic acetylcholine receptor; alpha-7 subunit;
brain tissue; screening; NAChR; antibody; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V12197 standard; cDNA; 1876
V12197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-APR-1997
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T48239;
                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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Neuronal nicotinic acetylcholine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             414 CTATAACAGTGCTGATGAGCGCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTC
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                                                                                                                                                                                                                                                                 Location/Qualifiers 73. .1581
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                                                                                                                                                                                                           /product=
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                                                                                                                                                                   "neuronal nicotinic acetylcholine receptor
alpha-7 subunit"
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Pred. No. 9.1e-23;
0; Mismatches 5
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Result

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Match

Length

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Query

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Neuronal nicotinic
Neuronal nicotinic
Neuronal nicotinic
Neuronal nicotinic
Neuronal nicotinic
Alpha4 subunit of
Alpha4 subunit of
Alpha4 subunit of
CDNA sequence of f
hnRNP U protein co
Human cyclin-depen
Human cardiac hype
Human cardiac hype
Human cardiatrophi
Tylactone synthase
BamHI J-I fragment
BamHI J-I fragment
Pertactin antigen

Q14319 Q34566 Q73500 T12908 T78203

Signal portion of Streptomyces fradi Human cystatin B g Human mutant EPMI

Physiologically ac Actinomadura hibis prn gene.

DNA enco

DNA encoding Pseud

344.44.4 344.44.4 344.44.4 44.44.4

16 17 18

X06987 V12196 V70195 N70195 Q44491 T35520

> DNA encoding cytop Human neuronal nic Mouse neuregulin r Human neuronal nic

Streptomyces prote Thermus aquaticus

Freacil gene. New Soluble starch syn Zea mays soluble s Neuronal nicotinic

Maize starch synth

Neuronal alpha-bun Neuronal alpha-bun Plasmid pZPC13 enc Human adenosine Al

Neuronal nicotinic Human neuronal nic V274T variant huma

Description

Human BAZ1-beta cD Human BAZ1-beta cD

774. 44.661.6 42.43.6 401.2 400.2 35.40.2 Title:
Perfect score:
Sequence:
Scoring table:

IDENTITY\_NUC

US-08-956-518A-103

CAGGCCGCCACATAGCTCCC.....CAAGAGTTCCTGCTACATCG 641

arched:

N\_Geneseq\_36:\*

311585 seqs, 125096042 residues

Pred. No. is the number of results predicted by chance to hav score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.

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SUMMARIES

Run

on:

OM nucleic -

nucleic search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

September 18, 1999, 00:35:12;

2 ; Search time 425.19 Seconds
(without alignments)
377.180 Million cell updates/sec

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC The present sequence encodes a human neuronal nicotinic acetylcholine CC receptor (NAChR) subunit. The cells expressing the alpha and/or beta CC NAChR subunits may be used in a method of screening compounds to CC identify any which modulate the activity of human neuronal NAChR. CC Subunit specific antibodies may be used to monitor the distribution and expression density of various subunits in normal vs diseased brain CC tissues. Testing of single receptor subunits or specific receptor CC provides informations with a variety of potential agonists or antagonists or combinations with a variety of potential agonists or antagonists of individual subunits and should lead to the identification and design of compounds that are capable of very specific interaction with one or unwanted side effects than drugs identified e.g. screening with cells that express a variety of subtypes.

Sequence 1876 BP; 369 A; 553 C; 530 G; 423 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
Claim 14; Fig 2; 44pp; English.
Claim 14; Fig 2; 44pp; English.
This sequence encodes the V247T variant of human alpha7 nicotinic acetylcholine receptor (nAChR) subunit of the invention. Cells containing the DNA are used to express the protein and to identify modulators of alpha7 nAChR activity or cytoprotective agents, e.g. antisense compounds or antagonists that are potentially useful for treating neurodegeneration, enzyme dysfunction, affective disorders and immune dysfunction, such as cancer, post-herpetic neuralgia, diabetic dysfunction, such as cancer, post-herpetic neuralgia, diabetic
                                                                                                                                                                                                                                               P-PSDB; W69216.

Nucleic acid encoding variant of human alpha7 nicotinic nodulators to identify modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-OCT-1998 (first entry)
V274T variant human alpha7 nAChR coding sequence.
Alpha7 nAChR; alpha7 nicotinic acetylcholine receptor subunit; cancer; neurodegeneration; enzyme dysfunction; affective disorder; therapy;
                                                                                                                                                                                                                                                                                                                                (ABBO ) ABBOTT LAB.
Briggs CA, Gopalakrishnan M,
Roch J, Sullivan JP, Touma E;
WPI; 98-377593/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activity of the receptor
Claim 8; Page 78-79; 99p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human neuronal nicotinic acetylcholine receptor subunits and DNA also transformed cells useful for screening cpds. which modulate
                                                                                                                                                                                                                      the receptor, potentially useful for treating neuro-degeneration, cancer, affective disorders etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           schizophrenia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Elliott KJ, Ellis WPI; 94-303024/37. P-PSDB; W44153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V44687 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              586 TTCTGGGCATTGCCAGTACCTGCCTCCAGGCATATTCAAGAGTTCCTGCTACATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mmune dysfunction; diabetic neuropathy; Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTATAACAGTGCTGATGAGCGCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTC 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCTGGGCATTGCCAGTACCTGCCTCCAGGCATATTCAAGAGTTCCTGCTACATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    U23405.
US-771737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
9. .1517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.8%;
95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harpold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                           McKenna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 108; DB 1;
Pred. No. 9.1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                         Monteggia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                    containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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Query Match Best Local Matches 9

Similarity

11.6%;

Score 74.4; DB 1; Pred. No. 1.4e-12;

Conservative

0

Mismatches

0

Gaps

0

526 CTGCGATATTGCTGATGAGCGCCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTC 585

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
subunit (W12368) and alpha2 subunit (W12369) of chick neuronal
calpha-bungarotoxin binding protein (ABBP). They were isolated from
an 18-day embryo chick brain cDNA library using a probe (see also
can 18-day embryo chick brain cDNA library using a probe (see also
can 18-day embryo chick brain amino acid sequence of chicken
brain ABBP. The probe isolated partial clone pCh29-1, which
encoded the N-terminal portion of alpha1. A subclone, pCh29-3
can (ATCC 40641), was used to rescreen the library yielding clone
pCh31-1 (ATCC 40640), which encoded the entire alpha2 sequence.
A probe based on the C-terminal region of pCh31-1 was used obtain
calpha1. The cDNA clones can be used as probes to identify further
ABBP subunits, and in the recombinant prodn. of ABBP.
Sequence 2769 BP; 790 A; 604 C; 571 G; 804 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            psychosis and schizophrenia. Probes based on the DNA are used to detect the DNA in usual hybridisation or amplification tests, while monoclonal antibodies are used to detect the protein for diagnosis (in vitro or by in situ immuno-fluorescent assay). Compared with wild-type alpha7 nAChR, the protein has about 100-fold greater sensitivity to cholinergic receptor agonists (nicotine or acetylcholine) and response to these agonists decays more slowly, but the wild-type inward rectification is
                                                                                                                                                                                                         binding, ion channel or other activities of the protein.
Claim 1; Fig 2A-B; 18pp; English.
2 cDNA clones (T59196 and T59197) respectively code for the alphal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T59196;
                                                                                                                                                                                                                                          New isolated neuronal alpha-bungarotoxin-binding protein DNA to screen cholinergic agents and other drugs which may affect binding, ion channel or other activities of the protein.
                                                                                                                                                                                                                                                                                                         WPI; 97-118297/11.
                                                                                                                                                                                                                                                                                                                                  04-FEB-1997.
28-SEP-1989; 413947.
28-SEP-1989; US-413947.
(SALK ) SALK INST BIOLOGICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neuronal alpha-bungarotoxin
                                                                                                                                                                                                                                                                                           P-PSDB; W12368
                                                                                                                                                                                                                                                                                                                                                                                                                                   mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               retained
                                                                                                                                                                                                                                                                                                                        Lindstrom JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     igand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       586 TTCTGGGCATTGCCAGTACCTGCCTCCAGGCATATTCAAGAGTTCCTGCTACATCG 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCTGGGCATTGCCAGTACCTGCCTCCAGGCATATTCAAGAGTTCCTGCTACATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1590 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                        Schoepfer
                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
71. .136
/*tag= b
137. .1510
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ion channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.8%;
95.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                322 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            binding binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 8.4e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ss.
                                                                                                                                                                                                                                                                                                                                         STUDIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  471 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein alphal subunit cDNA. protein alpha 1; cholinergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                449. G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  348
                                                                                                                                                                                                                                                          affect ligand
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RESULT
T59197
ID T1
AC T
DT 1
DE N
KW N
KW N
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       E B B B B B B
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                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                    S Claim 1; Fig 3A-B; 18pp; English.

2 cDNA clones (T59196 and T59197) respectively code for the alphal cubunit (W12368) and alpha2 subunit (W12369) of chick neuronal cubunit (W12368) and alpha2 subunit (W12369) of chick neuronal class of chick neuronal class of chick protein (ABBP). They were isolated from 18 day embryo chick brain cDNA library using a probe (see also T59198) based on the N-terminal amino acid sequence of chicken coded the N-terminal amino acid sequence pCh29-1, which class of chicken of alpha1. As subclone, pCh29-3 class of the N-terminal portion of alpha1. As subclone, pCh29-3 class of the N-terminal portion of alpha1. As subclone, pCh29-3 class of the N-terminal portion of alpha1. As subclone, pCh29-3 clone pCh31-1 (ATCC 40640), which encoded the entire alpha2 sequence. A probe based on the C-terminal region of pCh31-1 was used obtain clone pCh34-1 (ATCC 40639), encoding the C-terminal portion of alpha1. The cDNA clones can be used as probes to identify further abpha clones condition of ABBP subunits, and in the recombinant prodn. of ABBP.

Sequence 2101 BP; 582 A; 406 C; 454 G; 659 T;
                                                                                                                                                                                                                                                                                                                                       Best Local
Matches
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
24-JAN-1991 (first entry)
Plasmid pZPC13 encoding neuronal nicotinic acetylcholine receptor beta 4 subunit.
Rat; nAChR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T59197 standard, cDNA, 210
T59197,
17-JUN-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neuronal alpha-bungarotoxin
Neuronal alpha-bungarotoxin
ligand binding; ion channel
                                                                         Q06086 standard;
Q06086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated neuronal alpha-bungarotoxin-binding protein DNA - used to screen cholinergic agents and other drugs which may affect ligand binding, ion channel or other activities of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; W12369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lindstrom JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          signal_peptide
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                                                                                                                                                                                                                                                                                                  526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              472
                                                                                                                                                                                     481 CTCTGGATCCTGTCAATATATTCCTCCAGGCATTTTGAAGAGCACATGTTACATTG
                                                                                                                                                                                                                     586 TTCTGGGCATTGCCAGTACCTGCCTCCAGGCATATTCAAGAGTTCCTGCTACATCG 641
                                                                                                                                                                                                                                                            421 CTATAACAGTGCGGATGAAAGATTCGATGCAACATTTCACACAAATGTGCTGGTGAATTA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     412
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                                                                                                                                                                                                                                                                               CTGCGATATTGCTGATGAGCGCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTC 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCTGGGCATTGCCAGTACCTGCCTCCAGGCATATTCAAGAGTTCCTGCTACATCG 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCGGGACACTGCCAATATCTGCCACCAGGCATATTTAAAAGCTCATGCTACATAG 527
                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INST BIOLOGICAL Schoepfer RD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= b
146. .1498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
56. .145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ion channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 56. .1501
                                                                                        CDNA; 2460
                                                                                                                                                                                                                                                                                                                                                        9.68;
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                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  binding protein alpha2 subunit cDNA. binding protein alpha 2; cholinergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΒP
                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                                                                                   Score 61.6; DB 1; Length 2101;
Pred. No. 8.3e-09;
D; Mismatches 34; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STUDIES
                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                     536
                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                           New neuronal nicotinic acetyl:choline receptor - compsns. contg.

The sequence and sequences encoding them.

Claim I; Fig 3; 47pp; English.

The sequence encodes a novel neuronal nicotinic acetylcholine
receptor subunit, beta 4. Plasmid pzPC13 (ATCC 67893) was
isolated from a cDNA library in lambda ZAP II prepd. from rat
isolated from a cDNA library in lambda ZAP II prepd. from rat
the sequence of the cDNA in the region encoded by the 5th
exon is identical to that determined for the genomic clone with.
the exception of a sustn. at posn. 720 of a t for a c (this does
not alter the AA sequence); this may be due to a polymorphism
between the rat strains used for the genomic library and the cDNA
library, or could have resulted from a reverse transcriptase error
during prepn. of the cDNA. A sequence, the core of which is 44 bp
long is repeated three times at the beginning of the 3' UT region.
The function of this remains unknown. The protein subunit can
combine with the known subunits, alpha-2,-3, and -4, and beta-2
to form previously unknown functional receptors. The new subunit
is expressed in the central and peripheral nervous systems and in
Secuence 2460 RB. 510 A. 767 C. 587 T.
                                                                                                              Query Match
Best Local S
Matches 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-MAR-1990; U01403.
14-MAR-1989; US-321384.
12-MAR-1990; US-492555.
(SALK) SALK INST FOR BIOL STUD.
Heinemann SF; Deneris ES; Duvoisin RM; Patrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_unit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mat_peptide
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Key
                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polya_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_unit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-SEP-1990.
14-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9010648-A
                          587 TCTGGGCATTGCCAGTACCTGCCTCCAGGCATATTCAAGAGTTCCTGCTACATCG 641
                                                        409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PI; 90-304987/40.
-PSDB; R07143.
 AACGGCAGCATCCAGTGGCTGCCCCCTGCTATCTACAAGAGTGCCTGCAAGATTG
                                                     TGCGATATTGCTGATGAGCGCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTCT 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rattus
                                                                                                                           Similarity
                                                                                                                                                                                     2460 BP;
                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conflict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2436. .2441
/*tag= 1
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/*tag= g
/number= 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product-nAChR beta
416. .417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note-"conflict between genomic and cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              number-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   number=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            label-splice
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                                                                                                                           7.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .1545
                                                                                                                                                                                    519 A;
                                                                                                              Score 44.6; DB 1;
Pred. No. 0.0012;
0; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         site
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                                                                                                                                                                                    767 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 subunit
                                                                                                                                                                                    587 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ä
                                                                                                                                         Length 2460;
                                                                                                                                                                                    587 T;
                                                                                                              0;
523
                                                                                                              Gaps
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CC The specification describes antisense oligonucleotides (X52869-X55271) CC directed against at least 2 mRNAs selected from target genes, coding and CC non-coding regions of RNAs corresponding to target genes, gene CC initiation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding CC regions and all segments of RNAs encoding proteins associated with one CC may be derived from sequences X55272-74. These multiple target CC may be derived from sequences X55272-74. These multiple target CC are those associated with impaired respiration and inflammation, CC are those associated with impaired respiration and inflammation, CC allergic rhinitis, acute asthma, allergies, asthma, impeded respiration, pulmonary vasoconstriction, emphysema, chronic obstructive CC hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive cancer, hepatoccellular carcinoma, kidney cancer, breast cancer, pancreatic cancer, hepatoccellular carcinoma, kidney cancer, may metastasize or have metastasized to the lungs, including breast and prostate cancer. 21328 T; Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X X S 3 4 9 1 1 1 1 2 3 4 9 1 1 1 2 3 4 9 1 1 2 3 4 2 1 2 3 4 2 1 2 3 4 2 1 2 3 4 2 1 2 3 4 2 1 2 3 4 2 1 2 3 4 2 1 2 3 4 2 1 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 2 3 4 
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Best Local
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T95785 standard; cDNA to mRNA;
T95785;
22-MAY-1998 (first entry)
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17-SEP-1997;
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WPI; 99-229400/19
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-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCACATAGCTCCCGGCCAAGTCCTCGGTGCCCCTTGCCATTTTCCAGCCGCGCGCTCCCACG
                                                                                                                                                                                                                                                                             GGCCGCGGCCATGACAGCGGCTCGGGACTGGCTCCTTTTCCGCGCCCCCTCCCGCCGG 183
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73; Conser
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US-059160.
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41.2%;
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Pred. No. 0.02
L5; Mismatches
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New transcription factor designated FREACI1 - which regulates adipose tissue expressed genes involved in lipid metabolism and adipocyte differentiation, used to, e.g. inhibit gene expression Claim 1; Fig 1; 23pp; English.

This sequence represents the Freacil gene of the invention. The encoded protein has transcription regulative function directed against adipose tissue expressed genes. The protein is involved in lipid metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conventional starch applications, e.g. starch hydrolysate productions, papermaking, adhesives, textiles, building materials, so stabilisation, agrochemicals, pharmaceuticals, cosmetics, coal briquettes, ore and coal slurries, foundry casting, rubber, lea and synthetic polymers. The enzyme produces a starch stated to different physicochemical properties, especially viscosity and gelling properties, from wild type starch.

Sequence 2383 BP; 582 A; 546 C; 633 G; 622 T;
                                                                                                                                                                                                                                                             Freacll; transcription factor; adipose tissue expressed gene; obesity; lipid metabolism; adipocyte differentiation; obesity-related condition; non-insulin dependent diabetes mellitus; cardiovascular disease; catabolic condition; anorexia; bulimia; therapy; ss.
                                                                                                                      P-PSDB; Y01097
                                                                                                                                        (PHAA ) PHARMACIA & UPJOHN Carlsson P, Enerbaeck S; WPI; 99-070211/06
                                                                                                                                                                                26-MAY-1998; SE0989.
26-MAY-1997; SE-001963.
                                                                                                                                                                                                                                                                                                                            Freacl1 gene.
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Frohberg C, Kossmann
WPI; 98-000821/01.
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                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                             X28103 standard; DNA; 2106
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20-NOV-1997.
17-MAY-1996; 019918.
17-MAY-1996; DE-019918.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 GGCCGAGCCCACGGGTGAGCCGGCATTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 CGCCGGAGGTGAGGGGAAGATGTCCATGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 GCTCCCACGAGGGTCACGGCGGGGGGAGAGGTGGAGCCGCGAGAGCTCGGCCGGGGGCC 117
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Pred. No. 0.0039;
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RESULT
T67285
T67285
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DT 11
DE S0
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                                                                                        PT CDNA encoding soluble starch synthase - used to produce transgenic properties with increased capacity for producing and storing starch producing soluble starch producing starch synthase (SSS). They were isolated from a maize CC cDNA clones SSS10.52, SSS6.31 and SSS56 (T67285-87) code for maize CC inbred line W64A library by screening with a probe (T67288) based CC on pea SSS, rice SSS and maize GBSS. The cDNAs can be used to CC produce plants with an increased capacity for producing starch, or CC a capacity to produce starch with an altered fine structure. They CC can also be used to isolate the corresponding genomic sequences CC from crop plants, to determine the contribution of the SSS gene to CC of starch produced by the plant. Transgenic plants (sep. maize) CC can be used to produce hybid plants which have higher rates of CC starch synthesis at temperatures above the normal optimum.

SS sequence 2992 BP; 758 A; 655 C; 801 G; 776 T;
    Query Match
Best Local Sin
Matches 72;
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Matches 109
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06-DEC-1995; GB-024938.

(ZENE) ZENECA LTD.

Keeling PL, Knight ME;

WPI; 97-319782/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chesity-related conditions to increase or decrease the activity of adipocyte expressed genes. The DNA or protein can be used as drugs for treating obesity-related conditions to increase or decrease the activity of adipocyte expressed genes, e.g. FREACII can be used as a drug that blocks the cis elements of adipose expressed genes to inhibit gene expression; antisense constructs of Freacil can be used to down regulate expression. The FREACI1 protein can also be used for high throughput screening for substances that affect the activity of FREACI1, such as inhibitors, antagonists, or agonists. Conditions which can be treated include obesity, non-insulin dependent diabetes mellitus, cardiovascular diseases, catabolic conditions, anorexia, bulimia.

Sequence 2106 BP; 419 A; 757 C; 602 G; 328 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-SEP-1997 (first entry)
Soluble starch synthase cDNA clone SSS10.52.
Soluble starch synthase; SSS10.52; transgenic plant; cereal;
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T67285;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays inbred line W64A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109;
                      Similarity
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      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                      6.3%;
57.6%;
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                    Score 40.2;
Pred. No. 0
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Pred. No. 0.011;
      Mismatches
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                      DB 1;
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                                       Length 2992;
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Best Local Sim
Matches 72;
                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecule, used to produce transgenic plants - comprises nucleotide sequence encoding polypeptide having soluble starch synthase activity, where polypeptide is encoded by maize gene Claim 1; Column 25-28; 29pp; English.

The present sequence represents an isolated nucleic acid molecule which has been isolated and comprises a nucleotide sequence encoding a polypeptide having soluble starch synthase (SSS) activity, where the polypeptide is encoded by a maize gene. The isolated nucleic acid molecule can be used to produce transgenic plants with altered starch production. The transgenic plants produced using the nucleic acid molecule have an enhanced ability to produce structurally-altered starch sequence 2990 BP; 758 A; 655 C; 801 G; 776 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1995; 572951.
15-DEC-1995; US-572951.
21-UUN-1994; US-263921.
29-NOV-1994; US-346602.
                   Neuronal nicotinic acetylcholine receptor beta-4 subunit DNA 
Neuronal nicotinic acetylcholine receptor; nAChR; neurotransr 
ligand-gated receptor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ZENE ) ZENECA LTD.
Guan H, Keeling PL, Knight ME;
WPI; 98-582626/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zea mays soluble starch synthase gene SSS1052 and SSS64. Zea mays; US yellow-dent corn line; maize; soluble starc SSS; glycogen biosynthetic pathway; branching enzyme; ss
           Homo sapiens.
                                                              09-APR-1997 (first entry)
                                                                           T48241 standard; DNA; 1915
T48241;
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US5824790-A.
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                                   neurotransmitter;
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Location/Qualifiers

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RESULT
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Best Local
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29-OCT-1998; J01783.
17-APR-1998; JP-310027.
24-OCT-1997; JP-116570.
18-APR-1997; JP-116570.
18-APR-1997; JP-116570.
Transcriptional regulator gene family containing bromodomain - may be expressed in testis tissue and is useful for treatment of cancer and other proliferative disorders

Claim 2; Page 125-137; 187pp; Japanese.

This sequence encodes the human BA21-beta protein, a member of a family of transcriptional regulator genes containing a bromodomain (BAZ, Bromodomain with Atypical Zinc finger) which are expressed specifically in testis tissue and also in certain tumour lines. Transgenic cells may be used for the preparation of the BAZ1-alpha, BAZ1-beta, BAZ2-alpha and BAZ2-beta proteins. These proteins can be used in the treatment of cancer and other proliferative disorders, and in screening of compounds for their binding ability to the expression products (e.g. for use as drugs by modulation of transcriptional regulation).

Sequence 5561 BP; 1665 A; 1261 C; 1471 G; 1164 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding nicotinic acetylcholine receptor sub-units used in screening to determine the effect of drugs on the receptor Disclosure; Page 83-85; 108pp; English.

A DNA sequence (T48241) codes for the beta-4 subunit (W09027) of the human neuronal nicotinic acetylcholine receptor (nAchR). Host cells, esp. mammalian cells or amphibian occytes, carrying beta-4 nucleic acids, opt. in combination with other alpha and/or beta subunit nucleic acids (see also T48232-40), express recombinant nAchR subunits useful for identifying cpds. that modulate the activity of human nAchRs.

Sequence 1915 BP; 374 A; 631 C; 505 G; 405 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transcriptional regulator; transcription; BAZ1-alpha; bromodomain; BAZ; atypical zinc finger; testis; human; tumour; BAZ1-beta; BAZ2-alpha; dru BAZ2-beta; treatment; cancer; proliferative disorder; screening; ds.
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07-JUN-1995; US-484722.
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RESULT 1
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the expressed in testis tissue and is useful for treatment of cancer
and other proliferative disorders
Claim 2; Page 145-157; 187pp; Japanese.
This sequence encodes the human BAZ1-beta protein, a member of a
cfamily of transcriptional regulator genes containing a bromodomain (BAZ,
Bromodomain with Atypical Zinc finger) which are expressed specifically
in testis tissue and also in certain tumour lines. Transgenic cells may
be used for the preparation of the BAZ1-alpha, BAZ1-beta, BAZ2-alpha and
BAZ2-beta proteins. These proteins can be used in the treatment of cancer
and other proliferative disorders, and in screening of compounds for
their binding ability to the expression products (e.g. for use as drugs
by modulation of transcriptional regulation).
Sequence 5573 BP; 1668 A; 1267 C; 1472 G; 1166 T;
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Best Local Similarity
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Transcriptional regulator; transcription; BAZ1-alpha;
Atypical zinc finger; testis; human; tumour; BAZ1-beta
BAZ2-beta; treatment; cancer; proliferative disorder;
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24-OCT-1997; JP-310027.
18-APR-1997; JP-116570.
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29-OCT-1998.
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                                                                                                                TCGGGTCCCGGCGGCCGGCAGTCACGACTCCTCCTCAGCAGCACCGGAGG
                                                                                                                                                                                                       CGCCACATAGCTCCCGCCAAGTCCTCGGTGCCCCTTGCCATTTTCCAGCCGCGCTCCCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64;
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Pred. No. 0.51
0; Mismatches
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Q84888 standard; cDNA Q84888; 26-OCT-1995 (first e

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cytoplsmic tyrosine kinase

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29-MAR-1994; JP-058553.

(ASAH) ASAHI KASEI KOGYO KK.

Sakano S;

WPI; 95-106842/14.

P-PSDB; R71129-33.
                                                                                                                                                                                                                                                                                        cytoplasmic tyrosine kinase and antibody recognising it for screening chemical substances for tyrosine kinase inhibitory or activating activity for use as cancer therapy claim 7; Page 49-50; S8pp; English.

This DNA encodes a cytoplasmic tyrosine kinase which has enhanced expression in connection with blood cell line. The DNA sequences and isolated from the human UT-7 blood cell line. The DNA sequences and antibodies raised against the enzyme, are usful for screening agents for inhibiting or activating activity on the tyrosine kinase, for use as anticancer agents.

Sequence 1942 BP; 365 A; 615 C; 651 G; 311 T;
                                                                                                                                        1791
                                                                  1731 TCAGGGCTCCTGGCTTCGGGGCGAGGTGGAGCCGTCGGCGTCCTGCCCTGAGACGGAGGC 1672
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/product= cytoplasmic_tyrosine_kinase
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Search completed: September 18, 1999, 00:35:22 Job time: 19082 sec

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## ALIGNMENTS

TITLE 641 bp mRNA PRI 16-DEC-1998 Homo sapiens alpha 7 neuronal nicotinic receptor mRNA sequence. AF029838 93757793 AF029838.1 GI:3757793 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 641)

Gault, J., Robinson, M., Berger, R., Drebing, C., Logel, J., Hopkins, J., Moore, T., Jacobs, S., Meriwether, J., Choi, M.J., Kim, E.J., Walton, K., Buiting, K., Davis, A., Breese, C., Freedman, R. and Leonard, S. Genomic organization and partial duplication of the human alpha7 neuronal infootinic acetylcholine receptor gene genomics 52 (2), 173-185 (1998) 2 (bases 1 to 641)
Leonard,S., Gault,J., Logel,J., Drebing,C., Robinson,M., Berger,R.,
Breese,C., Davis,A., Hopkins,J. and Freedman,R.
Direct Submission

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leonard, S., Gault, J., Logel, J., Breese, C., Davis, A., Hopkins, J. Direct Submission
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 689)
Gault, J., Robinson, M., Berger, R., Drebing, C., Logel,
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/note-"alpha 7 neuronal nicotinic
alternative splicing"
a 210 c 196 g 141 t
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/db_xref="taxon:9606"
/chromosome="15"
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Pred. No. 2.5e
0; Mismatches
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2.5e-117;
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                                                              al Similarity
219; Conserv
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read cpg2e10.ft11d.
z58126
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                                                   CCTGGTGGTCGCGGNCATGACAGCGGCTCGGGACAGGCTCCTTTTCCGCGCCCCCTCCCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross,S.H., Charlton,J.A., Nan,X. and Bird,A.P.
Purification of CpG islands using a methylated DNA binding
Nat. Genet. 6 (3), 236-244 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-OCT-1995) The Sanger Centre, Hinxton, Cambridgeshire, CB10 1RQ, England. E-mail contact: humquery@sanger.ac.uk
2 (bases 1 to 291)
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MacDonald, M., Huckle, E., Wilkinson, P. and Micklem, G.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                              http://www.hgmp.mrc.ac.uk/ for details
or contact: biohelp@hgmp.mrc.ac.uk,
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vector: pGEM-5Zf(-)
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Primates; Catarrhini; Hominidae; Homo.
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/clone_lib="CGI-1"
/clone="2e10"
a 95 c 103 g
                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/sex="male"
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                                                                                                                                                                                                                                                                                                                                   /dev_stage="adult"
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Pred. No. 3.5e-45;
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Best Local Similarity
Matches 243; Conserv
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                                                                                                                                                                                                  CTATCTTCCAGGAGAACCAGGAGCCACAGCCGCGCGCCCCACCCGCAACATTAAGA
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                                                                                                                             TGA 47760
                                                                                                                                                                                    CTATCTTCCACAAGAACCAGGAGCCGCCGCCGCAGCTCACGCTCCACTGCAACATCACGG
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HS2G7F 298
H.sapiens CpG isl
read cpg2g7.fla.
Z60646
g1032750
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On Jan 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 (bases 1 to 137699)
Waterston, R.H.
Direct Submission
Submitted (15-JAN-1999) Genome
University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (08-SEP-1998) Genome
University School of Medicine,
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Waterston, R.H.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 137699)
Waterston, R. H.
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/db_xref="taxon:9606"
/clone="DJ1129D05"
/ 30670 c 32412 g 3770
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Pred. No. 1.2e-39;
0; Mismatches 59
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                                         Msel fragment,
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                                                                                                                                                                                                                                                                                                                                          AGGTGAGGGAAGATGTCCATGTCAGGGTTCAAGGCCAAACCGAAGTTACTGGCCT 239
                                                                                                                                                                                                                                                                                                                                                                                                                       ACGAGGGTCACGGCGGGGGGGGGGGGGGGGGGGGGCCCCGCCT 123
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                                                                                                                                                                              mRNA, al
AF036903
g3757807
                                                          Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Ver
Eutheria; Primates; Catarrhini; Hominidae;

1 (bases 1 to 1712)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-OCT-1995) The Sanger Centre, Hinxton, Cambridgeshire, CB10 1RO, England. E-mail contact: humquery@sanger.ac.uk 2 (bases 1 to 298)
Cross,S.H., Charlton,J.A., Nan,X. and Bird,A.P.
Purification of CpG islands using a methylated DNA binding column Nat. Genet. 6 (3), 236-244 (1994)
Gault, J., Robinson, M., Berger, R., Drebing, C., Logel, J., Hopkins, J., Moore, T., Jacobs, S., Meriwether, J., Choi, M.J., Kim, E.J., Walton, K., Buiting, K., Davis, A., Breese, C., Freedman, R. and Leonard, S. Genomic organization and partial duplication of the human alpha?
                                                                                                                                                                                                            AF036903 1712 bp
Homo sapiens alpha-7
mRNA, alternatively s
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MacDonald,M., Huckle,E., Wilkinson,P. and Micklem
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Primates; Catarrhini; Hominidae; Homo.
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/clone_lib="CGI-1"
/clone="297"
a 99 c 102 g
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/db_xref="taxon:9606"
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Pred. No. 2.3e-39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192;
Submitted (14 MAY-1999) Genome Sequencing Center, Washing University School of Medicine, 4444 Forest Park Parkway, MO 63108, USA
On Jun 5, 1999 this sequence version replaced gi:4827309.
* NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                                                                     Pieces.
AC007562
                                                                                                                        2 (bases 1 to 192439)
Waterston, R.H.
                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Primates; Catarrhini; Hominida
1 (bases 1 to 192439)
Waterston, R. H.
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                                                                                                           Direct Submission
                                                                                                                                                        The sequence of Homo sapiens Unpublished
                                                                                                                                                                                                                                                               Homo sapiens
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Leonard, S., Gault, J., Logel, J., Drebing, C., F
Breese, C., Davis, A., Hopkins, J. and Freedman,
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ilarity 100.0%;
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/db_xref="taxon:9606"
/db_xref="dbEST:W52861"
/db_xref="dbEST:AA037389"
/chromosome="15"
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alternatively spliced"
a 489 c 457 g 410 t
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Reseach Genetics/IMAGE Consortium, LLNL"
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NH0497C14, WORKING DRAFT SEQUENCE, 4 unordered
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Pred. No. le-38;
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                                                                      Sequencing Center, Washington 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                               Hominidae;
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Denver, CO 80262, USA
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Direct Submission
Submitted (09-JAN-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                             2 (bases 1 to 178307) Waterston, R.H.
                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 178307)
Waterston,R.H.
                                                                                              Unpublished
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                                                                                                              he sequence of Homo sapiens
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3: gap of unknown length
5: contig of 14652 bp in length
5: gap of unknown length
0: contig of 78057 bp in length
8: gap of unknown length
9: contig of 94341 bp in length.
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                                      TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCTGGTGGCCGGGCCATGACAGCGGCTCCGGGACTGGCTTTTTCCGCGCCCCCTCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                TTA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTATCTTCCACAAGAACCAGGAGCCGCTGCCGCAGCTCATGCTCCACTGCAACATCACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTATCTTCCAGGAGAACCAGGAGCCACAGCCGCGCGCTCACGCCCCACCGCAACATTAAGA
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                                                                                                                                                                                                                                   precursor
AF037646
g3757808
Gault,J., Robinson,M., Berger,R., Drebing,C., Logel,J., Hopkins, Moore,T., Jacobs,S., Meriwether,J., Choi,M.J., Kim,E.J., Walton,I Buiting,K., Davis,A., Breese,C., Freedman,R. and Leonard,S. Genomic organization and partial duplication of the human alpha7 neuronal nicotinic acetylcholine receptor gene (CHRNA7) Genomics 52 (2), 173-185 (1998)
                                                                                                                                                                                                                                                                                     AF037646 1836 bp
Homo sapiens alpha-7
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                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 o 63108, USA

Mar 13, 1999 this sequence version replaced gi:4138780.

NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    be preserved
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4 11181: gap of unknown length
2 57066: contig of 45885 bp in length
7 57084: gap of unknown length
5 178307: contig of 121223 bp in length
Location/Qualifiers
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38822 c 39355 g
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                       acetylcholine receptor
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                                                                      Walton, K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
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                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                           ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACCTGCCTCCAGGCATATTCAAGAGTTCCTGCTACATCG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGCGCTTTGACGCCACATTCCACACTAACGTGTTGGTGAATTCTTCTGGGCATTGCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Human a7 nicotinic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (03-DEC-1997) Psychiatry, University of Colorado Health Sciences Center, 4200 E. 9th Ave., Denver, CO 80262, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                               Cloning and sequence of the human
                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                              nicotinic acetylcholine receptor alpha 7 subunit; transmembrane
                                                                                                                                                                                                                Doveette-Stamm,L., Monteggia,L.M.,
Lee,J., Tian,J. and Giordano,T.
                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                            Homo sapiens (library: Clontech HL1065b; ATCC 37433) fetus brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMA7NAR
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                                                                                                                                          Dev. Res. (1993) In press
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                              to mRNA.
             /organism="Homo sapiens"
/db_xref="taxon:9606"
/dev_stage="fetus"
/tissue_type="brain"
/tissue_lib="Clontech HL1065b; A'
a 463 c 440 g 342 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="alpha-7 neuronal nicotinic acetylcholine
precursor; intron included in 5' region"
a 503 c 469 g 481 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="dbEST:W03952"
/db_xref="dbEST:N73891"
/chromosome="15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S., Gault,J., Logel,J., Drebing,C., Robinson,M.,
, Davis,A., Hopkins,J. and Freedman,R.
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/clone_11b="Soares fetal liver spleen library,
Genetics/IMAGE Consortium, LLNL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="unprocessed mRNA with intron"
<1. .1836</pre>
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1. .1836
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                                                                                                                                                                                             nicotinic acetylcholine
                                ATCC
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Best Local Sim
Matches 111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (04-FEB-1993) M. Katz, Univ of Pennsylvania
Medicine, Dept of Neuroscience, 36th & Hamilton Walk,
Stemmler Hall, Philadelphia, PA 19104, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peng, X., Katz, M., Gerzanich, V., Anand, R. and Lindstrom, J. Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from the SH-SSY cell line and determination of pharmacological properties of native receptors and functional 7 homomers expressed in Xenopus occytes

Mol. Pharmacol. 45 (3), 546-554 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2087)
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                                                                                                                                 /db_xref="GI:496607"
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VQHCKLKFGSWSYGGWSLDLONGADISGYINGEWDLVGIFOKRSERPYEGCKEYF
VQHCKLKFGSWSYGGWSLDLONGADISGYINGEWDLVGIFOKRSERPYEGCKEYF
VQHCKLKFGSWSYGGWSLDLONGADISGYINGEWDLVGIFOKRSERPYEGCKEYF
                     DESEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFVEAVSKDFA" 176. ,1609
                                                               LLVAEIMPATSDSVPLIAQYFASTMIIVGLSVVVTVIVLQYHHHDPDGGKMPKWTRVI
LLNWCAWFLRMKRPGEDKVRPACQHKQRRCSLASVEMSAVGPPPASNGNLLYIGFRGL
DGVHCVPTPDSGVVCGRMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:496606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="brain"
/cell_type="neuroblastoma"
/cell_line="SHSY-5Y"
                                                                                                                                                                                                                                                                                                                                                /product="neuronal
alpha-7 subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="neuronal nicotinic acetylocholine receptor
alpha-7_subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                    'protein_id="CAA49778.1"
'db_xref="PID:g496607"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'clone-"SHSY3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone_lib="lambda zap II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2087 bp
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95.7%;
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Pred. No. 1.7e-17;
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RESULT 12
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Cloning and sequence of full-length cDNAs encoding the human neuronal nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and expression of seven nAChR subunits in the human neuroblastoma cell line SH-SY5Y and/or IMR-32

FEBS Lett. 400 (3), 309-314 (1997)
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Y08420.1
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H.sapiens mRNA for nicotinic acetylcholine receptor alpha7 subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (27-SEP-1996) P.J. Groot Kormelink, Janssen Research
Foundation, Exp. Mol. Biol. Dept., Turnhoutseweg 30, B-2340 Beerse,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Revised by author 22-JAN-1998
On Jan 25, 1998 this sequence version replaced gi:1702915.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97162233
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/gene="nAChRA7"
67. .1506
                                                                                                                                   /protein_id="CAA69697.1"
/protein_id="CAA69697.1"
/db_xref="piD:e1246208"
/db_xref="piD:e1246208"
/db_xref="piD:e12808624"
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/translation="MRCSPGGVWLALAASLLHVSLQGBFQRKLYKELYKNYNPLERPV
/translation="MRCSPGGVWLALAASLLHVSLQGBFQRKLYKEYPGVKTVRF
PDGQIRKPDILLYNSAADERFDATFHTNYLVNSSGHCVLPFGTFKSSCYIDVRWFPFFD
PDGQIRKPDILLYNSAADERFDATFHTNYLVNSSGHCVLPFKSSCYIDVRWFPFFD
VQHCKLKFGSWSYGGWSLDLQWGAADISGYIRMGEWDLVGIPGKRSERFFECKEFFY
POTFTVMRRRTLYYGLNLLIFCVLISALALLVFLLPADSGEKISLGITVTLSLTVFN
LLVAEIMPATSDSVPLIAQYFASTMIIVGLSVVVTVIVLQYHHLDPDGGKMPKWTRVI
                                                                                                                                                                                                                                                                                                                                                                                  /product="nicotinic acetylcholine receptor alpha7 subunit
precursor"
                                                                     DESEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFVEAVSKDFA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_type="neuroblastoma"
/cell_line="IMR-32"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:2808623
                                                                                            LLNWCAWFLRMKRPGEDKVRPACQHKQRRCSLASVEMSAVAPPPASNGNLLYIGFRGL
DGVHCVPTPDSGVVCGRMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene="nAChRA7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ′gene="nAChRA7"
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95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  line="SH-SY5Y"
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Pred. No. 1.7e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Elliott, K.J., Ellis, S.B., Berckhan, K.J., Urrutia, A., Chavez. Noriega, L.E., Johnson, E.C., Velicelebi, G. and Harpold, M.M. Comparative structure of human neuronal alpha 2-alpha 7 and beta 2-beta 4 nicotinic acetylcholine receptor subunits and functional expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSU62436 1876 bp mRNA PRI 11-JAN-1997 Human nicotinic acetylcholine receptor alpha7 subunit precursor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (28-JUN-1996) Kathryn J. Elliott, SIBIA Neurosciences, Inc., 505 Coast Blvd. So., La Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 1876)
Elliott, K.J.
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Elliott, K.J., Ellis, S.B.,
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1.1876
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DGVHCVPTPDSGVVCGRMACSPTHDEHLLHGGQPPEGDPDLAKILEEVRYIANRFRCQ
                                                                                                         DVTFTVTMRRRTLYYGLNLLIPCVLISALALLVFLLPADSGEKISLGITVLLSLTVFM
LLVAEIMPATSDSVPLIAQYFASTMIIVGLSVVVTVIVLQYHHHDPDGGKMPKWTRVI
                                                                                                                                                                                                                                                                                              precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="nAChRA7"
451 c 42
                                                                                                                                                     VQHCKLKFGSWSYGGWSLDLQMQEADISGYIPNGEWDLVGIPGKRSERFYECCKEPYP
                                                                                                                                                                       PDGQIWKPDILLYNSADERFDATFHTNVLVNSSGHCQYLPPGIFKSSCYIDVRWFPFD
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                                            DESEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFVEAVSKDFA"
                                                                                                                                                                                                                                                                                                                           /product="nicotinic acetylcholine receptor alpha7 subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="SIBIA lambda gtll library #3 (M. Williams)"
/cell_line="IMR32"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                 codon_start=1/
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95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  _type="neuroblastoma"
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Pred. No. 1.7e-17;
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receptor alpha7 subunit"
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Best Local Similarity
Matches 111; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Montpellier, 34094 Cedex, 5,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (29-JUN-1993) BICE CHINI, CCIPE, Rue de la Cardonille, Montpellier, 34094 Cedex, 5, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7-nicotinic receptor subunit gene (CHRNA7)
Genomics 19 (2), 379-381 (1994)
94245214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1555)
Chini,B., Raimond,E., Elgoyhen,A.B., Moralli,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Vertebrata; Primates; Catarrhini; Hominidae; Homo.
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H.sapiens CHRNA7 mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heinemann, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 1555)
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                                                                                                                                                                                                                                                                                                                          /product="cholinergic receptor,
polypeptide 7"
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1 553 c
                                                                                                                                                                                                               polypeptide 7"
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                                                                                                                                                                                                                           /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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95.7%;
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Pred. No. 1.7e-17;
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1 (bases 1 to 1977)

Logel, J., Drebing, C., Barnhart, M., Antle, C. and Leonard, S.

Nucleotide Sequence and Transcript Size of the Alpha-7 Neuronal

Nicotinic Acetylcholine Receptor in Human Postmortem Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (13-NOV-1995) Sherry Leonard, University of Colorado Health Sciences Center, C-268-71 Pharmacology, 4200 E. Ninth Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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LLVAEIMPATSDSVPLIAQYFASTMI VGLSVFVLIVIQYHHIDDGGKMPKWPRVL
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                                                                                                                                                                                                                                                                                                                                                            /product="alpha 7 receptor"
                                                                                       DESEAVCSEWKFAACVVDRLCLMAFSVFTIICTIGILMS!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
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/db_xref="taxon:9606"
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